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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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Match Length DB
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Gapop 10.0 , Gapext 0.5
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   GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd
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pir3:*
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S40314
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Ig kappa chain v

Ig kappa chain v

Kappa chain v

Ig kappa chain v
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75.4	75.7	76.0 75.7	76.2 76.1 76.0	76.2 76.2	76.4 76.2
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830521 K1HUBN	\$46376 K1HUKA	\$40353 \$36262 T69017	S31981 PC2397 I39154	KIHUBI KIHURY YAUHIX	S52793 JL0139
ig kappa chain V r Ig kappa chain V r	kappa c	chain 1 a chain 1 envelo	Ig kappa chain - h anti-tetanus toxin Ig kappa chain (BR		Ig kappa chain V r Ig kappa chain V r

ALIGNMENTS

RESULT 1

RESULT 2 S46370 1G kappa chain V-J region (T23-9) - human (fragment) C;Species: Homo sapiens (man) C;Date: 27-Jan-1995 #sequence revision 01-Sep-1995 #text_change 21-Jan-2000 C;Accession: S46370; S38644 R;Bensimon, C; Chastagner, P.; Zouali, M. EMBO J. 13, 2951-2962, 1994	Oy 1 DIOMIGSPASISASVODRVITTCWYLOKBOKSPQ-LIY	Query Match 80.5%; Score 335; DB 1; Length 108; Best Local Similarity 67.3%; Pred. No. 4e-26; Matches 72; Conservative 5; Mismatches 2; Indels 28; Gaps 4;	A; Gene: GDB:18KV1 A; Cross-references: GDB:136264 A; Map position: 2p12-2p12 C; Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds; in some cases, such as IgA and IgW, the subunits associate into la C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F;16-90/Domain: immunoglobulin homology < IMM> F;23-88/Disulfide bonds: #status predicted	A,Title: Chemical modification of the carboxyl groups of protein substrates enhances the A,Reference number: S02572; MUID:88005152; PMID:3118831 A,Contents: annotation C;Comment: This is a Bence Jones protein. C;Genetics:	C;Species: Homo Baptens (man) C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 21-Jan-2000 C;Accession: A01868; S03574 R;Watenabe, S.; Hilschmann, N. Hoppe-Seyler's Z. Physiol. Chem. 351, 1291-1295, 1970 A;Title: The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subg A;Reference number: A01868; MUID:71032830; PMID:4097974	II RADIO Chain V-I region (Hau) - human

Gaps

4;

60

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Ig lambda chain V region (clone alpha-TNF-A1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36269
C;Accession: S36269
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
A;Cross-references: EMBL:Z18838; NID:g33422; PIDN:CAA79290.1; PID:g939915 (?Superfamily: immunoglobulin V region; immunoglobulin homology C:Keywords: heterotetramer; immunoglobulin C:Keywords: heterotetramer; immunoglobulin F:16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                         EMBO J. 12, 725-734, 1993
A;Title: Human anti-eelf antibodies with high specificity from phage display libraries.
A;Reference number: 336256; MUID:93178448; PMID:7679990
A;Accession: S36269
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A;Title: Expressed human immunoglobulin chi genes and their hypermutation A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40331
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C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: $40331
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;26-100/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-120 <BEN>
                                                                                                           A; Residues: 1-107 <GRI>
                                                                                                                                      A; Molecule type: mRNA
                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown
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A; Residues: 1-123 < KLE>
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A;Reference number: S46369; MUID:94313975; PMID:8039491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 RFSGSGSGTDFSFTISSLQPEDFATYYC-----FGQGTKLEIK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 DIOMTOSPSSISASVGDRVTITCRASOSISSYLWWYQOKPGKAPKLLIYAASSLOSGVPS
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Pred. No. 5.7e-26;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
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C;Superfamily: immunoglobulin Vegion; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;33-107/Domain: immunoglobulin homology <IMY>
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A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: S40312, MUID:94080891, PMID:8258341
A;Accession: S40367
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C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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                       22 DIOMTOSPSSISASVGDRVTITCRASHVISNHLVWFQQKPGKAPKSLIYAASSLQSGVPS
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                                                                          1 DIOMTOSPASLSASVGDRVTITC-----WYLQKPGKSPQ-LIY-----GVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.3%;
                                                                                                                                                              79.3%; Score 330; DB 2; 66.4%; Pred. No. 1.5e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 330; DB 2;
Pred. No. 1.4e-25;
6; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 330; DB 2;
Pred. No. 1.2e-25;
                                                                                                                                      Mismatches
                                                                                                                                                                                      Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 28;
                                                                                                                                      Indels
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C;Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000 C;Accession: S46371; S38645 R;Bensimon, C:;Chastagner, P:; Zouali, M. EMBO J. 13, 251-2962, 1994 A;Pitle: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rea A;Pitle: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rea A;Reference number: S46374 MUID:94313975; PMID:8039491 A;Refeucle type: mRNA A;Residues: 1-117 essNA A;Residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 DIOMIQSPSTLSASVGDRVTITCRASRSISTWLAWYQQKPGKAPKLLIYKASTLESGVPS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1g kappa chain V-J region - human
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cibacesion: 540313
Riklein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      If kappa chain V-J region - human C; Species: Homo sapiens (man) C; Accession: S40333 Species: Jacks-221, 1993 Bur. J. Immunol. 23, 3248-321, 1993 A; Title: Expressed human immunoglobulin chi genes and their hypermutation. A; Reference number: S40333 S40313 MUID: 94080891; PMID: 8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: EMBL:X72423; NID:g441314; PIDN:CAA51091.1; PID:g441315 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;32-106/Domain: immunoglobulin homology <!WM->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIOMIOSPASISASVGDRVTITC-----GVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,CTOSSTORES. Efferences: EMBL:Z27172; NID:g415959; PIDN:CAA81696.1; PID:g415960
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
P;23-97/Domain: immunoglobulin homology <INM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFSGSGGTEFILTISSLOPDDFATYYCQQYNSYFPPYTFGQGTKLEIK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 RESGSGSGTDFSFTISSLOPEDFATYYC-----FGQGTKLEIK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 RFSGSGSGTEFTLTISSLQPEDFATYYCLQYNGYPRTFGQGTKVEIK 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 78.4%; Score 326; DB 2; Length 117 Best Local Similarity 64.2%; Pred. No. 3.3e-25; Aatches 70; Conservative 7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 326; DB 2; Length 12
Pred. No. 3.5e-25;
7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Status: preliminary, translation not shown A,Molecule type: mRNA A,Residues: 1-125 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: $40313
A; Status: pueliminary; translation not shown
A; Molecule type: mRNA
A; Residues: 1-123 <KLE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.4%;
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Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89
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B49047
Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-IA) - human (fragm C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C; Jaccession: B49047
R; Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Ext. J. Immunol. 22, 2231-2236, 1992
A; Vittle: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A; Reference number: A49047; MUID: 92387224; PMID: 1516616
A; Residues: 1-108 acid
A; Residues: I-108 acid
A; Residue
                                                                                                                                                                                                                                                                                         RESULT 7
S52789
IG kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Deret, S;Rocca, A.; Khamlichi chain V region gene usage restriction and peculiarities in myeloma-A;Reference number: S52789
A;Reference number: S52789
A;Residus: preliminary
A;Molecule type: mRNA
A;Residus: Preliminary
A;Molecule type: mRNA
A;Residus: 1-129 <ROC>
A;Cross-references: EMBL:X85995; NID:9758588; FIDN:CAA59987.1; PID:9758589
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIQMIQSPSSLSASVGDRVIIITGRASQSISSYLNWYQQKPGKAPKILIYAASSLQSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 DIQMIQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIHAASSLETGVPS
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                                                                                                                            S KFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSYPYTFGQGTKLEIK 128
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                                                      -----FGOGTKLEIK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 330; DB 2; Length 129;
Pred. No. 1.5e-25;
5; Mismatches 4; Indels
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                                                      42 RFSGSGSGTDFSFTISSLQPEDFATYYC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 65.4%;
Matches 70; Conservative
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S46371
S kappa chain V-J region (T2
C,Species: Homo gapiens (man)
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A)Complexerences: GDB:136264
A; Map position: 2pp2-2pp12
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka C; Complex: An immunoglobulin heterotetramer subunit sassociate into l hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 16-90/Domain: immunoglobulin homology < IMM>
F; 16-90/Domain: immunoglobulin homology < IMM>
F; 23-88/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 24-Apr.1984 #sequence_revision 24-Apr.1984 #text_change 21-Jan-2000
C;Date: 24-Apr.1984 #sequence_revision 24-Apr.1984 #text_change 21-Jan-2000
C;Accession: A01871; F3069
R;Capra, J; Klapper, D.G.
Scand, J. Immunol. 5, 677-684, 1976
Scand, J. Immunol. 5, 677-684, 1976
A;Title: Complete amino acid sequence of the variable domains of two human IgM anti-gam A;Reference number: A01871; MUID:77038198; PMID:824717
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A; Residuas: 1-108 cdps
A; Residuas: 1-108 cdps
A; Rocaluas: 1-108 cdps
A; Note: the second and third hypervariable regions of this chain are identical with tho
A; Note: the second and third hypervariable regions of this character, J.; Carson, D.; Sol
R; Goni, P.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sol
A; Title: Structural and idiotypic characterization of the L chains of human IgM autoant
A; Reference number: A30601; MUID:89215279; PMID:2496160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Accession: F30609
A,Molecule type: protein
A,Residues: 1-104 <GON>
C,Comment: This chain was isolated from an IgM with anti-gamma globulin activity.
C,Genetics:
A,Gene: GDB:IGKV1
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1 DIQMTQSPSTLSASVGDRVTITCRPSQAFGSWLAWYQQKPGKAPELLIYRVSSLQSGVPS 60
                                                                                                                                                                                                                                                                                   Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: S40315
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;File: Expressed human 1mmunoglobulin chi genes and their hypermutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 11125 cKLLs
A; Cross-references: EMBL:X72425; NID:g441318; PIDN:CAA51093.1; PID:g441319
C; Superfeanily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;31.105/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSHSAPPYTFGQGTRLEMK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 RESGSGSGTDFSFTISSLOPEDFATYYC-----FGQGTKLEIK
                                                                                                       61 RFSGSGSGTEFTLTISSLQPDDVATYYCQQANRYFGQGTKLEIK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                    RESGSGSGTDFSFTISSLOPEDFATYYC----FGQGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.5%; Score 322.5; DB 2, 62.0%; Pred. No. 7.8e-25; iive 8; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DВ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Accession: S40315
A,Status: preliminary; translation not shown
A,Molecule type: mRNA
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Best Local S
Matches 67
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19 kappa chain V-I region (Wil[2]) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 30-Un-1988 #sequence_revision 30-Jun-1988 #text_change 21-Jan-2000
C;Accession: A27585
R;Goni, F.; Chuba, J.; Buxbaum, J.; Frangione, B.
C;Accession: A27585
A; Immunol. 140, 551-57, 1988
A;Title: A double monoclonal IgG1-kappa and IgG2-kappa in a single myeloma patient. Vari
A;Reference number: A92620; MUID:88088871; PMID:3121749
A;Accession: A27585
A;Aocession: A27585
A;Aocession: A27585
A;Aocession: A27585
A;Aocession: A27585
A;Aocession: Immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 DIQLTQSPSFLSASVGDRVTITCRASQGISSYLAWYQQKPGKAPKLLIYAASTLQSGVPS 75
                                                                                                                                                                                                                                                                                                        41
                                                                                                                                                                                                                                                                                                                                                                  78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grappa chain V-J region - human
CjSpecies: Homo sapiens (man)
CjAccession: S40336
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 2348-3271, 1993
A;Ttlein. Expressed human immunoglobulin chi genes and their hypermutation.
A;Ttlein: Expressed human immunoglobulin chi genes and their hypermutation.
A;Ttlein: Expressed human immunoglobulin chi genes and their hypermutation.
A;Accession: S40336
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-124 <KLE>
                                                                                                                                                                                                                                                                                                                                              19 DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYKASSLESGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-124 «KLE»
A;Cross-references: EMBL:X72446; NID:g441360; PIDN:CAA51114.1; PID:g441361
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-105/Domain: immunoglobulin homology «IMM»
          A;Cross-references: BMBL:X72443; NID:g441354; PIDN:CAA51111.1; PID:g441355 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;34-108/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                        1 DIOMIOSPASISASVGDRVIITC------WYLQKPGKSPQ-LIY-----GVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESGSGSGTDFSFTISSLQPEDFATYYC-----FGQGTKLEIK 79
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                                                                                                                                                                        Score 324; DB 2; Length 125; Pred. No. 5.5e-25; Mismatches 2; Indels
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66.3%; Pred. No. 6.5e-25;
iive 7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 77.8%; Score 323.5; DB 2; Length Best Local Similarity 64.8%; Pred. No. 6.1e-25; Matches 70; Conservative 6; Mismatches 3; Indels
                                                                                                                                                                                                           Pred. No. 5.5e
8; Mismatches
                                                                                                                                                                                                    1 Similarity 64.5%;
69; Conservative
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Matches 69; Conservative
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Best Local Similarity
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Pred. No. 7.5e-25;	6; Mismatches
64.5%;	rative
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Best Local Similarity 64.5%;	Matches

1 DIOMICSPASLSASVGDRVIITCWYLOKPGKSPQ-LIYGVPS 41		
1 DIQMTQSPASLSASVGDRVTITCWYLQKPGKSPQ-LIYGVPS	41	9
	-	1 DIOMTQSPSSLSVSVGDRVTITCQASQNVNAYLNWYQQKPGLAPKLLIYGASTREAGVPS

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Search completed: January 13, 2004, 12:44:39 Job time : 5.72664 secs

homo sapien mus musculu mus musculu mus musculu homo sapien

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1 DIOMTOSPASISASVGDRVTITC-----WILOKPGKSPQ-LIY-----GVPS
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                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                 P01623
P04206
P18135
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P01649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 335; DB 1; Length 108; Pred. No. 4.6e-31; 5; Mismatches 2; Indels
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COMPLEMENTARITY-DETERMINING-1.
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subgroups.";

i subgroups.";

i hoppe-seyler's Z. Physiol. Chem. 351:1291-1295(1970).

-! MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV

-! MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV

-! MISCELLANEOUS: THE IS A BENCE-JONES PROTEIN.

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R SSPP, P800362; 1WTL.

GO; GO:0005926; C:extracellular; NAS.

GO; GO:0005929; F:antigen binding activity; NAS.

R O; GO:0006955; P:immune response; NAS.

R InterPro; IPR003106; Ig-like.

R InterPro; IPR003106; Ig-like.

R PÉAM; PR00047; 149; 1.

R PRMART; SN00406; IG_IKE; 1.

R PROSITE; PS50835; IG_LIKE; 1.

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11671 MW; 08D3A6160D8D0618 CRC64;
                                                                                                                                                                                                                                                                                21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region Hau.
                                                                                                                                                                                                                                                           108 AA
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                                                                            KV3L_HUMAN
KV5K_MOUSE
KV5L_MOUSE
KV5N_MOUSE
KV4C_HUMAN
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                                                                                                                                                                                                                                                           PRT;
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KV3E
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88
97
107
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108 AA;
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NCBI_TaxID=9606;
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P01600;
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SEQUENCE.
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                                                                                           January 13, 2004, 12:19:34 ; Search time 3.44978 Seconds (without alignments) 1076.912 Million cell updates/sec
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                                                                                                                                                                           1 DIQMTQSPASLSASVGDRVT.....QPEDFATYYCFGQGTKLEIK 79
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P01594
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              GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                               127863 seqs, 47026705 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KV1R HUMAN
KV1B HUMAN
KV1L HUMAN
KV1C HUMAN
KV1F HUMAN
KV1F HUMAN
KV1F HUMAN
KV1Y HUMAN
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Maximum Match 100%
Listing first 45 summaries
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                                                                    protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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KV1Y
KV1A
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seq length: 200000000
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Perfect score:
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Maximum DB
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                                                                                                                                                                                                                                                                                                                           Laure C.J., Watanabe S., Hilschmann N.;

"The primary structure of a monoclonal IgM-immunoglobulin

"The primary structure of a monoclonal IgM-immunoglobulin

(macroglobulin Gal.), I. The amino acid sequence of the L-chain of

Kappa-type, subgroup I.";

Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973)

HOSPELANEOUS: THE CREGION OF THIS CHAIN HAS THE INV (3) MARKER.

-I. MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
16 kappa chain V-I region Lay.
19 kappa chain V-I region Lay.
19 kappa chain V-I region Lay.
19 kappa chain Netazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
19 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
10 NCBI_TaxID=9606;
                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-I region Gal.
17 kappa chain V-I region Gal.
18 kappa chain (V-I region Gal.
18 kappa chain V-I region Gal.
19 kappa chain V-I region Gal.
10 kappa chain V-I region Gal.
10 kappa chain V-I region Gal.
10 kappa chain V-I region Gal.
11 kappa chain V-I region Gal.
12 kappa chain V-I region Gal.
13 kappa chain V-I region Gal.
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15 kappa chain Gal.
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18 kappa chain V-I region Gal.
19 kappa chain V-I region Gal.
10 kappa chain Chai
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Pred. No. 1.4e-29;
7; Mismatches 3; Indels
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COMPLEMENTARITY-DETERMINING-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A01867; KIHUGL.
HSSP; PO1607; IREI.
GO; GO:0003873; F:antigen binding activity; NAS.
GO; GO:0003833; F:antigen binding activity; NAS.
GO; GO:0006555; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-MGC.
InterPro; IPR003596; Ig-V.
                                                                             108 AA
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BY SIMILARITY
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PROSITE; PS50835; IG_LIKE; 1.
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KVIM HUMAN

ID KVIM HUMAN

AC 21-01L-1986

DT 21-01L-1986

DT 15-01L-1999

DE 19 kappa cha:
CS Homo sapiens

OC Bukaryota;
Mammalia; Full.

OX NCBI_TAXID=9
                                                                       KV1G HUMAN
P01599;
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A MELLINEST (JOSSIS).

B Scand, J. Immunol. 5.677-684 (1976).

B Scand, J. Immunol. 5.677-684 (1976).

C -- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS CHAIN ARE IDENTICAL WITH HOSE OF THE HUMAN POW V-III KAPPA CHAIN,

C -- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.

C -- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.

DR RSP PO1607, IREI.

R HSSP; PO1607, IREI.

R GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0005575; P:immune response; NAS.

BR InterPro; IPR003106; Ig_MHC.

DR InterPro; IPR003106; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIGMIDSPASISASVGDRVTITC-----WYLOKPGKSPQ-LIY-----GVPS
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-!- MISCELLANBOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-!- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN:
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Kohler H., Shimizu A., Paul C., Putnam F.W.;
"Macroglobulin structure: variable sequence of light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYNNWPPTFGGGTKVEVK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.4%; Score 322; DB 1; Length 108; 64.5%; Pred. No. 1.4e-29; ive 6; Mismatches 4; Indels 5
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
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21-UUL-1986 (Rel. 01, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
15 kappa chain V-I region OU.
Homo sapiens (Human)
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[1]
SEQUENCE.
MEDLINE=77038198; PubMed=824717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam, PF00047; ig; 1.
SMARY; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
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HSSP; P01607; 1REI.
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108 AA;
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P01606;
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us-09-990-586-79.rsp

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KV1R_HUMAN
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Palm W., Hilschmann N.;
Palm W., Hilschmann N.;
"The primary structure of a crystalline monoclonal immunoglobulin kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation and characterization of the tryptic peptides; the complete amino acid sequence of the protein; a contribution to the elucidation of the three-dimensional structure of antibodies, in particular their combining site.";
Hoppe-Seyler's Z. Physiol. Chem. 356;167-191(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMIZSPSSLSASVGBRVTITCRASZTISSYLBWYZZKPGKAPBLLIYAASBLHSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=76039968; PubMed=1182131;
Epp O., Lattman E.E., Schiffer M., Huber R., Falm W.;
"The molecular structure of a dimer composed of the variable portions
of the Bence-Jones protein REI refined at 2.0-A resolution.";
Biochemierry 14:4943-4952(1975).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -------WYLQKPGKSPQ-LIY------GVPS
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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PRAMEWORK-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 108;
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Pred. No. 1.4e-29;
3; Mismatches 2; Indels
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PIR; A91663; KIHURE.
PDB; 1RE1; 17-FEB-84.
PDB; 1AR2; 12-NOV-97.
PDB; 1BWW; 29-DEC-99.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR07110; Ig-like.
InterPro; IPR03066; Ig-MC.
InterPro; IPR03596; Ig-v.
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(Rel. 01, Last sequence update)
(Rel. 42, Last annotation update)
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21-JUL-1986 (Rel. 01, Last sec
15-SEP-2003 (Rel. 42, Last ant
11g kappa chain V-I region Rei.
Homo sapiens (Human).
                                                                                                                                                                                                                               Pfam; PF00047; ig; i. SWART; SM00406; iGv; i. PROSITE; PS50835; ig LIKE; i. Immunoglobulin V region.
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108 AA;
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P01607;
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"Amino acid sequence of the Fv region of a human monoclonal IgM
"Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3,4-pyruvylated
galactose in Klebsiella polysaccharides K30 and K33.";
Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
-!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTHEODY
AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIQMIQSPASLSASVGDRVIITC------WYLQKPGKSPQ-LIY-----GVPS
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Catarrhini, Hominidae, Homo.
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COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                              Bence-Jones protein; 3D-structure. FRAMEWORK-1.
                                                                                                                                                                                        COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                    COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.9%; Score 320; DB 1; Length 10 ilarity 65.1%; Pred. No. 2.3e-29; Conservative 6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 RFSGSGSGTDFSFTISSLQPEDFATYYC-----FGQGTKLBI
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-I region WEA.
Homo Sapiens (Human).
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR00306; Ig_MC.
InterPro; IPR003596; Ig_W.
Pfam; PF00047; ig; 1.
SWART; SW00406; IGV; 1.
Immunoglobulin V region; Bence-Jones prot.
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MEDLINE=83273707; PubMed=6410398;
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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P01610;
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GO:0003823; F:antigen binding activity; NAS.
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Rehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,

Schwager P., Steigemann W., Schraum H.J.;

Schwager P., Steigemann W., Schraum H.J.;

"The structure determination of the variable portion of the

Bence-Jones protein Au.";

Biophys. Struct. Mech. 1:139-146(1975).

INSCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY

MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V

REGION OF THE KAPPA CHAIN REI.

-:- MISCELLANEOUS: THE S REGION OF THIS CHAIN HAS THE INV (3) MARKER.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Homo sepiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"Rule of antibody structure. The primary structure of a monoclona;
immunoglobulin L-chain of the Kappa-type, subgroup I (Bence-Jones
                                                                                                                                                                            InterPro; InterPro; From State State
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 320; DB 1; Length 108; Pred. No. 2.3e-29; 8; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11840 MW; 9249B61F0945618C CRC64;
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                                                                               GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0066855; P:immune response; NAS.
InterPro; IPR00110; Ig-like.
InterPro; IPR003065; Ig_MHC.
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           WALDENSTROM'S MACROGLOBULINEMIA.
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Matches 68; Conservative
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484
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                                       PIR; A01876; K1HUWE
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AC POL1
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DIQMIQSPASISASVGDRVIIIC------WYLQKPGKSPQ-LIY-----GVPS 41
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Klobeck H.G., Combriato G., Zachau H.G.;
"Immunoglobulin genes of the Kappa light chain type from two human
lymphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 108;
                                                                                                                                                   PROSITE, PS50835; IG LIKE; 1.
Immunoglobulin V region; Bence-Jones protein; 3D-structure.
DOMAIN
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COMPLEMENTARITY-DETERMINING-3.
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Pred. No. 3.9e-29;
5; Mismatches 5; Indels
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13-AUG-1987 (Rel. 05, Last sequence update)
15-AUG-1987 (Rel. 38, Last annotation update)
1G kappa chain V-I region Walker precursor.
Homo sapiens (Human).
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GO, GO:0003823; F:antigen binding activ
GO, GO:006955; P:immune response; NAS.
InterPro; IPR007110; IQ-1ike.
InterPro; IPR003006; IG-NHC.
InterPro; IPR003596; IG-V.
Pfam; PF00047; IG; 1.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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ilarity 64.5%;
Conservative
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Homo sapiens (Human)
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       Query Match
Best Local Similarity
Matches 69; Conserv
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KV1F_HUMAN
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                                                                                                                                                                                     1 DIOMTOSPASLSASVGDRVTITC------WYLQKPGKSPQ-LIY-----GVPS
                                                                                                                                                     Gaps
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-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=73029807; PubMed=4563064; Baraikol H.U., Hilschmann N.; Leibold W., Barnikol H.U., Hilschmann Structure of a "Principle of antibody structure. The primary structure of a monoclonal kappa 1-type immunoglobulin L-chain (Bence Jones protein 81). 3. The complete amino acid sequence and the genetic significance of the variability principles for the mechanism of antibody formation.";
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                     28;
                 KAPPA CHAIN V-I REGION WALKER
                                                                                                                                                                                                                        RFSGSGSGTDFSFTISSLQPEDPATYYC-----FGQGTKLEIK 79
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FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                   Length 129;
                 IG KAPPA CHAIN V-I REGION WALK
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-3.
                                                       COMPLEMENTARITY-DETERMINING-2.
                                                                       COMPLEMENTARITY-DETERMINING-3. FRAMEWORK-4.
                                                                                                                                                    4; Indels
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                                                                                                               14069 MW; F941FA07D4AFC2F9 CRC64;
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005825; F:antigen binding activity; NAS.
GO; GO:0006955; F:immune response; NAS.
INCEPTO; IPRO07110; IG-1ike.
InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03596; Ig_V.
                                                                                                                                Score 318; DB 1;
Pred. No. 4.7e-29;
5; Mismatches 4;
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SM00406; IGY. 1.
;; PS50835; IG LIKE; 1.
globulin V region; Bence-Jones protein.
                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 kappa chain V-I region Bi.
Homo sapiens (Human).
                                                                                             BY SIMILARITY
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Immunoglobulin V
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P01595;
21-JUL-1986 (
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Local Sim.
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                                                                                                                                       1 DIOMTOSPSPLSASVGDSVTITCOASODIRNSLIMYQOKPGKAPKFLIYDAENLEIGVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochemistry 9:3188-3196(1970).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE.

MEDLINE-71064023; PubMed=5489770;
Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";
Biochemistry 9:3155-3161(1970).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDLINE=71064027; PubMed=4923144;
Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds.";
                                                                                                                                                                                                                 61 RFRGSGSGTDFALSISSLQPEDFATYYCQQYYNLPYTFGQGTKLBIK 107
                                                                                                                                                                                      42 RFSGSGSGTDFSFTISSLQPEDFATYYC-----FGQGTKLEIK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEMENTARITY-DETERMINING-1.
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Length 108;
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COMPLEMENTARITY-DETERMINING-3.
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                                              5; Indels
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11788 MW; 9CD294F2F4D88823 CRC64;
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GO: GO: 0003823; F: antigen binding activity; NAS.
GO: GO: 0006955; P: immine response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig-MC.
InterPro; IPR003506; Ig-MC.
  Score 317; DB 1;
Pred. No. 5e-29;
5; Mismatches 5
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21-JUL-1986 (Rel. 01, Last sequence update)
11-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-I region EU.
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Pred. No. 56
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                                                                                                1 DIOMIOSPASISASVGDRVTITC--
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; PS50835; IG LIKE; 1.
lobulin V region.
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    76.2%;
illarity 64.5%;
Conservative
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SMART; SM00406; IGV;
PROSITE; PS50835; IC
Immunoglobulin V reg
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Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;
[In] Franek F., Shugar D. (eds.);
[Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).
                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                             FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
    RFSGSGSGTDFSFTISSLQPEDFATYYC-----FGQGTKLEIK 79
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
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PIR; ASJONATION THEN TO A DENNE FOLIDIN.
HSSP; P80362; IWTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:000555; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003306; Ig-WHC.
InterPro; IPR003306; Ig-V.
Pfam; PF00047; ig; 1.
SWART; SW0406; IG-V.
PROSITE; PS0835; IG LIKE; 1.
Immunoqlobulin V region; Bence-Jones protein.
DOMAIN.
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                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
11 kappa chain V-I region Roy.
Home sapiens (Human)
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nes 68; Conservative
                                                                                                                                                      STANDARD;
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108 AA;
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RESULT 12 KVIK HUMAN ID KVIK HUMAN

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                                                                                                                                                                                                                                                                "Comparative structural studies on the light chains of human immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker.";
J. Biochem. 77.1277-1296(1975).
I. BIOCHEM. 77.1277-1296(1975).
II. MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
II. MISCELLANEOUS: THE IS A BENCE-JONES PROTEIN.
BIR, A01869; KIHUKA.
HISSP; P80362; MTL.
GO, GO:0005576; C:extracellular; NAS.
GO, GO:0005576; C:extracellular; NAS.
GO, GO:0005576; C:extracellular; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003506; Ig_WHC.
InterPro; IPR003506; Ig_WHC.
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Homo sapiens (Human).

Bykarycta: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butharia; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
PO1603;
21-UTL-1986 (Rel. 01, Created)
21-UTL-1986 (Rel. 01, Last Sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region Ka.
19 kappa chain N-I region Ka.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
Mol. Immunol. 23:73-78(1986).
PIR; A01678; KIHUBN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 RFSGSGSGTDFSFTISSLOPEDFATYYC-----FGQGTKLEIK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.5%; Score 314; DB 1; Length 108; 58.9%; Pred. No. 1.1e-28; ive 13; Mismatches 3; Indels ::
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COMPLEMENTARITY-DETERMINING-2.
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13-AUG-1987 (Rel. 05, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
11g kappa chain V-I region BAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on; Bence-Jones protein.
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BY SIMILARITY
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MEDLINE=86174817; PubMed=3083240;
                                                                                                                                                                                                                                  MEDLINE=76189985; PubMed=818073;
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SMART; SM00406; 1Gv; 1.
PROSITE; PS50835; 1G LIKE; 1.
Immunoglobulin V region; Beno
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108 AA;
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P04430;
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Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
Sconcon A., Stevens F.J., Schiffer M.;
"Comparison of crystal structures of two homologous proteins:
structural origin of altered domain interactions in immunoglobulin
light-chain dimers.";
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-i. Mol. abl. 147:185-193(1981).
-i. MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PDB; 1WTL; 01-NOV-94.
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01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
19 kappa chain V-1 region WAT.
19 kappa chain W-1 region WAT.
19 kappa chain (Human).
19 kappa chain (Human).
19 kappa chain (Human).
10 kappa chain W-1 region WAT.
10 kappa chain WAT.
10 kappa chai
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Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
Popp R.A., Solomon A.;
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FRAMEWORK-2.
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COMPLEMENTARITY-DETERMINING-3.
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              GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding activity; NAS.
GO; GO:0005855; F:antigen binding activity; NAS.
GO; GO:0006955; F:antigen binding activity; NAS.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_N.
InterPro; IPR003006; Ig_N.
InterPro; IPR003006; Ig_N.
ISWART; SM00406; IGV; 1.
INTERPROSTIE; PSS0833; IG_LIKE; 1.
Immunoglobulin V region; Amyloid.
InterPro; IPR030006; Ig_N.
InterPro; IPR030006; IGV; 1.
IMMUNOGLOBULIN V region; Amyloid.
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GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
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108 AA;
   HSSP; P80362; 1WTL
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P80362;
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1 DIQMIQSPSSLSASVGDRVIITCRASQDIINYVNWFQQRPGQAPKVLIYGASILEIGVPS 60
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P0153; VIA HUMAN STANDARD; PRT; 108 AA.
21-07L-1986 (Rel. 01, Last sequence update)
12-07L-1986 (Rel. 38, Last sendence update)
15-07L-1999 (Rel. 38, Last sendence update)
15-07L-1999 (Rel. 38, Last sendence update)
16 Kappa chain V-I region AG.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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FRAMEWORK-2.
COMPLEMENTARIY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARIY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARIY.
TN -> SD (IN REF. 2).
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                                                                                          Bence-Jones protein; 3D-structure
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Benc
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Best Local Similarity 62.6%;
Matches 67; Conservative 9
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1 DIGMIGSPASISASVGDRVIIIC-----WYLOKPGKSPQ-LIY-----GVPS 41
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Best Local Similarity 64.5%; Pred. No. 1.8e-28;
Matches 69; Conservative 4; Mismatches 6; Indels 28; Gaps
InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig MHC.

DR InterPro; IPR003596; Ig_v.

DR PRAMI; SM00406; Igv.

DR PROSITE; PS50835; IG LIKE; 1.

DR PROSITE; PS50835; IG LIKE; 1.

TOWALIN 1 23 COMPLEMENTARITY-DETERMINING-1.

PT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-2.

SO 56 COMPLEMENTARITY-DETERMINING-2.

PRAMEWORK-3.

COMPLEMENTARITY-DETERMINING-3.

FRAMEWORK-4.

PRAMEWORK-4.

TAPOCAF CRC64;
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Search completed: January 13, 2004, 12:39:25 Job time : 4.44978 secs

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9ul80 homo sapien Q9jl82 mus musculu Q9jl80 mus musculu

41

28;

-GVPS Gaps

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE=98277139; PubMed=9614934;
MY X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
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Best Local Similarity 66.4%; Pred. No. 1.2e-31;
Matches 71; Conservative 5; Mismatches 3; Indels
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1-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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108 AA; 11738 MW; C06681716C4D16F3 CRC64;
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Clin Immunol. Immunopathol. 87:184-192(1998)
EMB1, APO35037; AAD56273.1; -.
HSSP; PO1607; IREI.
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InterPro; IPR003106; Ig_MHC.
InterPro; IPR003506; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PR0SITE; PS50835; IG_LIKE; 1.
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Q9u181 homo sapien
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                                                                                                                                                                                                                                                                                                                                        416
1 DIQMTQSPASLSASVGDRVT.....QPEDFATYYCFGQGTKLEIK 79
                                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPNLLIYAASSLQSGVPS 60
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KINDLINE-981375893; PubMed=9712075;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
Adderson E.G., Shikhman A.R., Ward K.E., Cunningham M.W.;
Adderson E.G., Shikhman A.R., Ward K.E., Cunningham M.W.;
Molecular analysis of polyreactive monocloral antibodies from rheumatic carditis; human anti-N-acetylglucosamine/anti-myosin antibody V region genes.", J. T. Tamunol. 161:2020-2031(1998).

R MRL; U96396; AAB68785.1; -
R InterPro; IPR003066; Ig.Mc.
R InterPro; IPR003066; Ig.Mc.
R InterPro; IPR003566; Ig.Mc.
R InterPro; IPR00407; Ig. Id.
R SMART; SM00406; IGV. 1.
R SMART; SM00406; IGV. 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 19, Last sequence update)
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain variable region (Fragment).
Enkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=98277139; Pubmed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                          RFSGSGSGTDFTLTISSLOPEDFATYYCQQSYSTSWTFGEGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 RFSGSGGTDFSFTISSLOPEDFATYYC-----FGQGTKLEIK 79
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01-MAR-2003 (TIENBLIE] 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.7%; Score 327.5; DB 4; Length 367.0%; Pred. No. 2.4e-31; ive 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
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(TrEMBLrel. 13, Last seq
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Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RFSGSGSGTDFTLTISSLQPEDVATYYCOKYNSAPRTFGPGTKLEIK 107
                                                                                                                                                                                                                                                           77.2%; Score 321; DB 4; Length 108; larity 66.4%; Pred. No. 1.5e-30; Conservative 3; Mismatches 5; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 RFSGSGGTDFSFTISSLQPEDFATYYC-----FGQGTKLEIK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDILINE-98277139; PubMed-9614934;
Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 RFSGSGSGTDFSFTISSLQPEDFATYYC-----FGQGTKLEIK 79
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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107 AA; 11501 MW; 070549FDE0754748 CRC64;
                                                                                                                                                                                                               108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clin. Immunol. Immunopathol. 87:184-192 (1998)
EMBL; AF035033; AAD56269.1; -.
HSSP; PO1607; JREI.
InterPro; IPR007110; Ig-like.
InterPro; IPR03306; Ig_MHC.
InterPro; IPR03396; Ig_W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
HSSP; POIGO7; IREI.
InterPro: IRRO07110; Ig-like.
InterPro: IRRO03006; Ig_MHC.
InterPro: IPR003596; Ig_v.
ShTan; PR00047; ig; I.
SNART; SMO0406; IGv; I.
PROSITE; PS50835; IG_LIKE; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam, PF00047; ig; 1. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG_LIKE; 1.
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Best Local Similarity 63.2
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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71.9%; Score 299; DB 11; Length 109; 60.7%; Pred. No. 6.2e-28; ive 5; Mismatches 9; Indels 28
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
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                                                                                   65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                           Best Local Similarity
Matches 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. TISSUE=Colon;
                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8VCP0
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
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Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
"Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
"In Mammalian Cells.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR307938; AAL09422.1;
InterPro; IPR00710; Ig-like.
InterPro; IPR003506; Ig_MC.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RFSGSGSGTDFTLTISCLQSEDFATYYCQQYYSFPPTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 301; DB 4; Length 108; Pred. No. 3.6e-28; 6; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
pterin-mimicking anti-idiotope kappa chain variable region
                                                        01-MAY-2000 (TrEMBirel. 13, Created)
--MAY-2000 (TrEMBirel. 13, Last sequence update)
01-MAY-2003 (TrEMBirel. 23, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
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108 AA; 11787 MW; DB5845F19724FB4E CRC64;
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EMBL; AF035035; AAD56271.1; -.
HSSP; P01607; IREI.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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108 AA
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PRT;
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Pfam; PF00047; ig; 1.
SWART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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PROSITE; PS50835; IG_LIKE; 1.
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1 Similarity 61.7%;
66; Conservative (
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PRELIMINARY;
                                                                                                                                                                                                                     Homo sapiens (Human)
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Best Local S
Matches 66
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                                                    1 DIGMIQSPASISASVGDRVILIC------WYLQKPGKSPQLIY-----GVPS 41
                                                                                                         1 DIQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNAKTLADGVPS 60
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   Gaps
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CN 8.
CN 8.
Enks musculus (Mouse).
Enksryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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STRAIN=Balb/c; TISSUE=Spleen;
MEDLINE=20183931; PubMed=10706631;
Shinobara N., Demura T.,
"Isolation of a varcular cell wall-specific monoclonal antibody recognizing a cell polarity by using a phage display subtraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28;
   58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 RPSGSRSGTQFSLKINSLQPEDFGSYYCQHHSGIPFTFGSGTKLEIK 127
                                                                                                                                                                                                               42 RESGSGSGTDFSFTISSLQPEDFATYYC-----FGQGTKLEIK 79
                                                                                                                                                                       42 RESGSGSGTDFSFTISSLOPEDFATYYC-----FGQGTKLEIK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Straubberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019474; AAH19474.1; -.
InterPro; BC019474; AAH19474.1; -.
InterPro; IPR00306; Ig_WHC.
InterPro; IPR003596; Ig_V.
Pfam; PPC0047; ig; 2.
SMART; SMO0406; IGV.
PROSITE; PSC00290; IG WHC; 1.
Hypothetical protein.
SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                QBVCEO;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25-7 kDa protein.
Mus musculus (Mouse)
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Last annotation update)
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21361171; PubMed=11468171; Comean K., Herrera G.A.; Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.; The tropism of organ involvement in primary systemic amyloidosis: contributions of Ig V(L) germ line gene use and clonal plasma cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESGGGSATNFTVTISSLQPEDFATYXCQQYHHLPFTFGPGTKVDFK 107
                                                                                                                                                                                                                                                                                            233 RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWTTPYTFGGGTKLEIK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 69.0%; Score 287; DB 4; Length 116; Best Local Similarity 57.9%; Pred. No. 1.8e-26; Matches 62; Conservative 9; Mismatches 8; Indels 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 RFSGSGSGTDFSFTISSLQPEDFATYYC-----FGQGTKLBIK 79
                                                                                               InterPro; IPR007110; Ig-1ike.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig MHC.
Pfam; PF00047; ig; 2.
SWART; SM0406; IGv, 2.
SWART; SR05085; IG LIKE; 2.
SEQUENCE: 298 AA; 31867 MW; E0F96B8A17004317 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 AA; 12735 MW; E796FC2217BFCF57 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 23, Last annotation update)
Kappa 1 light chain variable region (Fragment).
SDNK1.
                       Acad. Sci. U.S.A. 97:2585-2590(2000).
341; BAA88633.1; -.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 58.9%
The 63, Conservative
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                          Proc. Natl. Acad
EMBL; AB036341;
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COS 676 PR
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241 AA

PRELIMINARY;

RESULT 10 Q921A6 ID Q921A6

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MEDINE=98170165; PubMed=9509426;

MEDINE=98170165; PubMed=9509426;

MEDINE=98170165; PubMed=9509426;

MINE AND F. R. R. R. R. L. Kim H.J., Choi I.H., Lee S.D.,

Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;

The monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and

Generation of a single-chain FV molecule (ScFV).";

MOI. Cells 7:816-819(1997).

MOI. Cells 7:846-819(1997).

MINE PROBOGY 189067; ABA84044.1;

MINE PROBOGY 1990396; Ig_WHC.

MINE PROBOGY 1990396; Ig_WHC.

MERE PROBOGY 1990396; Ig_W.

MER PROBOGY 1990396; IG_W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMIQSPASLSASVGDRVIIIC-----WYLQKPGKSPQL----IY---GVPS 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                  Eukaryoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 67.4%; Score 280.5; DB 11; Length 241; 1 Similarity 55.7%; Pred. No. 2.6e-25; 59; Conservative 12; Mismatches 8; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 RFSGSGSGTDFSFTISSLOPEDFATYYC----FGOGTKLEIK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Colon;
Strausberg R.;
Submitted (P. 1) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013496; AAH13496.1; -.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003506; Ig_WHC.
InterPro; IPR003596; Ig_V.
Pf00047; ig; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26086 MW; 0276887248E9C771 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 AA; 25781 MW; BIC184DA149A16EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9JWS9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25:8 kDa protein (Fragment).
Mus musculus (Mouse).
Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.3%; Score 280; DB 11; 58.9%; Pred. No. 2.9e-25;
   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence updat
01-PEC-2003 (TrEMBLrel. 19, Last annotation upd
Anti-CEA 79 single chain Fv fragment (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
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                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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Gaps

28;

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21 DIQMIQTISSLSASLGDRVTISCSASQGISNYLNWYQQKPDGTVKLLIYYTSSLHSGVPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIQMTQSPASLSASVGDRVTITC------WYLQKPGKSPQLIY-----GVPS 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nowno appens, nomman,.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                      1 DIQMTQSPASLSASVGDRVTITC------WYLQKP-GKSPQLIY---
                                                                                                                                                                                                                                                                                                                                                                                                              81 RFSGSGSGTHYSLTISNLBPEDIATYYCQQYSQFPFTFGSGTKLEIK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RFSGSGSGTEFILTISSLÖSEDFAVYYCQQYNKWPHTFGQGTKLDIK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
InterPro; IPR00311, 19-11ke.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_W.
Ffam; PR00407; Igc. 2.
SMART; SM00407; Igc. 1.
SMART; SM00406; Ig_L1.
PROSITE; PS00299; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 65.6%; Score 273; DB 4; Length 234; Local Similarity 53.3%; Pred. No. 2e-24; Nosmatches 10; Indels 18
                                                                                                                                                                                                                      Query Match 66.1%; Score 275; DB 11; Length 23: Best Local Similarity 57.9%; Pred. No. 1.2e-24; Matches 62; Conservative 7; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                        42 RFSGSGSGTDFSFTISSLOPEDFATYYC-----FGOGTKLEIK
                 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
Pram; PR00047; ig; 2.
SMART; SM00406; IGv; 1.
PROSTTE; PS50835; IG_LIKE; 2.
PROSTTE; PS00290; IG_MHC; 1.
PROCHEL(all protein_ Hypothetical protein_ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEABI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 AA; 25530 MW; 6316E8DEF8D132F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (
01-OCT-2002 (
01-MAR-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q91WF8;
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42
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Q91WF8
ID Q91WF
AC Q91WF
DT 01-DE
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                                      1 DIQMTQSPASLSASVGDRVTITC------WYLQKP-GKSPQLIY-----GVPS 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41
                                                                             20 DIÓMIQITSSLSASLGDRVIISCSGSQGIANYLNWYQQKPDGIVKLLIYYISSLHSGVPS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIQLTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS
    Gaps
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                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Kappa light chain of Mab7 (Fragment).
Kappa light chain of Mab7 (Fragment).
Bukaryota, Metazoa, Orordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN 2002 (TrEMBLrel. 21, Created)
01-JUN 2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25.9 kDa protein.
Hypothetical 25.9 kDa protein.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilde K.G., Yu X., Exramoddoullah A.K.M., Misra S.,;
"Cloning of cDRAs encoding for anti-white pine blister rust mo antibody (Mab 7, its light and heavy chains) and construction single chain antibody (scPV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFIS2371; AAD40242.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003066; Ig_MGC.
Pfam; PF00047; ig; 2.
                                                                                                                                              61 RPSGSGGODYSLTISSLEYEDMGIYYCLQYDEPPFTFGSGTKLEIK 107
                                                                                                                       42 RFSGSGSGTDFSFTISSLQPEDFATYYC-----FGQGTKLEIK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 RFSGSGSGTDFSFTISSLQPEDFATYYC------FGQGTKLEIK 79
  9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Indels
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 214
214 AA; 23922 MW; 52BA205FDE995E2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 66.8%; Score 278; DB 11; Scinilarity 57.0%; Pred. No. 4.5e-25; 61; Conservative 9; Mismatches 9;
  7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam, PF00047; ig; 2. _____SMART; SM00406; IGv; 1. PROSITE; PS50835; IG_LIKE; 2. PROSITE; PS00290; IG_MHC; 1.
63; Conservative
                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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NON TER
SEQUENCE
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Matches
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Gaps

28;

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DT 01-WAR-2003 (TrEMBLrel. 23, Last annotation update)

B Hypothetical 25.9 KDa protein.

C Mamalia, Educatea, Chordata, Craniata, Vertebrata, Buteleostomi,

B Musaryora, Metaza, Chordata, Craniata, Vertebrata, Buteleostomi,

C Mamalia, Entheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.

RN 11

RN 11

RN 11

RN 125UB-Colon,

RN 125UB-Colo
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Search completed: January 13, 2004, 12:43:05 Job time : 17.1441 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - pr	OM protein - protein search, using sw model
Run on:	January 13, 2004, 12:18:44; Search time 18:4218 Seconds (without alignments) 680.681 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-990-586-79 416 1 DIQMIQSPASLSASVGDRVTQPEDFATYYCFGQGTKLEIK 79
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	1107863 segs, 158726573 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

1107863

Total number of hits satisfying chosen parameters:

19Jun03:*	ö	2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*	à	7	5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*	/gcgdata/geneseq/geneseqp-embl/AA1985.	IDS1/gcgdat	8: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*	a/geneseq/geneseqp-emb1/AA1988.	: /SIDS1/gcgdata/	. /SIDS1/gcgdata/geneseg/genesegp-embl/AA1990.	: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.	: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.	: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.	: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.	: /SIDS1/gcgdata/geneseg/genesegp-embl/AA1995.	: /SIDS1/gcgdata/geneseg/	: /SIDS1/gcgdata/geneseq/geneseqp-	'geneseg/genesegp-embl/AA1998.	: /SIDS1/gcgdata/geneseg/genesegp-emb1/AA1999.	gcgdata/	1/gcgdata/geneseq/geneseqp-emb1/AA2001.	geneseg/genesegp-emb1/AA2002.	24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:
: ee:																								
Database																								

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Murine humanised M	Human ICR-1.1 V-K	Humanised murine a	Antibody against I	Humanised antibody	Humanised ICR-1.1	Humanised ICR-1.1	Humanised murine a	Humanised monoclon
	Ω	ABG74720	AAW76130	AAW71260	AAY00786	AAW81454	AAB13050	AAY82449	AAY50757	AAU70942
	DB		13	19	20	20	21	21	21	23
	Query Match Length DB	80	110	110	110	110	110	110	110	110
*		:	81.1	81.1	81.1	81.1	81.1	81.1	81.1	81.1
	Score	376.5	337.5	337.5	337.5	337.5	337.5	337.5	337.5	337.5
	Result No.		7	٣	4	ഹ	9	7	æ	on

i-human VEGF r	ti-human Flt-1	\$	ligh	Humanised 23F2G li	fusic	anti	light	Anti-CEA antibody	Anti-CEA antibody		anti	11-6	Anti-human IL-4 hu	Anti-human VEGF re	Anti-human Flt-1 a	DNA encoding TRA-8	Anti-human IL-4 hu	Humanised antibody	ised	aci	Human anti-placent	Ĕ	Ci H	Ligh	sed muri	sed ant	ised	Vl consen	i-Er	eus hum	ised	riabl	nised anti-VE	body libr	, humanis
AAY7759	AAB7886	AAR3014	AAR4793	AAW8935	AAW0430	AAR5009	AAR4722	AAW413	AAW4139	ABP96012	AAE1206	AAR6765	AAR8947	AAY7759	AAB7886	AAU7281	AAR 8061	AAW4139	AAW4141	AAY2188	AAR1198	AARS	. AAR6030	AAW8680	AAW7062	AAW8745		AAB6208	AAB6039	AAB6040	AAB6158	AAB6158	ABP6119	ABJ1872	AAW7061
26 2	26 2	10 1	11 1	11 2	13 1	1 60	07 1	07 1	07 1	107 24	08 2	25 1	26 1	28 2	28 2	12 2	32 1	35 1	35 1	41 2	07 1	07 1	07 1	07 1	07 1	07 2	07 2	07 2	07 2	07 2	07 2	07 2	07 2	07 2	08 1
9.6	9.6	5.5	5.5	5.5	0.5	0.5	0.4	0.4	4.0	4	0.4	4.0	4.0	0.4	4.0	4.0	4.0	4.0	0.4	4.0	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3
35.		m	m	m	m	m	34.	34.	34.	334.5	34.	34.	34.	34.	34.	34.	34.	34.	34.	34.	m	334	3	ო	ന	3	ო	ന	E	m	က	E	3	m	m
10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	5	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4

ALI GNMENTS

us-09-990-586-79.rag

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This sequence represents a human ICR-1.1 V-K region amplified PCR product. This sequence is used in the isolation of a novel human product. This sequence is used in the isolation of a novel human in the recellular adhesion molecule, ICAM-R. This sequence is used in a method which investigates modulators of the interaction between ICAM-R and the 14.3.3 family member H31-beta and tubulin. An anti-ICAM-R antibody optionally coupled to toxin or radionuclide, or an ICAM-R perticularly its effector functions involved in (non) specific immune responses. ICAM-R related agents may be used to treat or monitor inflammation, disorders involving T cell activation or macrophages, e.g. adult respiratory distress syndrome, stroke, Crohn's disease, multiple sclerosis, rheumatoid arthritis, asthma, tumour growth, human immune deficiency virus infection, diabetes, graft vs. host disease and anny others. Antibodies may also be used for passive immunisation, ic rumbre syntessing cells. ICAM-R and for identifying ICAM-R expressing cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIOMIQSPASLSASVGDRVTITC-----WYLOKPGKSPO-LIY-----GVPSR 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 DIQMTQSPSSLSASVGDRVTITCSASSSVSYIYWYQQKPGKAPKLLIYLTSNLASGVPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, ICAM-R; intercellular adhesion molecule; adhesion; treatment; inflammatory condition; asthma; tumour growth; metastasis; viral infection; antibody ICR-1.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised murine antibody ICR-1.1 light chain amino acid sequence.
                                                                                                                                                         identifying compounds that modulate interaction of intercellular adhesion molecule R - with ligands HS1-beta and tubulin using two-hybrid assay, useful for treating inflammation, T cell activation etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.1%; Score 337.5; DB 19; Length 110; 68.9%; Pred. No. 3e-23; ive 4; Mismatches 2; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSGSGSGTDFTLTISSLQPEDFATYYCQQWKSIPLTFGQGTKLEIK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSGSGSGTDFSFTISSLOPEDFATYYC-----FGQGTKLEIK 79
                                                                                                                                                                                                                                                                                               Example 13; Column 135-136; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW71260 standard; Protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-0483389.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 68.9
                                                                Vazeux R;
                                                                                                          NPI; 1998-386989/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 AA;
                   ICOS CORP.
                                                                                                                                     N-PSDB; AAV56428
                                                                Gallatin WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
18-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                   (ICOS-)
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Intercellular adhesion molecule; human; ICAM-R; modulator; 14.3.3 family; HSI-beta; tubulin; inhibitor; stimulator; effector; immune response; inflammation; disorder; T cell activation; macrophage; Crohn's disease; adult respiratory distress syndrome; stroke; multiple sclerosis; asthma; rheumatoid arthritis; tumour growth; human immune deficiency virus; infection; diabetes; graft vs. host disease; passive immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                    treating allergy, septic or endotoxic shock, septicaemia, stroke, asthma, graft versus host disease, Crohn's disease, or inflammatory bowel disease. This sequence represents a protein associated with the humanised murine Mu007 antibody described in the disclosure of the
                                                                                                                                                                                                                         This invention describes a novel antibody that specifically binds mature human interleukin (IL) lbeta, and binds the same epitope on mature human IL-lbeta as mouse monoclonal antibody Mu007 or humanized antibody Hu007. The antibody of the invention have antirhewmatic, antiarchritic, antiaflammatory, osteopathic, antiallergic, cerebroprotective, antiasthmatic, immunosuppressive and antibacterial activity and can be used in a vaccine. The antibody is useful for manufacturing a medicament for treating rheumatoid arthritis or osteoarthritis, or for inhibiting cartilage destruction in a subject. The antibody is also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIQMIQSPSSLSASVGDRVTITCWFQQKPGKAPKSLIYGVPSRFSGSGSGTDFTLTISSL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIOMIQSPASLSASVGDRVIIICMYLQKPGKSPQ-LIYGVPSRFSGSGSGTDFSFTISSL 59
                                                                                    New IL-1beta antibodies, useful for treating allergy, septic or endotoxic shock, septicemia, stroke, asthma, graft versus host disease, Crohn's disease, or inflammatory bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 376.5; DB 24; Length 80;
Pred. No. 6.8e-27;
5; Mismatches 2; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ICR-1.1 V-K region PCR product protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW76130 standard; Protein; 110 AA
                                                                                                                                                                                  Disclosure, Fig 1, 98pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 QPEDFATYYCFGQGTKLEIK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 OPEDFATYYCFGOGTKLEIK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-0286754.
92US-0827689.
92US-0889724.
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9308-0009266
9300-0800787.
9308-0102852.
9508-0482882.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.0
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JAN-1993;
05-AUG-1993;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5773218-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-1998
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26-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW76130;
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do ò AMY 6130
AMY 6130
AMY 6130
AMY 6130
AMY 6130
AMY 6130
AMY 6130
AMY 70-0-N
AMY

64

27; Gaps

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This sequence represents an antibody specific for ICAM-R.

The invention relates to antibodies (AD) which bind specifically

The invention relates to antibodies (AD) which bind specifically

to the interaction between ICAM-R and alpha d/CDI8. Abs with specific ICAM-R

interaction between ICAM-R and alpha d/CDI8. Abs with specific ICAM-R

binding are useful in compositions for immunisation, and for purifying

ICAM-R polypeptides and identifying cells expressing ICAM-R on their cell

involving ICAM-R, especially inflammatory responses of the specific

immune system, the non-specific immune system, monitoring and treating

immune system, the non-specific immune system, monitoring and treating

infection. In particular diseases involving an essential T cell

activation (e.g. asthma, psoriasis, diabetes, graft vs. host disease,

tissue transplant rejection, and multiple sclerosis) may be treated with

anti-ICAM-R antibodies. The Abs specifically bind to and identify ICAM-R

and disrupt ICAM-R to cell adhesion molecule, especially alpha d/CD18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIĞMTÖSPSSLSASVGDRVTITCSASSSVSYIYMYQQKPGKAPKLIYLTSNLASGVPSR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Intercellular adhesion molecule polypeptide; ICAM-R; humanised; ICR-1.1; ICR-8.1; monoclonal antibody; therapeutic; inflammatory; asthma; tumour; graft-versus-host disease; viral infection; toxin; radionuclide; neovascularisation site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DIOMIOSPASISASVGDRVTITC-----WYLOKPGKSPQ-LIX-----GVPSR
                                                                                                                                                                                                                                                    New intercellular adhesion molecule receptor (ICAM-R) specific antibodies - useful for modularing ligand/receptor binding and biological activities involving ICAM-R, especially those of the specific and non-specific immune systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 337.5; DB 20; Length 110;
Pred. No. 3e-23;
4; Mismatches 2; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSGSGSGTDFTLTISSLQPEDFATYYCQOWKSIPLTFGQGTKLEIK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSGSGSGTDFSFTISSLOPEDFATYYC-----FGQGTKLEIK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised antibody ICR-1.1 Vk region (HuVK).
                                                                                                                                                                                                                                                                                                                                                 Example 13; Column 135-136; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW81454 standard; Protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n
Similarity 68.9%;
               92US-0894061.
93US-0009266.
93WO-US00787.
93US-0102852.
92US-0889724
                                                                                       95US-0483932
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                                                                                                                                                                    Vazeux R;
                                                                                                                                                                                                   WPI; 1999-204041/17.
N-PSDB; AAX21883.
                                                                                                                            (ICOS-) ICOS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 AA;
                 05-JUN-1992;
22-JAN-1993;
26-JAN-1993;
05-AUG-1993;
                                                                                                                                                                    Gallatin WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US5837822-A
                                                                                         07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ICAM; immunoglobulin-like loop; intercellular adhesion molecule receptor; alpha d/CD18; antibody; immunisation; inflammatory response; asthma; tumour growth; viral infection; therapy.
                                                                                                                                                                                                                                                                                                                                                               The present sequence represents the humanised light chain of murine antibody ICR-1.1. This antibody is specific for ICAM-3 (intercellular adhesion molecule-R). ICAMs are polypeptides that are expressed on blood vessel endothelial cell surfaces and are involved in the adhesion events in various conditions. ICAM-8 variants (see AAW71264-69) can be used to treat or monitor inflammatory conditions involving specific on be used to trospecific immune responses, asthma, tumour growth and/or metastasis and viral infections. The ICAM variants are produced recombinantly, from expression libraries of mutated sequences, and the ones that are adhesion events. They can also be used to raise antibodies, also for use as therapeutic or diagnostic agents.
(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIOMIOSPASISASVGDRVTITC-----WYLQKPGKSPQ-LIY-----GVPSR 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape
                                                                                                                                                                                                                                                      DNA encoding mutant ICAM-R poly;peptide(s) - useful for diagnosis and treatment of cell adhesion based disease conditions e.g. inflammation or asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.1%; Score 337.5; DB 19; Length 110; 68.9%; Pred. No. 3e-23; cive 4; Mismatches 2; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSGSGSGTDFTLTISSLQPEDFATYYCQQWKSIPLTFGQGTKLEIK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 FSGSGSGTDFSFTISSLOPEDFATYYC-----FGQGTKLEIK 79
                                                                                                                                                                                                                                                                                                                                      Example 13; Columns 135-136; 111pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY00786 standard; Protein; 110
 93WO-US00787.
92US-0827689.
92US-0889724.
92US-0894061.
93US-0009266.
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92US-0827689.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibody against ICAM-R.
                                                                                                                                                                      Gallatin WM, Vazeux R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-530940/45.
N-PSDB; AAV54866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 110 AA;
                                                                                                                                    CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-AUG-1994;
27-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
                                                                                                                                    (ICOS-) ICOS
                                                              05-JUN-1992;
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                                                                            22-JAN-1993
05-AUG-1993
                                         26-MAY-1992
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Op ਨੇ

42

Gaps

94US-0286754. 93WO-US00787. 92US-088724. 92US-0894061. 93US-0009266. 93US-0102852.

Vazeux R;

95US-0475680

us-09-990-586-79.rag

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Hybrid fusion proteins comprising intercellular adhesion molecule or its variants useful, for treating inflammatory conditions, Crohn's disease, atherosclerosis and diabetes
                                                                                                                                                                                                                                    Example 13; Column 135-138; 109pp; English.
                                                                                                                                                        WPI; 2000-542449/49.
N-PSDB; AAA97170.
                                                                                                              (ICOS-) ICOS CORP.
                                                                                                                                  Gallatin WM,
                    05-AUG-1994;
26-JAN-1993;
27-JAN-1992;
07-JUN-1995;
                                                                                     05-AUG-1993;
                                                     26-MAY-1992
05-JUN-1992
                                                                            22-JAN-1993
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Matches
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-human immunodeficiency virus, HIV, cytostatic, ICAM-R, ARDS; stroke, intercellular adhesion molecule, immunoglobulin heavy chain; septicaemia, inflammatory conditions; glomerulonephritis, arthritis, dermatosis; haemodialysis; leukapherseis, ulcerative colitis; Crohn's disease; necrotising enterocolitis; atherosclerosis; psoriasis, asthma; transplant rejection; diabetes; tumour.
                                                                                                                                                                                                                                                                     The invention relates to humanised ICR-1.1 and ICR-8.1 antibodies targeted to the human intercellular adhesion molecule polypeptide (ICAM-R) polypeptide. Antibodies specific for ICAM's are potentially useful as therapeutic compounds, for treating e.g. immune-mediated inflammatory conditions (e.g. graft-versus-host disease), aschma, tumours or viral infections. Monoclonal antibodies specific for ICAM-R, or their conjugates formed with e.g. toxins or radionuclides are useful for therapeutically targeting or detecting neovascularisation sites. The present sequence tepresents the amino acid sequence of the Vk region of the humanised antibody ICR-1.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIOMIOSPASISASVGDRVTITC-----WYLQKPGKSPQ-LIY------GVPSR 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIOMIQSPSSLSASVGDRVITICSASSSVSYIYWYQQKPGKAPKLLIYLTSNLASGVPSR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                 Humanised antibodies specific for intercellular adhesion molecule polypeptide - useful for therapeutic or diagnostic purposes
                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                    81.1%; Score 337.5; DB 20; Length 110; 68.9%; Pred. No. 3e-23; ive 4; Mismatches 2; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 FSGSGSGTDFSFTISSLQPEDFATYYC-----FGQGTKLEIK 79
                                                                                                                                                                                                                                                    Example 13; Columns 145-148; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised ICR-1.1 Vk protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB13050 standard; Protein; 110 AA.
                                           95US-0487113.
92US-0827689.
92US-0889724.
92US-0009266.
93WO-US07787.
                        95US-0487113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             Vazeux R;
                                                                                                                                                                                 WPI; 1999-023535/02
                                                                                                                                      CORP.
                                                                                                                                                                                                                                                                                                                                                                                                    110 AA;
                                                                                                                                                                                           N-PSDB; AAV69196
                                                                                                                                      (ICOS-) ICOS
                                                                                                                                                           Gallatin WM,
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                        07-JUN-1995;
                                                                                                   26-JAN-1993;
05-AUG-1993;
  17-NOV-1998
                                             07-JUN-1995
                                                        27-JAN-1992
                                                                  36-MAY-1992
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This invention relates to a hybrid fusion protein comprising an intercellular adhesion molecule (ICAM-R) amino acid fragment at its amino terminus and a constant domain of an immunoglobulin heavy chain at its carboxy terminus. ICAM-R polypeptides are useful for treating and monitoring inflammatory conditions such as adult respiratory distress syndrome, multiple organ injury syndrome secondary to septicacemia or cranma, reperfusion injury of tissue, acute glomerulonephitis, reactive arthritis, dermatosis, stroke, thermal injury, haemodialysis, enterocolitis, granulocyte transfews, acute glomerulorephitis, reactive also useful for treating conditions response of the also useful for treating conditions respectively. ICAM-R polypeptides are also useful for treating conditions repetiding from a response of the specific immune system in a mammal e.g. postasis, organ/tissue arthritis, diabetes and lupus erythematosus. ICAM-R products and ICAM-R cransplant rejection and autoimmune diseases including Raymand's syndrome, autoimmune thyroiditis, multiple solerosis, rheumatoid cransplant and or metastasis and viral infection (e.g. HIV infection). Sequences AAA97090 and AAB13036 represent the human ICAM-R DNA sequences AAA97090 and AAB13036 represent the human ICAM-R antibody ICR-8.1, and fragments of the humanised anti-ICAM-R antibody. Sequences AAA97112-A97123 and AAA97132-A97132 represent cransplant approacher metastasis and probes, all used in the production of mannised anti-ICAM-R antibody. Sequences AAA97135-A97156 and AAA97132-A97136 represent murine (ICC ICR-1) sequences AAA97155-A97156 represent primers used in the production of continual and peptide sequences used in the humanised anti-ICAM-R antibody ICR-8.1, and including AAA97132-A97136 and AAB97133-A997156 and AAB97131-A997132 represent murine (ICC ICR-1) sequences DNA and peptide sequences used in the production of the chimaric protein of the invention include AAA971717-A97188 and chimaric protein of the invention include sequences used in the production of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 DIQMTQSPSSLSASVGDRVTITCSASSSVSYIYWYQQKPGKAPKLLIYLISNLASGVPSR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSGSGSGTDFTLTISSLQPEDFATYYCQQWKSIPLTFGQGTKLEIK 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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nes 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 AA;
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AAY82449 standard; Frotein; 110

AAY82449 ID AAY8

RESULT

US6100383-A. 08-AUG-2000

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(first entry)

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The present invention describes a monoclonal antibody (WAb) (I),

produced by the hybridoma cell line 81K2F (ATCC HB 11692). Also described

are: (1) a hybridoma cell line 81K2F; and (2) a MAb (II), that competes

with (1) for binding to ICAM-R (intracellular adhesion molecule

creeptor) (III). (II) mimics the activity of natural binding proteins

through which intercellular and intracellular activities of (III) are

modulated. (II) is also used for modulating the immune responsee. (I) is

useful in modulating the ligand/receptor binding biological activity

involving (III) especially those effector functions of (III) involved in

specific and non-specific immune system responsee. Inflammatory

conditions which may be treated or monitored with related products of

(III) include conditions resulting from a response of the non-specific

immune system in a mammal e.g. adult respiratory distress syndrome,

creparfusion injury of issue, acute glomerulonephritis, reactive

arthritis, stroke, ulcrative colitis and atherosclarosis, and conditions

resulting from a response of the specific immune system in a mammal, e.g.

specials, organ/tissue transplantation rejectorion, autofmunne diseases

cuch as autoimmune thyroiditis multiple sclerosis, rheumatoid arthritis,

diabetes and lupus erythematosue, and the exemplification of the present
                                                                                                                          Human; ICAM-R; chromosome 19; intracellular adhesion molecule receptor; Adm, ICAM-1; ICAM-2; humanised; antibody; mutagenic; chimeric; vulnerary; nephropathic; antiarthritic; cerebroorcective; antiulcer; cytostatic; antiarteriosclerotic; immunosuppressive; antidiabetic; neuroprotective; antithyroid; dermatological; antiasthmatic; antiviral; antihiflammatory; anti-HIV; vasotropic; antipsoriatic; immunosodulator; antirheumatic; cell adhesion mediator; inflammatory condition; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel monoclonal antibody directed against ICAM-R proteins useful for treating acute glomerulonephritis, ulcerative colitis, psoriasis, rheumatoid arthritis, diabetes, multiple sclerosis, asthma and viral
                                                                                        Humanised ICR-1.1 antibody HuVK protein sequence SEQ ID NO:96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 13; Column 151-153; 117pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                      12-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-AUG-1993
                                                      28-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                  AAY82449
                                                                                                                                                                                                                                                                    Immune
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Vazeux R;

CORP.

94US-0286754. 92US-0827689. 92US-0889724. 92US-0694061. 93US-0009266.

93US-0102852

96US-0714017

sapiens

DB 21; Length 110;

Score 337.5;

81.1%;

Query Match

110 AA;

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4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel method for identifying a compound that modulates phosphorylation of human intercellular adhesion molecule polypeptide (ICAM-R) by protein kinase C isoform. The method comprises: (a) exposing a purified peptide consisting of the cytoplasmic domain of ICAM-R to protein kinase C isoform and labeled adenosine triphosphate in the presence and absence of a test compound; (b) measuring labeled thosphosphate transferred to the peptide; and (c) identifying a test compound that affects transfer of the labeled phosphate as a modulator compound. The method is useful for identifying compounds that modulate the phosphorylation of human intercellular adhesion molecule polypeptide which might form the basis for the development of therapeutic and diagnostic agents. This sequence represents the humanised murine ICR-1.1 antibody VK region which is used in the method of the invention.
                                            42
                                                                       64
                                         1 DIGMTOSPASUSASVGDRVTLTC-----WYLQKPGKSPQ-LIY-----GVPSR
                                                           5 DIOMIQSPSSLSASVGDRVIITCSASSSVSYIYWYQQKPGKAPKLLIYLISNLASGVPSR
                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying modulators of protein kinase C phosphorylation of human intercellular adhesion molecule polypeptide -
                                                                                                                                                                                                                                                                                                                     ICAM-R; murine; intercellular adhesion molecule; phosphorylation; protein kinase C; modulator; ICR-1.1; antibody.
                  27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21; Length 110;
                                                                                                                         FSGSGSGTDFTLTISSLQPEDFATYYCQQWKSIPLTFGQGTKLEIK 110
                                                                                                     79
                  Indels
                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 337.5; DE
Pred. No. 3e-23;
      Pred. No. 3e-23;
                                                                                                                                                                                                                                                                                            Humanised murine antibody ICR-1.1 VK protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 14; Column 153-154; 122pp; English.
                   Mismatches
                                                                                                      43 FSGSGSGTDFSFTISSLQPEDFATYYC-
                                                                                                                                                                                                          Ā
                   4;
                                                                                                                                                                                                          AAY50757 standard; Protein; 110
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68.98;
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92US-0889724.
92US-0894061.
93US-0009266.
93WS-0102852.
95US-0487113.
   68.9%;
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                                                                                                                                                                                                                                                               16-FEB-2000 (first entry)
                   73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vazeux R;
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Best Local Similarity
Best Local Similarity
Matches 73; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallatin WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICOS-) ICOS
                                                                                                                                                                                                                                                                                                                                                                                    Mus sp.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JAN-1993;
26-JAN-1993;
05-AUG-1993;
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                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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                                                                                                                                                                             RESULT 8
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-----GVPSR

Gaps

27;

Indels

Length 110;

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8

Matches

65 43

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transplant rejection, autoimmune diseases including Raynaud's syndrome, autoimmune thyroiditis, multiple sclerosis, rheumatoid arthritis, lugus erythematosus, asthma, tumnour growth and/or metastasis, viral infection, tissue transplant rejection, graft versus host disease and multiple sclerosis. (II) is also useful for immunisation, for purifying ICAM-R polypeptides and for identifying cells that display the polypeptides on their surfaces. AAUF0928-AAUF0946 represent ICAM amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a gene recombinant antibody that has specific reaction with human vascular endothelial growth factor (VEGF) receptor Pit-1. The antibodies are useful for diagnosis and as remedies for diseases due to abnormal neovascularisation such as proliferation or metastasis of solid tumor, arthritis in rheumatoid arthritis, diabetic
                                                                                                                                                                                                                                                                                                                                                                                 DIOMIOSPSSLSASVGDRVIITCSASSSVSYIYWYQQRPGRAPKLLIYLTSNLASGVPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recombinant antibodies, useful for diagnosis and as remedies for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diseases due to abnormal neovascularization e.g. proliferation or metastasis of solid tumor, rheumatoid arthritis, diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-human VEGF receptor Flt-1 antibody related peptide sequence #94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody; human; vascular endothelial growth factor; VEGF receptor; Flt-1; neovascularisation; cell proliferation; metastasis; tumour; rheumatoid arthritis; retinopathy; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rscsescrbririssiorabrarycoowksipitrecorkieik 110
                                                                                                                                                                                                                                                                                                                                                                                                                              43 FSGSGSGTDFSFTISSLOPEDFATYYC-----FGQGTKLEIK 79
                                                                                                                                                                                                                                                                                                                                        1 DIQMIQSPASLSASVGDRVTITC------WYLOKPGKSPQ-LIY
                                                                                                                                                                                                                                                   Score 337.5; DB 23;
Pred. No. 3e-23;
4; Mismatches 2; 1
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Pred. No. 5.2e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 28; Page 202; 210pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ġ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY77599 standard; peptide; 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.6%;
69.2%;
                                                                                                                                                                                                                                                       81.1%;
68.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-JP02661.
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                                                                                                                                                                                                                               Query Match
Query Match
Best Local Similarity be..
Best Local Almilarity be..
Angle Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shitara K, Ito M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-072431/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                               110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAZ87771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAY-1998;
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                                                                                                                                                                                                               Sequence
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              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Auman; intercellular adhesion molecule; ICAM; antiinflammatory; stroke; antibacterial; vulnerary; vasotropic; nephrotropic; antiarthritic; cerebroprotective; dermatological; antiulcer; immunosuppressive; tumour; antipsoriatic; antiarteriosclerotic; neuroprotective; antithyroid; virucide; antirheumatic; antiabetic; antiasthmatic; cytostatic; asthma; hybridoma cell line; ATCC HB 12190; inflammation; septicaemia; trauma; adult respiratory distress syndrome; multiple organ injury syndrome; tissue reperfusion injury; acute glomerulonephritis; arthritis; vaccine; dermatosis; thermal injury; amemodialysis; leukopheresis; psoriasis; Crohn's disease; ulcerative colitis; multiple sclerosis; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel hybridoma cell line (I) ATCC HB 12190. (I) is useful for producing an intercellular adhesion molecule (TCAM) monoclonal antibody (II). (II) is useful for treating inflammatory conditions including adult respiratory distress syndrome, multiple organ injury syndrome secondary to septitoemia or trauma, tissue repertuaion injury, acute glomerulonephisis, reactive arthritis, dermatcosis with acute inflammatory components, stroke, thermal injury, haemodialysis, leukopheressis, ulcerative collis, crohn's disease, necrotishing entercoclisis, granulocyte transfusion associated syndrome, diabetes, atherosclerosis, cytokine-induced toxicity, psoriasis, organ/tissue
                                                           42
                                                                                               DIĞMTĞSPSSLSASVGDRVTITCSASSSVSYIYMYQQKPGKAPKLLIYLTSNLASGVPSR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel hybridoma cell line useful for producing monoclonal antibody for treating inflammatory conditions, immune system disorders and infectious diseases, is deposited under specified ATCC accession number
                                                         ----WYLQKPGKSPQ-LIY-----GVPSR
                Gaps
                27;
                                                                                                                                                                             FSGSGGGTDFTLTISSLQPEDFATYYCQQWKSIPLTFGQGTKLEIK 110
                                                                                                                                                 79
              2; Indels
                                                                                                                                                 FSGSGSGTDFSFTISSLQPEDFATYYC-----FGQGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised monoclonal antibody ICR-1.1 VK region
                   Mismatches
                                                           1 DIQMIQSPASLSASVGDRVTITC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 83; Example 14; 126pp; English.
                                                                                                                                                                                                                                                                                                            standard; Protein; 110 AA
                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0382289.
92US-0827689.
92US-0889724.
92US-0894061.
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93US-0102852.
95US-0487113.
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                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABK09359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2001029293-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallatin WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JAN-1992
                     73;
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Synthetic

AAU70942;

AAU70942

AAU70942 RESULT

Length 126;

DB 21;

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4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to a reagent for detecting differentiation of monocytes and macrophages from haematopoietic stem cells, containing a substance which binds to human vascular endothelial growth factor (WEGF) receptor Fit-1. The invention also includes a method for diagnosing a disease in which the differentiation of monocytes and macrophages is limplicated, using the reagent, and an agent for the treament of diseases diagnosed using the method, containing a substance which binds to Fit-1 or a substance which inhibits the signal transduction of Fit-1. Diseases which may be diagnosed or treated include inflammation, delayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypersensitivity, malignant tumours and arteriosclerosis.

AAF70190 - AAF70244, AAF70251 and AAF70258 represent DNA sequences encoding anti-human Fit-1 monoclonal antibody fragments and oligomuclectides used in the construction of the antibody. The monoclonal antibody is used in the reagent of the invention. FCR primers AAF70245 - AAF78870 (excluding AAF70251) are used in the isolation of the antibody DNA sequences. Protein sequences AAB78848 - AAB78870 represent fragments of the anti-human Fit-1 antibody.
                         42
                                                82
                                                                                                                                                                                                                                                                    Differentiation, monocyte, macrophage, haematopoietic stem cell; cancer, vascular endothelial growth factor; VEGF; Flt-1; inflammation; antibody; delayed hypersensitivity; malignant tumour; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Substances binding to human vascular endothelial growth factor receptor Flt-1, used for diagnosis and treatment of inflammatory diseases, arteriosclerosis, cancer and delayed hypersensitivity -
                                       23 DIQMTQSPSSLSASVGDRVTITCSASSSVSYMHWYQQKPGKAPKLLIYRTSNLASGVPSR
Gapa
25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 335.5; DB 22; Length 126; Pred. No. 5.2e-23; 5; Mismatches 2; Indels 25;
                                                                                                                                                                                                                                               Anti-human Flt-1 antibody VL CDR protein sequence SEQ ID 90.
                          1 DIOMIQSPASISASVGDRVTITC------WYLOKPGKSPQ-LIY-
                                                                                          83 FSGSGSGTDFTLTISSLQPEDFATYYCHQWSMYTFGQGTKVEIK 126
2; Indels
                                                                           43 FSGSGSGTDFSFTISSLQPEDFATYYC----FGQGTKLEIK 79
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Page 157; 164pp; Japanese
                                                                                                                                                                     Æ
                                                                                                                                                                    AAB78868 standard; Protein; 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                          16-JUN-2000; 2000WO-JP03957.
                                                                                                                                                                                                                     20-APR-2001 (first entry)
72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shibuya M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-080847/09.
N-PSDB; AAF70244.
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                                                                                                                                                                                                                                                                                                                                                      WO200079275-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                               28-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shitara K,
                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                             AAB78868;
                                                                                                                                        Matches
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----WYLQKPGKSPQ-LIY-----GVPSR

1 DIQMTQSPASLSASVGDRVTITC--

Query Match
Best Local Similarity 69.2%;
Matches 72; Conservative

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42
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The 431/26 VH and VK antibody fragments represented in AAQ26757-58 are pref. for the prodn. of the fuelon proteins of formula huruwAk.L-beta-dluc (1) (huruwAk= humanised, tumour-specific monoclonal antibody, or its tumour-binding fragments); L= linker; beta-dluc= human beta-glucuronidase). BetaGlc Linker 1 and betaGlc Linker 2 oligonucleotides are given in AAQ26759-60. Hinge 1 and hinge 2b oligonucleotides are given in AAQ26761-62.

(1) are used to activate prodrugs. The antibody component provides for specific targetting to tumours while the beta-dluc component activates a suitable prodrug by cleavage of glucuronic acid. The combination of the prodrug and (1) is useful in tumour treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIOMIOSPASISASVGDRVIIIC------WYLOKPGKSPQ-LIY-----GVPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 DIGMIQSPSSLSASVGDRVTITCSTSSSVSYMHWYQQXPGKAPKLLIYSTSNLASGVPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VH; VK; huTuMAK-L-beta-Gluc; monoclonal antibody; tumour; linker;
beta-glucuronidase; hinge; prodrug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56;
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Pred. No. 5.1e-23;
5; Mismatches 2; Indels 26
                                                                                                          83 FSGSGSGTDFTLTISSLQPEDFATYYCHQWSMYTFQQTKVEIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 FSGSGSGTDFSFTISSLQPEDFATYYC-----FGQGTKLEIK 79
                                                                               79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fusion protein for diagnosis and treatment - comprises
tumour-specific monoclonal antibody (fragment), linker
beta-glucuronidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sedlacek H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kolar C,
                                                                                  43 FSGSGSGTDFSFTISSLOPEDFATYYC-
                                                                                                                                                                                                                                                          AAR30147 standard; Protein; 110 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hoffman D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 68.6%;
Matches 72; Conservative 5
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                                                                                                                                                                                                                                                                                                                                                         (updated)
(first entry)
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(FARH ) HOECHST AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Czech J,
Hoffmann I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-293718/36.
N-PSDB; AAQ26758.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    431/26 VK hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-1991;
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11-FEB-1993
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Seemann G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                          AAR30147;
                                  53
                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                       AAR30147
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38 GVPSRFSGSGSGTDFSFTISSLOPEDFATYYC-

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65

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                           Amplification, 23F2G; humanised antibody; heavy chain; light chain; hybridoma; inflammation, CD18; human leukocyte integrins; mAb 60.3; monoclonal antibody; LFA-1; adhesion; migration; multiple sclerosis; MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                migration to inflammatory sites. The MAb is an anti-CD18 integrin antibody which competes with MAb 60.3 for binding to LFA-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibodies immunologically reactive with the CD18 of human leukocyte integrins and/or competing with mAb 60.3 for binding to human LFA-1 - for alleviating symptoms associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.5%; Score 335; DB 15; Length 111;
65.8%; Pred. No. 5.1e-23;
ive 4; Mismatches 2; Indels 32;
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(Updated on 10-MAR-2003 to add missing OS field.)
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                        Humanised light chain region of 23F2G.
                                                                Ā
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                                                                AAR47935 standard; Protein; 111
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93US-0060699.
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                                                                                                                                                                                       (updated)
(updated)
(first entry)
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(UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-048551/06.
N-PSDB; AAQ55917.
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Best Local Similarity
Matches 73; Conserv:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 AA;
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10-MAY-1993;
                                                                                                                                                                                                                         10-MAR-2003
24-JUL-1994
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Synthetic.
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                                                                                                                             AAR47935;
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ARRA7935

DAR47935

ARA77935

ARA77935

AXX
AAR47935

DT 25-MA
DT 25-MA
DT 10-MA
DR WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes the hybridoma cell line 23F2G (ATCC HB 11801) and the Chinese hamster ovary (CHO) cell lines 656 (ATCC CRL 11398) and B13-24 (ATCC CRL 11397). Monoclonal antibody (MAD) 23F2G (and its humanised variants 666 and B13-24) is an anti-human CD18 antibody for the treatment of inflammation, specifically multiple sclerosis. The present sequence represents humanised 23F2G light chain variable region from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 bigwigspsslsasvedrytitcrasesvesygnnemywygokegkapkiliylasnies
                                                                                                                                                                                 Mouse; humanised; antibody; heavy chain variable region; light chain; 23F2G; inflammatory disease; multiple sclerosis; common beta chain; CD18; human leukocyte integrin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.5%; Score 335; DB 20; Length 111;
65.8%; Pred. No. 5.1e-23;
ive 4; Mismatches 2; Indels 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 GVPSRFSGSGGTDFSFTISSLQPEDFATYYC-----FGQGTKLEIK 79
61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCHQDNEDPPTFGQGTKLEIK 111
                                                                                                                                                            Humanised 23F2G light chain variable region.
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                                                                            AAW89351 standard, Protein, 111
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93US-0060699.
95US-0396089.
97US-0785571.
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(UNIW ) UNIV WASHINGTON.
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Best Local Similarity
Matches 73; Conserval
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10-MAY-1993;
28-FEB-1995;
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Synthetic.
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RESULT 15

1 DIOMIOSFASISASVGDRVIITC------37

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AAW04301 standard; Protein; 213 AA.

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fragment/enzyme fusion proteins can be used for tumour therapy, fragment/enzyme fusion proteins can be used for tumour therapy, c especially when the fusion protein comprises a tumour-specific especially when the fusion protein comprises a unon-toxic prodrug to a toxic drug. The fusion proteins are constructed in expression vectors and expressed in thioredoxinreductase deficient B.coli, allowing expression products to be isolated in soluble functional form without renaturation. The Ab fragment is an FAb fragment or an antigen binding region. In the fusion protein, the Ab component is humanised and the enzyme component is a human cytoplasmic enzyme. This fusion protein comprises the antibody constant and variable light chain regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prodn. of recombinant antibody (Ab), Ab fragment or Ab/enzyme fusion protein - by cytoplasmic expression in thio:redoxin:reductase deficient E. coli
                                                                                                                                Antibody; fusion protein; recombinant antibody; tumour therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.5%; Score 335; DB 17; Length 213; 68.6%; Pred. No. 9.4e-23; tive 5; Mismatches 2; Indels 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Figure 5a; 12pp; German
                                                                                                                                                                                                                                                                                                    96EP-0103913.
                                    (updated)
(first entry)
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Best Local Similarity 68.6
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                              (BEHW ) BEHRINGWERKE AG.
                                                                                          Antibody fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                    Bosslet K, Czech J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-457328/46.
N-PSDB; AAT38397.
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                                25-MAR-2003
14-FEB-1997
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                                                                                                                                                                                        Synthetic.
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AAW04301;
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Search completed: January 13, 2004, 12:38:23 Job time : 19.4218 secs

FSGSGGTDFTFTISSLQPEDIATYXCHQWSSYPTFGQGTKVEIK 106 43 FSGSGSGTDFSFTISSLQPEDFATYYC-----FGQGTKLEIK 79

42 61

26; Gaps

1 DIOMIOSPASISASVGDRVTITC-----WYLQKPGKSPQ-LIY-----GVPSR 2 DIQMIQSPSSLSASVGDRVTITCSTSSSVSYMHWYQQKPGKAFKLLIYSTSNLASGVPSR

à d à us-09-990-586-79.rai

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90.7%; Score 377.5;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Sequence 104, App
Sequence 85, Appl
                                                                                       ; Search time 6.83057 Seconds (without alignments) 489.353 Million cell updates/sec
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1 DIQMTQSPASLSASVGDRVT......QPEDFATYYCFGQGTKLEIK 79
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1. /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/BECOMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
version 5.1.6
- 2004 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
GenCore
Copyright (c) 1993
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seq length: 200000000
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Perfect score:
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US-08-255-501A-55
US-09-265-231-55
US-09-171-945-99
US-09-171-945-99
US-09-171-945-99
US-08-441-44-80
US-07-341-37-64-18
US-08-44-26-18
US-08-44-26-18
US-08-446-265A-130
US-08-446-265A-130
US-08-446-265A-130
US-08-446-265A-130
US-08-446-265A-130
US-08-446-265A-130
                                                                                         US-08-407-620A-10
US-08-407-620A-32
US-07-934-373C-3
                                                                              US-08-974-899-2
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                                                                                                                         ALIGNMENTS
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(202) 672-5399
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TOPOLOGY:
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US-09-416-557-104
                                  RESULT 3
US-09-205-231-85
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                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                               Sequence 104, Application US/08765783A
Sequence 104, Application US/08765783A
Patent No. 5994524
GENERAL INPORMATION:
APPLICANT: Matsumoto, Yoshihiro
APPLICANT: Sato, Yoshiki
APPLICANT: Sato, Koh
APPLICANT: Yamada, Yoshiki
APPLICANT: Yamada, Tutami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B: MORRISON & FOERSTER
2000 Pennsylvania Avenue, NW, suite 5500
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: DESCRIPTION
SYSTEM: DOS
SOFTWARE: FASISEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,783A
FILING DATE: O'-MAR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/765,783A
FILING DATE: WINDER: SOFTING APPLICATION NUMBER: SOFTING APPLICATION NUMBER: 20,959
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
TELECOMMUTCATION INFORMATION:
TELEPHONE: 202-887-1500
TELEPHONE: 202-887-1500
   90.0%; Pred. No. 1.5e-29; tive 5; Mismatches 2
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Best Local Similarity 90.0%;
Matches 72; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 72; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
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US-90-20-31-33-58

Sequence 8. Application US/9205231

Parent No. 6121-20-31

GARRILLOWIT STATE OF INVENTION: Reasouk:
APPLICATI STATE OF INVENTION: INTERLACENT: APPLICATION OF INVENTION: INTERLACENT: APPLICATION OF SECURIORS: ```

```
APPLICANT: HANNA, Nabil APPLICANT: BADLAN, Nabil APPLICANT: BADLAN, Nabil APPLICANT: BADLAN, Roland A. APPLICANT: BADLAN, Roland A. APPLICANT: NEWMAN, Roland A. TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF NUMBER OF SENDENS: 28

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Burns, Doane, Swecker & Mathis STATE: Virginia COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM: MEDIUM TYPE: READABLE FORM: MEDIUM TYPE: READABLE FORM: MEDIUM TYPE: Patentin Release #1.0, Version #1.30

COMPUTER: Datentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/554,840
 1 DIOMTÓSPSSLSASVGDRVTITCMYQÓKPGKAPKLLIYSASYRYSGVPSRFSGSGSGTDF
 Length 87;
 Indels
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: WO PCT/JP94/01763
PRIOR APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION NUMBER: US-291078
FILING DATE: 19-NOV-1993
ATTONEY/AGENT INPORMATION:
NAME: NAGNER, Harold C.
REGISTRATION NUMBER: 25,2886,794
 Score 364; DB 3;
Pred. No. 3.3e-28;
5; Mismatches 2
 53 SFIISSLOPEDFATYYCFGOGTKLEIK 79
 KEGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
 Sequence 10, Application US/08554840 Patent No. 6001358 GENERAL INFORMATION: APPLICANT: BLACK, Amelia
 TELEX: 904136
INFORMATION FOR SEQ ID NO: 112: SEQUENCE CHARACTERISTICS: LENGTH: 87 amino Types
 Query Match
Best Local Similarity 82.8%;
Matches 72; Conservative
 ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
 TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-646-265A-112
 amino acid
 FILING DATE: 07
 US-08-554-840-10
 g
 1 DIQMTQSPSSLSASVGDRVTITCWYQQKPGKAPKLLIYGVPSRFSGSGSGTDFTFISSL 60
 1 DIQMIQSPASLSASVGDRVIITCWYLQXPGKSPQ-LIYGVPSRFSGSGGTDFSFTISSL 59
 1; Gaps
 DB 3; Length 80;
 Indels
 GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
APPLICANT: SATO, Koh
APPLICANT: STOY, KOH
APPLICANT: TSUCHIYA, Massyuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDUTILOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
 ISEE: MORRISON & FOERSTER: 2000 Pennsylvania Avenue, NW, suite 5500 Washington
APPLICANT: TBUChlya, Masayuki
APPLICANT: Yamazaki, Tatsumi
TITLE OF INVENTION: Reshaped Human Antibody to
TITLE OF INVENTION: Interleukin-8
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
STREFT:
 Query Match 90.7%; Score 377.5; DB 3; Best Local Similarity 90.0%; Pred. No. 1.5e-29; Matches 72; Conservative 5; Mismatches 2;
 OPERATING SYSTEM: DOS
SOFFWARE: Fast SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/416,557
FILING DATE: 12-October-1999
CLASSIFICATION:
PRION APPLICATION NUMBER: 08/765,783
FILING DATE: 7-March-1997
ATTORNEY/AGENT INFORMATION:
NAME: MULASAIGE, KALE H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 35029-20001.10
TELEOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
 ADDRESSEE: Foley & Largner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
 RESULT 5

20.08-646-265A-112

9. Sequence 112, Application US/08646265A

9. Patent No. 6214973
 60 QPEDFATYYCFGQGTKLEIK 79
 61 OPEDIATYYCFGOGTKVEIK 80
 TELEX:
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
 COUNTRY: CONDG-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 TELEFAX: 202-822-0168
 STRANDEDNESS: single TOPOLOGY: linear
 COMPUTER READABLE FORM:
 OPERATING SYSTEM:
SOFTWARE: FastSEC
 COUNTRY: U
 ;
US-09-416-557-104
 CITY: Wa.
STATE: D
COUNTRY:
 g
```

Gaps

```
Score 358.5; DB 4;
Pred. No. 1e-27;
8; Mismatches 3;
 Query Match

86.2%; Score 358.5;
Best Local Similarity 85.0%; Pred. No. 1e-2
Matches 68; Conservative 8; Mismatches
 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNUBER: US/08/554,840
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELEPHONE: (703) 836-6620
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 10, Application US/09332595
Patent No. 6506383
 61 QSDDFATYYCFGQGTKLEIK 80
 60 OPEDFATYYCFGOGTKLEIK 79
 60 QPEDFATYYCFGQGTKLEIK 79
 61 QSDDFATYYCFGQGTKLEIK 80
 Query Match
Best Local Similarity 85.0%;
Matches 68; Conservative
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
 MOLECULE TYPE: protein
 amino acid
 linear
 STRANDEDNESS:
 US-09-332-595-10
 RESULT 8
US-09-332-595-10
 8
 셤
 ઠે
 PAPELICANT: BLACK, Amelia
APPLICANT: BLACK, Amelia
APPLICANT: BLACK, Amelia
APPLICANT: PADLAN, Eduardo A.
APPLICANT: PADLAN, Eduardo A.
APPLICANT: PADLAN, Eduardo A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
NUMBER OF ESCURNES: 28
CORRESSEE: BLACK, ADAMESS:
ADDRESSEE: BLACK, ADAMESS:
ADDRESSEE: BLACK, ADAMESS:
ADDRESSEE: BLACK, ADAMESS:
ADDRESSEE: BLACK, ADAMESS:
COMPUTER: VIzginia
STRATE: VIzginia
COMPUTER: IBM PC Compatable
COMPUTER: IBM PC Compatable
COMPUTER: IBM PC Compatable
COMPUTER: BLOCK OF COMPATABLE
COMPUTER: BRADABLE FORM:
ADDICATION NUMBER: US/08/554,340
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/554,340
FILING DATE:
FRIENCE/CONCET NUMBER: 012712-127
TELECOMMUTICATION NUMBER: 012712-127
 1 DIQMIQSPSTLSASVGDRVTITCWYQQKPGBAPKVLIYGVPSRFSGSGSGTEFTLTISSL 00
 1 DIOMIQSPASLSASVGDRVIIICWYLQKPGKSPQ-LIYGVPSRFSGSGSGTDFSFIISSL
 Query Match

86.2%; Score 358.5; DB 3; Length 80;

Best Local Similarity 85.0%; Pred. No. 1e-27;

Matches 68; Conservative 8; Mismatches 3; Indels
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
 Sequence 10, Application US/08925339
Patent No. 6440418
 79
 60 OPEDFATYYCFGOGTKLEIK
 80 amino acids
 , MOLECULE TYPE: protein US-08-925-339-10
 single
 / MOLECULE TYPE: protein US-08-554-840-10
 linear
 RESULT 7
US-08-925-339-10
 엄
 ઠે
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GENERAL INFORMATION:

APPLICANT: BLACK, Amelia

APPLICANT: HANNA, Nabil

APPLICANT: FANNA, Nabil

APPLICANT: PADLAN, Eduardo A.

APPLICANT: PADLAN, Roland A.

TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,

TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF NUMBER OF SEQUENCES: 28
 1 DIOMIQSPASISASVGDRVIIICMYLOKPGKSPQ-LIYGVPSRFSGSGSGTDFSFIISSL 59
 1 DIQMIQSPSTLSASVGDRVTITCWYQQKPGBAPKVLIYGVPSRFSGSGSGTEFTLISSL
 1 DIOMIQSPASUSASVGDRVIIICMYLQKPGKSPQ-LIYGVPSRFSGSGSGTDFSFTISSL
 1 DIQMIQSPSTLSASVGDRVTITCWYQQKPGEAPKVLIYGVPSRFSGSGSGTEFTLISSL
 Gaps
 .5; DB 4; Length 80; 1e-27;
Length 80;
 Indels
 3; Indels
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRETY APPLICATION DATA: APPLICATION NUMBER: US/09/332,595
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria STRXE: Virginia
COUNTRY: United States
ZIP: 22213-1404
```

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US/09/332,595
 Sequence 12, Application US/09332595
Patent No. 6506383
GENERAL INFORMATION;
 60 QPEDFATYYCFGQGTKLEIK 79
 61 <u>OPEDFADÝFCFGGGTKLEÍK</u> 80
 Query Match
Best Local Similarity 85.0%;
 LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS: single
 CURRENT APPLICATION DATA: APPLICATION NUMBER: US
 68; Conservative
 TOPOLOGY: linear
MOLECULE TYPE: protein
 CLASSIFICATION
 US-09-332-595-12
 US-08-925-339-12
 Matches
 δ
 셤
 ઠે
 Sequence 12, Application US/08925339
Patent No. 6440418
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabil
APPLICANT: BADLAN, Redardo A.
APPLICANT: PADLAN, Redardo A.
TITLE OF INVENTION: HUMANIZAD ANTIBODIES TO HUMAN gp39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
 Parent No. 6001358
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Mabil
APPLICANT: PADLAN, Eduardo A.
APPLICANT: PADLAN, Eduardo A.
APPLICANT: HUMAN, POLINA, EDUAN A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN 9939,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNE, DORNES.
 9
 1 DIQMTQSPASLSASVGDRVTITCWYLQKPGKSPQ-LIYGVPSRFSGSGSGTDFSFTISSL
 1 DIVMTQSPSFLSASVGDRVTITCMYQQXPGKSPXLLIYGVPDRFSGSGSGTDFTLTISSL
 Length 80;
 Indels
 84.0%; Score 349.5; DB 3;
85.0%; Pred. No. 7.3e-27;
vative 4; Mismatches 7;
 3: Burns, Doane, Swecker & Mathis P.O. Box 1404
 E: Burns, Doane, Swecker & Mathis
P.O. Box 1404
 Seguence 12, Application US/08554840
 60 OPEDFATYYCFGQGTKLEIK 79
 OPEDFADYFCFGGGTKLEIK BO
 TELEPAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 Query Match
Best Local Similarity 85.0°
 STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
 , MOLECULE TYPE: protein US-08-554-840-12
 CITY: Alexandria STATE: Virginia
 linear
 amino acid
 STRANDEDNESS:
 RESULT 10
US-08-925-339-12
RESULT 9
US-08-554-840-12
 g
```

```
APPLICANT: BLACK, Amelia
APPLICANT: BLACK, Amelia
APPLICANT: BLACK, Amelia
APPLICANT: BLACK, Amelia
APPLICANT: BADLAN, Reduand A.
APPLICANT: PADLAN, Reduand A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 28
CORRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: P.O. Box 1404
CITY: Alexandria
STATE: P.O. Box 1404
COUNTRY: United States
ZIP: 22231-31404
COUNTRY: United States
COUNTRY: Ploppy disk
 1 DIQMIQSPASISASVGDRVIITCWYLOKPGKSPQ-LIYGVPSRFSGSGSGIDFSFTISSL 59
 1 DIVMTÖSPSFLSASVGDRVTITCMYQQKPGKSPKLLIYGVPDRFSGSGSGTDFTLTISSL 60
 Gaps
 ٦,
 Score 349.5; DB 4; Length 80; Pred. No. 7.3e-27; A; Mismatches 7; Indels
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM
MEDIUM TYPE: FOLPOPY disk
COMPUTER READABLE FORM
MEDIUM TYPE: FOLPOPY disk
COMPUTER: IBM PC COMPATIBLE
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,339
FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/554,840
FILING DATE: 07-NOV-1995
ATPONEY AGENT INFORMATION:
NAME: TESERNCE/POCKET NUMBER: 35,030
REFTRATION NUMBER: 35,030
REFTRATIO
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATIS: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30.
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Gaps

19;

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1 DIQMIQSPASLSASVGDRVTITC-----WYLQKPGKSPQ-LIY-----GVPS 41
 1 DIOMIQSPSSLSASVGDRVITICRASENIYSNLAWYQQKPGKAPKLLIYAATYLADGVPS
 DB 3; Length 98;
 Length 98;
 Score 345.5; DB 2; Length 9 Pred. No. 2.2e-26; 6; Mismatches 2; Indels
 | Sequence 87. Application US/09205231 | Sequence 87. Application US/09205231 | Patent No. 6121423 | Patent No. 6121423 | Applicant: TSUCHIYA, Masayuki APPLICANT: SATO, Koh APPLICANT: HTATA, Yulchi TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN TITLE OF INVENTION: INTERLEUKIN-6 | NUMBER OF SEQUENCES: 91 | CORRESPONDENCE ADDRESS: ADDRESSE: FOley & Lardner | CORRESSE: Foley & Lardner | CORRESSE | CORRE
 COUNTRY: USA
COUNTRY: USA
CONTUTER: 20007-5109
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/205,231
FILING DATE:
 42 RFSGSGSGTDFSFTISSLOPEDFATYYCFGQGTKLEIK 79
 61 RFSGSGSGTDYTFTISSLQPEDIATYYCFGQGTKVEIK 98
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/553,501
FILING DATE: 20-FRB-1996
APPLICATION NUMBER: WO PCT/JP94/00859
FILING DATE: 30-MAY-1994
FILING DATE: 30-MAY-1894
APPLICATION DATA:
APPLICATION NUMBER: JP 5-129787
 AGENT INFORMANT.
WEGNER, Harold C.
WIMBER: 25,258
 STREET: FOLDY & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C. COUNTRY: USA
 83.1%; Score 345.5;
 APPLICATION NUMBER: JP 5-129787
FILING DATE: 31-MAY-1993
ALTORNEX/AGENT INFORMATION:
 RECISTRATION NUMBER: 25,256
REFERENCE/DOCKET NUMBER: 53
TELECOMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
 87:
 Query Match
Best Local Similarity 72.4%;
Matches 71; Conservative
 TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGIH: 98 aming acids
 INFORMATION FOR SEQ ID NO:
 single
 TYPE: amino acid
STRANDEDNESS: sir
 TYPE: amino acid
STRANDEDNESS: si
 linear
 ;
TOPOLOGY:
US-08-553-501A-87
 US-09-205-231-87
 US-09-205-231-87
 Query Match
 g
 1 DIQMIQSPASLSASVGDRVTITCWYLQKPGKSPQ-LIYGVPSRFSGSGSGTDFSFTISSL
 1 DIVMTQSPSFLSASVGDRVTITCMYQQKPGKSPKLLIYGVPDRFSGSGSGTDFTLTISSL
 Score 349.5; DB 4; Length 80; Pred. No. 7.3e-27;
 Sequence 87, Application US/08553501A
Patent No. 5856135
GENERAL INFORMATION:
APPLICANT: SATO, Koh
APPLICANT: HIRATA, Yuichi
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSES: FOLEY & Lardner
 Indels
 CORRESPONDENCES:
ADDRESSER: Folgy & Lardner
STREET: 3000 K Street, N.W., Suite 500
STATE: D.C.
COUNTRY: USA
ZIP: 2000-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,501A
FILING DATE: 20-FEB-1996
CLASSTEICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/00859
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/00859
PRIOR DATE: 30-MAY-1994
PRILING DATE: 31-MAY-1994
PRILING
 ; bc.
1.3e-27;
7;
 REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/177/AAOK
ELECOMMUNICATION INFORMATION:
 4; Mismatches
 ATTORNEY DATE:
ATTORNEY JAKET INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REPERENCE/DOCKET NUMBER: 012712-127
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/554,840
FILING DATE:
 60 OPEDFATYYCFGQGTKLEIK 79
 61 OPEDPADYFCFGGGTKLEIK 80
 Query Match
Best Local Similarity 85.0%;
Matches 68; Conservative
 TYPE: amino acid
STRANDEDNESS: single
 TOPOLOGY: linear MOLECULE TYPE: protein
 US-08-553-501A-87
 US-09-332-595-12
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us-09-990-586-79.rai

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Gaps
 Score 337.5; DB 2; Length 110;
Pred. No. 1.4e-25;
4; Mismatches 2; Indels 27;
 65 FSGSGSGTDFTLTISSLQPEDFATYYCQQWKSIPLTFGQGTKLEIK 110
 43 FSGSGSGTDFSFTISSLQPEDFATYYC-----FGQGTKLEIK 79
 ----MATÖKEGKSEÖ-LIX-
 GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GALILAT: GALIATION,
GALIATION:
GALIATE OF INVENTION:
ICAM-RELATED PROTEIN
NUMBER OF SEQUENCES:
GONUTES:
GONUTRY:
GONUTRY
 P-41,337
ER: 27866/32760
 US-08-483-389-96; Sequence 96, Application US/08483389; Patent No. 5811517
 DIOMTOSPASLSASVGDRVTITC-
 NAME: Suh, Young J.
REGISTRATUON NUMBER: 9-41,3
REFERENCE/DOCKET NUMBER: 2
TELECOMMUNICATION INFORMATION
 Query Match
Best Local Similarity 68.9%;
Matches 73; Conservative
 TELEFAX: (312) 474-0448
TELEX: (312) 474-6600
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
 : 110 amino acids
amino acid
3Y: linear
 MOLECULE TYPE: protein
 US-08-483-389-96
 ઠે
 d
 g
 8
 1 DIQMIQSPSSLSASVGDRVIITCRASENIYSNLAWYQQKPGKAPKLLIYAATYLADGVPS 60
 1 DIQMTQSPASLSASVGDRVTITC-----GVPS
 Gaps
 Gaps
 27;
 19;
 81.1%; Score 337.5; DB 1; Length 110; 68.9%; Pred. No. 1.4e-25; Indels 27; ive 4; Mismatches 2; Indels 27;
 Pred. No. 2.2e-26;
6; Mismatches 2; Indels
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
 APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OSPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,882
FLING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
APPLICATION NUMBER: US 08/286,754
 61 RFSGSGSGTDYTFTISSLQPEDIATYYCFGQGTKVEIK 98
 42 RESGSGSGTDFSFTISSLQPEDFATYYCFGQGTKLEIK 79
 APPLICATION NUMBER: US 08/102,852
PRILING DATE: 05-AUG-1993
PRICR APPLICATION NUMBER: US 08/102,852
PRICR APPLICATION NUMBER: US 08/009,266
PILING DATE: 22-OAM-1993
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/899,724
PILING DATE: 26-MAY-1992
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
PILING DATE: 27-DAN-1992
PRICR APPLICATION NUMBER: US 07/827,689
PILING DATE: 27-DAN-1992
PRICR APPLICATION NUMBER: US 07/827,689
 Sequence 96, Application US/08482882
Patent No. 5773218
GENERAL INFORMATION:
 REFERENCE/DOCKET NUMBER: 32178
ELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
 72.48;
 110 amino acids
amino acid
Best Local Similarity 72.4%
Matches 71; Conservative
 TELEX: 25-3856
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 110 amino acid
 Query Match
Best Local Similarity 68.9
Matches 73; Conservative
 MOLECULE TYPE: protein
 ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 CITY: Chicago
STATE: Illinois
COUNTRY: USA
 US-08-482-882-96
 US-08-482-882-96
```

Tue Jan 13 13:22:01 2004

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Search completed: January 13, 2004, 12:46:32 Job time: 7.83057 secs

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Query Match
Best Local Similarity
 RESULT 2
S37483
 RESULT 1
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 8
 Ig heavy chain pre Ig gamma -2a chain Ig heavy chain V r Ig gamma chain - m Ig gamma -2a chain Ig heavy chain V r ' Search time 6.30655 Seconds
(without alignments)
1326.664 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 1 QIQLVQSGGELVKPGASVRV.....DTAVYFCARWGQGTTVTVSS 87
 Description
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 283308 segs, 96168682 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 protein search, using sw model
 January 13, 2004, 12:22:35
 PC4402
S36265
F30502
C30560
S20640
 PH0960
 S53751
PH0958
MHMS18
 A54378
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 $21810
$38950
$40295
 H32513
B22769
JL0076
 855542
 2H0959
 538717
 50024
 PH0961
 71,0077
 length: 0
length: 2000000000
 US-09-990-586-90
 Query
Match Length DB
 Copyright
 PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
 sed
 Title:
Perfect score:
 Scoring table:
 Score
 OM protein
 Minimum DB
Maximum DB
 Sequence:
 Searched:
 Database
 Run on:
 Result
 No.
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| 30 330.5 73.8 120 2 PH0962<br>32 330.5 73.8 128 2 PH0952<br>33 330.5 73.8 128 2 PH0954<br>34 329.5 73.5 137 1 G2MS43<br>35 73.5 137 1 G2MS43<br>35 73.5 137 1 G2MS43<br>37 73.4 117 1 MHMSJS<br>329 73.4 117 1 MHMSJS<br>40 329 73.4 127 2 PH0955<br>40 329 73.4 127 2 PH0955<br>41 328 73.2 119 2 S20446<br>42 328 73.2 120 2 S2046<br>44 328 73.2 136 2 PL0208<br>45 327.5 73.1 120 2 P20208 |       | chain |       | _     |       | heavy chain | heavy | heavy |      | heavy | heavy | heavy | heavy | heavy | Ig heavy chain V r |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------|-------|-------|-------|-------|-------------|-------|-------|------|-------|-------|-------|-------|-------|--------------------|
| 330.5 73.8 128<br>330.5 73.8 128<br>320.5 73.8 138<br>229.5 73.7 133<br>329 73.4 117<br>329 73.4 117<br>329 73.4 117<br>329 73.4 117<br>329 73.4 121<br>329 73.4 121<br>329 73.5 119<br>328 73.2 123<br>328 73.2 123                                                                                                                                                                           |       |       |       |       |       |             |       |       |      |       |       |       |       |       | -                  |
| 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3                                                                                                                                                                                                                                                                                                                                                          |       |       |       |       | •     |             |       |       |      |       |       |       |       |       |                    |
|                                                                                                                                                                                                                                                                                                                                                                                                | 73.8  | 73.8  | 73.8  | 73.5  | 73.5  | 73.4        | 73.4  | 73.4  | 73.4 | 73.4  | 73.2  | 73.2  | 73.2  | 73.2  | 73.1               |
| ろうろうろうろう ちょう よみ よみ なら ひころう よら でっぱい しょえき よら できらい しょえき よら                                                                                                                                                                                                                                                                                                                                        | 330.5 | 330.5 | 330.5 | 329.5 | 329.5 | 329         | 329   | 329   | 329  | 329   | 328   | 328   | 328   | 328   | 327.5              |
|                                                                                                                                                                                                                                                                                                                                                                                                | 30    | 31    | m r   | υ (c) | 35    | 36          | 37    | 38    | 39   | 40    | 41    | 42    | 43    | 44    | 45                 |

```
A34672
Ig heavy chain precursor V region (VMU-3.2) - mouse (fragment)
Cjspecies: Mus musculus (house mouse)
Cjspecies: Mus musculus (house mouse)
Cjspecies: Mus musculus (house mouse)
Cjspecies: As a musculus (house mouse)
Cjaccession: A24672
R;Winter, E; Radbruch, A.; Krawinkel, U.
EMBO J. 4, 2861-2867, 1985
A;Reference number: A91022; MUID:86055722; PMID:2998759
A;Rolecule type: DNA
A;Residues: 1-119 < WIN.
A;Crossreficues: GB:X03088; NID:952378; PIDN:CAA26881.1; PID:9773578
A;Rolecule type: Musungolobulin to region immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: hetrotetramer; immunoglobulin homology cikeywords: hetrotetramer; immunoglobulin homology ciMC-3.2 #status predicted <MAT>
F;4-119/Product: Ig heavy chain V region; VMU-3.2 #status predicted <MAT>
 43
 63
 Ig gamma-2a chain - mouse
C;Species: Mus musculus (house mouse)
C;Dete: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37483
R;Ducancel, F.F.D.
 4 QVQLQQSGPELVKPGASVKISCKASGYAFSSSWMNWVKQRPGKGLEWIGRIYPGDGDTNY
 64 NGKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARDYYGSDYWGQGTTLTVSS 119
 A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253 CS.Superfamily: immunoglobulin C region; immunoglobulin cycycycas: immunoglobulin cycycycas: immunoglobulin homology cixeywords: immunoglobulin homology <IMM>
 Gaps
 44 -----GKATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS 87
 29;
 Length 119;
 Length 469;
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI
 Indels
 77.1%; Score 345.5; DB 2; 62.1%; Pred. No. 5.4e-27; rative 10; Mismatches 5;
 76.7%; Score 343.5; DB 2; 60.8%; Pred. No. 3.3e-26;
 submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Accession: S37483
A;Atatus: preliminary
A;Molecule type: mRNA
A;Residues: 1-469 <DUC>
ALIGNMENTS
 Query Match
Best Local Similarity 62.1%
Matches 72; Conservative
```

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Ig heavy chain V region pe2 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 2.7-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: 855542
R;Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
A;Moi. Biol. 247, 932-946, 1995
A;Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies usin utations in the variable region genes.
A;Reference number: 855528; MUID:95239763; PMID:7536850
 C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C.Speciession: PR0961
C.Speciession: PR0961
C.Speciession: PR0961
D. Exp. Med. 175, 983-991, 1992
A.Titlle: Svidence for somatic selection of natural autoantibodies.
A.Reference number: PR0952; MUID:92202880; PMID:1552291
 A/Cross-references: EMBL:X82581; NID:9854302; PIDN:CAA57917.1; PID:9854303 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P:14-97/Domain: immunoglobulin homology <IMM>
 61 EKFKSKATLITVDKSSSTAYMQLSSLTSEDSAVYYCTRGVVASMDYWGQGTIVTVSS 116
 61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGYYYYYGMDVWGQGTTVTVSS
 Gaps
 Gaps
 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS 87
 32;
 30;
 Length 116;
 C, Superfamily: immunoglobulin V region; immunoglobulin homology C, Keywords: heterotetramer; immunoglobulin E;1-30, Region: framework F;15-98, Domain: immunoglobulin homology < IMM> F;15-98, Domain: immunoglobulin homology < IMM> F;31-35, Region: complementarity-determining 1
 1 QIQLVQSGGELVKPGASVRVSCKASG----YSFTWVRQSPGKGLEWI
 2 IQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG-
 Indels
 Indels
 Score 337; DB 2; Le
Pred. No. 3.7e-26;
 (g heavy chain V region (G6+ T-L33) - human (fragment)
 75.2%; Score 337; DB 2; 1
60.3%; Pred. No. 3.6e-26;
tive 11; Mismatches 5;
 13; Mismatches
 F;68-98/Region: framework 3
F;99-107/Region: complementarity-determining 3
 --67/Region: complementarity-determining
3-98/Region: framework 3
 A;Status: nucleic acid sequence not shown A;Molecule type: DNA A;Residues: 1-119 <MAR>
 75.2%;
 Query Match
Best Local Similarity 60...
Best T0; Conservative
 69; Conservative
 F;36-50/Region: framework
 Local Similarity
 A;Residues: 1-116 <BOE>
 A;Status: preliminary A;Molecule type: mRNA
 A, Accession: 855542
 Query Match
 Best Loc
Matches
 RESULT
S41394
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 Ig heavy chain precursor V region (anti-phenyloxazolone, 18C10) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 3.1-Dec-1931 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C;Accession: JL0076
R;Kaartinen, M.; Rocca-Serra, J.; Maekelae, O.
Mol. Immunol. 25, 859-865, 1988
Mol. Immunol. 25, 859-865, 1988
A;Title: Combinatorial association of V genes: one VH gene codes for three non-cross-real A;Reference number: JL0076; MulD:89096973; PMID:3211160
A;Accession: JL0076; MulD:89096973; PMID:3211160
 RESULT 7
182769
19 Absorpty chain V region (B1-8.VI/V2) - mouse (tentative sequence)
19 Absorpty chain V region (B1-8.VI/V2) - mouse (tentative sequence)
2, Species: Mus musculus (house mouse)
2, Species: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996
C, Accession R. 1 Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
BMBO J. 1, 635-640, 1982
A;Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between A;Reference number: A90971; MUID:84236026; PMID:7188353
 A, Molecule type: protein
A, Residues: 1-120 <DLD.
A, Note: the sequences of two spontaneously arising somatic variants, B1-8.V1 and B1-8.V2
A, Note: peptides and unsequenced residues were positioned by homology with the B1-8 seque; Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: heterotetramer; immunoglobulin
P;15-98/Domain: immunoglobulin homology <IMM>
 ë
 'n
 120
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 87
 20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 79
 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARKNYGSSFDYWGQGTTLTVSS 137
---WGOGTTVTVSS 87
 61 NQKFKGKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDYYGSSYFDYWGQGTTLTVSS
 80 NEKFKSKATLITVDKPSSTAYMQLSSLTSEDSAVYYCAREGPAGDYWGQGTTLITVSS 135
 1 QVQLQQPGABLVKPGASVKVSCKASGYTFTSYWMHWVKQRPGQGLEWIGRIHPSDSDTNY
 Gaps
 Gaps
 45 -----KATLIVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTTVTVSS 87
 A.Cross-references: GB:A27788; NID:g195851; PIDN:AAA38441.1; PID:g195852 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin C; Keywords: heterotetramer; immunoglobulin F;1-19/Domain: signal sequence #status predicted <SIG>F;20-441/Product: Ig heavy chain #status predicted <MAT>F;34-117/Domain: immunoglobulin homology <IPM>F;50-54/Region: complementarity-determining 1 F;69-85/Region: complementarity-determining 2 F;123-135/Region: Oz segment
 33,
 29;
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWI----
 Length 141;
 Length 120;
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWIG
 Indels
 Indels
 ; Score 337.5; DB 2;
; Pred. No. 3.3e-26;
10; Mismatches 6;
 75.3%; Score 337.5; DB 2; 60.3%; Pred. No. 3.9e-26; cive 11; Mismatches 6;
 44 ----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-
----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR
 75.3%;
 Query Match
Best Local Similarity 59...
Best Tocal 71; Conservative 1
 Conservative
 Local Similarity
nes 70; Conserva
 A; Molecule type: mRNA
A; Residues: 1-141 < KAA>
 80
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119

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Gaps

35;

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"unward to the control of the contro
 A,Molecule type: DNA
A,Residues: 1.117 <1862>
A,Residues: 1.117 <1862>
A,Residues: 1.107 <1862>
A,Note: the B1-8 mu chain mRNA was cloned from a library of C57BL/6 DNA
A,Note: the 186-2 germline gene was cloned from a library of C57BL/6 DNA
R,Dildrop, R.; Bruggemann, M.; Rádbruch, A.; Rajewsky, K.; Beyreuther, K.
BEMBO J. 1, 635-640, 1982
A,Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between
A,Reference number: A90971; MUID:84236026; PMID:7188353
 A;Molecule type: protein
A;Residues: 20-139 <DIL>
A;Note: the V region of the B1-8 delta chain, derived as a spontaneous class switch var.
of the mu chain
 1-19/Domain: signal sequence #status predicted <SIG>
20-139/Product: Ig kappa chain V region (B1-8) #status experimental <MAT>
34-117/Domain: immunoglobulin homology <IMM>
 44 -----GKATLIVDKSTSTAYMELSSLRSEDTAVYFCAR-------WGQGTTVTV
 1 OVOLVOSGABVKKPGSSVKVSCKASGGTFSSYAISWVRQAPQQGLEWMGGIIPIFGTANY
 A;Cross-references: GB:J00529; NID:g195114; PIDN:AAA38170.1; PID:g195115
A;Accession: B90809
 Query Match 74.9%; Score 335.5; DB 1; Length 139; Best Local Similarity 58.3%; Pred. No. 6e-26; Matches 70; Conservative 11; Mismatches 6; Indels 33
 Length 122;
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWIG-
 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;1-30/Region: framework: immunoglobulin homology < INM**
F;15-98/Domain: immunoglobulin homology < INM**
F;31-35/Region: complementarity-determining 1
F;31-67/Region: framework 2
F;51-67/Region: framework 2
F;68-99/Region: framework 3
 C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immenoglobulin
C;Keywords: hererotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
 1 QIQLVQSGGELVKPGASVRVSCKASG----YSFTWVRQSPGKGLEWI
 Indels
 Score 335.5; DB 2;
Pred. No. 5.3e-26;
 74.9%; Sco...
56.6%; Pred. No. 5...
''ve 13; Mismatches
 F,99-110/Region: complementarity-determining 3
 F;118-124/Region: D segment F;125-139/Region: J segment (JH2)
 Query Match
Best Local Similarity 56.6%
Matches 69, Conservative
 SS 122
 87
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Ig heavy chain V region - mouse
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Accession: 541394
R;Margaritte, C.; Gilbert, D.; Brard, F.; Tron, F.
sibnitteed to the EMBL Data Library, January 1994
A;Description: Structural characterization of an (NZB X NZW)F1 mouse-derived IgM anti-DN A;Reference number: 841393
A;Accession: 841394
A;Accession: 841394
A;Accession: 841394
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <MAR>
A;Residues: 1-120 <MAR>
A;Cross-references: EMBL: 229586; NID: 9452354; PIDN: CAA82703.1; PID: 91334080
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <INMA>
 antibody Fab Jel 103 heavy châin - mouse
C;Species: Mus musculus (house mouse)
C;Dace: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 17-Mar-1999
C;Accession: S5375;
B;Pokkuluri, P.R.; Bouthillier, F.; Li, Y.; Kuderova, A.; Lee, J.; Cygler, M.
J. Mol. Biol. 243, 283-297, 1994
A;Title: Preparation, characterization and crystallization of an antibody Fab fragment
A;Reference number: S53750; MuID:95018269; PMID:7523684
 ñ
 61 NQKFKGKATLTVDKSSSTAYMQFSSLTSEDSAVYYCARRYYGSRVSMDYWQQGTSVTVSS 120
 43
 9
 43
 9
 87
 61 NQKFKGKATLIVDISSSTAYMQLSSLTSEDSAVYYCANLRGYFDYWQQGTTLIVUSS 116
 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 Gaps
 Gaps
 44 ~----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTTVTVSS
 29;
 33;
 14.9%; Score 335.5; DB 2; Length 116; larity 60.3%; Pred. No. 5e-26; Conservative 11; Mismatches 6; Indels 29
 DB 2; Length 120;
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWI
 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI
 5; Indels
 ; Score 336.5; DB 2; Pred. No. 4.1e-26; 12; Mismatches 5;
 75.18;
 Query Match
Best Local Similarity 58.3%
 Similarity
 A.Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-116 <POK>
 70;
 Query Match
Best Local S
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C,Accession: PC4402
R,Suzuki, C.; Ueda, H.; Suzuki, B.; Nagamune, T.
Blochem. 122, 322-329, 1997
A;Title: Construction, bacterial expression, and characterization of hapten-specific sin A;Reference number: PC4402
A;Accession: PC4402
A;Accession: PC4402
A;Accession: PC4402
C;Keywords: fusion protein
 pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein C;Species: synthetic
C;Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998
 220 NEKFKSKATLIVDKPSSTAYMQLSSLTSEDSAVYYCARYDYYGSSYFDYWGQGTTLIVSS 279
 80 NEKFKSKATLIVDKPSSTAYMQLSSLISEDSAVYYCARYDYYGSSYFDYWGQGTTLIVSS 139
 ----- 44
20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 79
 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 Query Match 74.9%; Score 335.5; DB 4; Length 287; Best Local Similarity 58.3%; Pred. No. 1.2e-25; Matches 70; Conservative 11; Mismatches 6; Indels 33; Gaps
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWIG-----
 RESULT 15
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Search completed: January 13, 2004, 12:44:40 Job time : 7.30655 secs

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 January 13, 2004, 12:19:34 ; Search time 3.79913 Seconds (without alignments) 1076.912 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 448
1 QIQLVQSGGELVKPGASVRV.....DTAVYFCARWGQGTTVTVSS 87
 Description
 P06330
P01147
P01146
P01746
P01744
P01744
P01749
P01759
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P01769
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 127863 seqs, 47026705 residues
 SUMMARIES
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MOUSE
HUMAN
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Minimum DB seg length: 0
Maximum DB seg length: 200000000
 US-09-990-586-90
 Query
Match Length DB
 SwissProt_41:*
 Title:
Perfect score:
Sequence:
 279
279
278.5
276.5
271.5
 Scoring table:
 Database :
 Searched:
 Run on:
 Result
No.
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| P01808 mus musculu P01761 homo sapien P01767 homo sapien P06326 homo sapien P01807 mus musculu P01783 mus musculu P01811 mus musculu P01810 mus musculu P01805 rattus norv |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| HV38 MOUSE<br>HV1E HUMAN<br>HV3E HUMAN<br>HV37 MOUSE<br>HV37 MOUSE<br>HV41 MOUSE<br>HV41 MOUSE<br>HV41 HUMAN<br>HV01 RAT<br>HV01 RAT                                                                                                                                                                                                                  |
| аннаннанна                                                                                                                                                                                                                                                                                                                                            |
| 1119<br>1119<br>1119<br>1119<br>1119<br>1119                                                                                                                                                                                                                                                                                                          |
| 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                                 |
| 22 23 22 22 22 22 22 23 24 24 25 25 25 25 25 25 25 25 25 25 25 25 25                                                                                                                                                                                                                                                                                  |
| W M M M M M M M M M M M M M M M M M M M                                                                                                                                                                                                                                                                                                               |

## ALIGNMENTS

| RESULT<br>HV07 M | LT 1<br>MOUSE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                         |            |             |                                    |            |                  |                |                                     |                                                                   |          |
|------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------|------------|-------------|------------------------------------|------------|------------------|----------------|-------------------------------------|-------------------------------------------------------------------|----------|
| Ω.               | HV07 MOUSE S                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | STA                                     | STANDARD;  |             | PRT;                               | 139        | AA.              |                |                                     |                                                                   |          |
| AC<br>C          | P01751; P01                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                         |            | 4000        |                                    |            |                  |                |                                     |                                                                   |          |
| , E              | 21-005-1966                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                         | 150        | tacted.     | ימעי<br>מסמיים מיממים מסמ          | יהמחי      | ā                |                |                                     |                                                                   |          |
| 1 5              | 15-SED-2003                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | (00)                                    | 42,        | Tagt of     | annotation undate)                 | 1100       | ate)             |                |                                     |                                                                   |          |
| DE               | Id heavy ch                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | in V                                    | edior      |             | -8/186-2 precursor                 | recur      | Bor.             |                |                                     |                                                                   |          |
| S                | =                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | SUOW) SI                                | (e)        |             |                                    |            |                  |                |                                     |                                                                   |          |
| S                | Eukaryota; Metazoa;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Metazoa                                 |            | Chordata;   | Craniata; Vertebrata;              | ta; V      | ertebr           |                | Euteleostomi                        | stomi;                                                            |          |
| Ö                | Mammalia; Eutheria;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Sutheria                                |            | Rodentia;   | Sciuro                             | gnath      | i; Mur           | idae;          | Sciurognathi, Muridae, Murinae, Mus | e; Mus.                                                           |          |
| ×o               | NCBI TaxID=10090;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 10000:                                  |            |             |                                    | ,          |                  |                |                                     |                                                                   |          |
| Z.               | [E]                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                         |            |             |                                    |            |                  |                |                                     |                                                                   |          |
| RP               | SEQUENCE FROM N.A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | N.A.                                    |            |             |                                    |            |                  |                |                                     |                                                                   |          |
| RC               | STRAIN=C57BL/6;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 317/6;                                  |            |             |                                    |            |                  |                |                                     |                                                                   |          |
| ž                | MEDLINE=81234548; PubMed=6788376;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 34548;                                  | PubMe      | d=6788      | 376;                               | 1          | •                |                |                                     |                                                                   |          |
| Z                | Bothwell A.L.M.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                         | askir      | Paskind M., | Reth M.,                           | , Ima      | Imanishi-Karı    | Karı T         | :                                   | кајемѕку к.                                                       |          |
| Æ                | Baltimore D.;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                         |            | •           |                                    | -          | •                | 1              |                                     |                                                                   |          |
| RŢ               | "Heavy chain variable region contribution                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | n varia                                 | bler       | egion       | contrib                            | it ion     |                  | e NPD          | to the NPD ramily                   |                                                                   |          |
| R.T              | antibodies: somatic mutation evident in a                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Bomati                                  | C mut      | ation       | evident                            | 다.<br>다    |                  | Za <           | rrapre                              | region.";                                                         |          |
| <u>.</u>         | Cell 24:625                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 5-637 (19                               | 81)        |             |                                    |            | 9                | T. C.          | 4                                   | Odradyn                                                           | 4        |
| Ŋ<br>U           | - I - MISCELI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | ANEOUS                                  | THE        | B1-8 M      | CHAIN                              | MRNA       | MAS C            | LONED          | F KOM                               | MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HIBKIDOWA | M.A      |
| បូ               | MAKING                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ANTIBOD                                 | LEST       | O THE       | HAPTEN                             | (4-HY      | DROXY-           | 3-N-T          | CPHEN                               | MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL) ACEIYL  |          |
| ပ္ပ              | (NPB AN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | (NPB ANTIBODIES)                        | ٠          |             |                                    |            |                  |                |                                     |                                                                   |          |
| ပ္ပ              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 1                                       |            |             |                                    |            |                  |                |                                     |                                                                   |          |
| ပ္ပ              | This SWISS-PROT entry is copyright. It is produced through a collaboration                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | PROT en                                 | try        | s copy      | right.                             | ıt is      | produ            | ced tr         | rough                               | a collab                                                          | oration  |
| ပ္ပ              | between th                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ne Swiss                                | Inst       | itute       | of Biol                            | ntorm      | atics            | and            | ine Er                              | BL outst                                                          | acion -  |
| ខួ               | the European                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | an Bioin                                | forme      | tics I      | nstitut                            | 6)         | here a           | re no          | restr                               | Bioinformatics Institute. There are no restrictions               | on its   |
| ပ္ပ              | use by no                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | non-profit                              | t ir       | nstitut     | institutions as long               | long       | as i             | as its content | tent                                | is in                                                             | n no way |
| ပ္ပ              | modified ar                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | and this statement                      | Btate      | ment i      | is not removed.                    | emove      | d. Us            | age 1          | Usage by and for                    | for com                                                           | mercial  |
| ပ္ပ              | entities requires a license                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | equires                                 | a lic      | ense a      | greemen                            | r (Se      | e http           | .//ww          | v.iBb-8                             | agreement (See http://www.isb-sib.ch/announce/                    | nounce/  |
| ပ္ပ              | or send an email to license@isb-sib.ch)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | email t                                 | 0 110      | cense@i     | sb-sib.                            | ch).       |                  |                |                                     |                                                                   |          |
| ខ្ល              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | -          |             |                                    |            |                  | 1              | -                                   | 1 1 1 1 1 1 1 1 1                                                 |          |
| E C              | EMBL: J0052                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | J00529; AAA38170.1;                     | 8170       | 1, - 1,     |                                    |            |                  |                |                                     |                                                                   |          |
| DR.              | PIR: A90809                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 3; MHMS1                                |            |             |                                    |            |                  |                |                                     |                                                                   |          |
| D.               | PDB: 1A6U:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 27-MAY-                                 | 98         |             |                                    |            |                  |                |                                     |                                                                   |          |
|                  | PDB: 126W: 15-,III,-98                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 15-1111,-                               | 98         |             |                                    |            |                  |                |                                     |                                                                   |          |
|                  | 11107070                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 11200001                                |            | 9411-1      |                                    |            |                  |                |                                     |                                                                   |          |
|                  | Interest ( TENCOLATE) 19 TENCOLATE ( TATANTAL TOPOLOGICAL TOPOLOGICA TOPOLOGICA TOPOLOGICA TOPOLOGICAL TOPOLOGICA TOPOLOGIC | 17,00401                                |            | NEW CI      |                                    |            |                  |                |                                     |                                                                   |          |
|                  | Throughou                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 000000000000000000000000000000000000000 |            |             |                                    |            |                  |                |                                     |                                                                   |          |
| 4 6              | Dfam: DEOO!                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 747. 10.                                | ?'<br>}    |             |                                    |            |                  |                |                                     |                                                                   |          |
|                  | DAMP . END                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 181 1010                                |            |             |                                    |            |                  |                |                                     |                                                                   |          |
|                  | OFFICE TARGET                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 70000                                   | - 0        | 1 2 2 2 2   |                                    |            |                  |                |                                     |                                                                   |          |
|                  | Taminoglobi                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 11:00:00;                               | 1          |             | Signal: 3D-structure               | 1          | 411.40           |                |                                     |                                                                   |          |
|                  | Tumunoa Ton                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 7 , 1111                                | 20.00      | 116.10 11   | יחה לידם                           | 1          | נה               |                |                                     |                                                                   |          |
|                  | SIGNAL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ÷ C                                     | פינ        |             | TE HEAVY CHAIN V REGION B1-8/186-2 | V CHA      | A V NT           | RGTON          | B1-8/1                              | 86-2.                                                             |          |
| 4 E              | NTAMOU                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 200                                     | 4 4        |             | FRAMEWORK-1                        | RK-1.      |                  |                |                                     |                                                                   |          |
| Ē                | DOMATN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 0 5                                     | 5.4        |             | COMPLEMENTARITY - DETERMINING - 1  | ENTAR      | ITY-DE           | TERMI          | NING-1.                             |                                                                   |          |
| <u> </u>         | DOMATN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | n<br>n                                  | 89         |             | FRAMEWORK-2                        | RK-2.      |                  |                |                                     |                                                                   |          |
| Ē                | NTAMOG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 9 6                                     | 000        |             | COMPLEMENTARITY-DETERMINING-2      | ENTAR      | ITY-DE           | TERMIN         | VING-2.                             |                                                                   |          |
| i i              | DOMATN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 9 0                                     | 117        |             | FRAMEWORK-3                        | RK-3.      |                  |                |                                     |                                                                   |          |
| Į.               | DOMAIN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 118                                     | 124        |             | D SEGMENT                          | N.         |                  |                |                                     |                                                                   |          |
| L.               | DOMAIN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 125                                     | 139        |             | JH2 SEG                            | SEGMENT.   |                  |                |                                     |                                                                   |          |
| H                | DISULFID                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 41                                      | . Н        |             | BY SIMI                            | SIMILARITY | Υ.               |                |                                     |                                                                   |          |
| H                | NON TER                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 139                                     | <b>t</b> 1 | 139         |                                    |            |                  |                |                                     |                                                                   |          |
| S                | SEQUENCE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 139 AA;                                 |            | 119 MW;     |                                    | D4FD0      | 1B57DD4FD0C9F465 | CRC64;         |                                     |                                                                   |          |

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heavy chain constant region domains.";
Biochemistry 21:5415-5424(1982).
--- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
--- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
 61 NOKFKGKATLITVDKSSSTAYMQLNSLTSEDSAVXYCARDYDWYFDVWGAGTIVTVSS 117
 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI TaxID=10090;
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 'Complete amino acid sequence of a mouse mu chain: homology among
 MEDLINE-83075344; PubMed=6816276;
Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
Hood L.E.;
 30;
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI----
 IĜ-LIKE.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (COMPLEX)
 73.4%; Score 329; DB 1; Length 117; 59.8%; Pred. No. 9e-31; ive 11; Mismatches 6; Indels 3
QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWIG-
 12983 MW; 3CF8ACE4BE447E41 CRC64;
 -i- SIMILARITY: Contains 1 immunoglobulin-like domain. PIR; A02039; MHMS4B.
HSSP; P01789; JMCP.
InterPro; IPR007110; IG-like.
InterPro; IPR003006; IG_MHC.
InterPro; IPR0030596; IG_V.
 ----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR---
 SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 heavy chain V region U558.

Mus musculus (Mouse).
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Iq heavy chain V region MOPC 104E.

Mus musculus (Mouse).
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 Z
 117
 Pfam; PF0047; 1g; 1.
SMAAR; SM00467; 1g; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Glycoprotein.
DOMAIN
 Local Similarity 59.8 tes 70; Conservative
 STANDARD;
 STANDARD;
 116
96
55
117
 117 1
117 AA;
 NCBI_TaxID=10090;
 HV12 MOUSE
P01756;
 MOUSE
 NON TER
SEQUENCE
 45
 20
 CARBOHYD
 Query Match
 HV13 M
P01757
 MOUSE
 HV12_MOUSE
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 ω
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 'n
 80 NEXFKSKATLIVDKPSSTAYMQLSSLISEDSAVYYCARYDYYGSSYFDYWGQGTTLIVSS 139
 79
 87
 44
 "Heary chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24.625-637(1981).
-!- MISCELLANBOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-------WGQGTTVTVSS
 Gaps
 Gabs
 MEDLINE-81234548; Pubmed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 31;
 33;
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG----
 73.5%; Score 329.5; DB 1; Length 137; larity 57.6%; Pred. No. 9.5e-31; Conservative 11; Mismatches 8; Indels 31.
 Length 139;
 COMPLEMENTARITY-DETERMINING-1
 COMPLEMENTARITY - DETERMINING - 2
 IG HEAVY CHAIN V REGION S43.
FRAMEWORK-1.
 6; Indels
 15200 MW; ADDS881BF44B8EC9 CRC64;
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse)
 137 AA.
 BY SIMILARITY.
 FRAMEWORK-3.
D SEGMENT.
JH2 SEGMENT.
 FRAMEWORK-2
 EMBL; J00539; AAA38172.1; -. PIR; A02038; G2MS43. HSSP; P01810; 2FBJ. InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_W.
 74.9%;
 Query Match
Best Local Similarity be...
Best Local 70; Conservative
 STANDARD;
 9
 (NPB ANTIBODIES)
 137
137 AA;
 Similarity
68; Conserv
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 Baltimore D.;
 MOUSE
 Query Match
Best Local S:
Matches 68
 DISULFID
NON TER
SEQUENCE
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 HV11 MO
 DOMAIN
 DOMAIN
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Gaps

43

us-09-990-586-90.rsp

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Length 118;
 Length 120;
 Indels
 Indels
 -1-SIMILARIY: Contains 1 immunoglobulin-like domain.
HSSP: P01789; IMCP.
InterPro; IPR003106; Ig_like.
InterPro; IPR003596; Ig_WG.
InterPro; IPR003596; Ig_V.
SMART; SM00406; Ig_V.
SMART; SM00406; Ig_V.
Immunoglobulin V region; Hybridome.
DOMAIN
 120 AA; 13307 MW; FF04E4A167B654AF CRC64;
 72.0%; Score 322.5; DB 1; 58.5%; Pred. No. 5.1e-30; ive 9; Mismatches 9;
 71.2%; Score 319; DB 1; I 55.8%; Pred. No. 1.3e-29; iive 12; Mismatches 7;
 RESULT 7

HV50 MOUSE

ID HV450 MOUSE

STANDARD; PRT; 120 AA.

AC R66329;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE 15-JUL-1999 (Rel. 38, Last annotation update)

DE 16-Mus musculus (Mouse).
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region 36-65.
Mus musculus (Mouse).
 120 AA
 Local Similarity 55.89
es 67, Conservative
 Conservative
 STANDARD;
 Query Match
Best Local Similarity
Matches 69; Conserv
 SEGMENT
 MOUSE
 SEQUENCE
 Query Match
 RESULT
 g
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 43
 9
 61 NOKFKGKATLIVDKSSSTAYMQLNSLTSEDSAVYYCARDRYWYFDVWGAGTIVIVSS 117
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI------
 MEDLINE-84182519; PubMed-6201362;
Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
"A V region determinant (idiotope) expressed at high frequency in B
"Imphocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523(1984).
 Gaps
 44 -----GKATLIVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTTVTVSS
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 SEQUENCE.
MEDLINE=80078170; PubMed=6765983;
Schilling J., Clevinger B., Davie J.M., Hood L.;
"Amino acid sequence of homogeneous antibodies to dextran and rearrangements in heavy chain V-region gene segments.";
Nature 283:35-40(1980).
 73.4%; Score 329; DB 1; Length.117; 59.8%; Pred. No. 9e-31; cive 11; Mismatches 6; Indels
 -!- MISCELLANBOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, I WHICH OCCUR IN THE D AND J SEGMENTS.
-!- MISCELLANBOUS: THIS PROTEIN BINDS DEXTRAN.
-!- SIMILARITY: CONTAINS 1 immunoglobulin-like domain.
PIR; A26242; MHNSJS.
FIRSP: POLITS9; INC.
InterPro; IPRO03006; IG_MHC.
InterPro; IPRO03006; IG_MHC.
 12934 MW; 94F7BEE4C762A018 CRC64;
 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;
 01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region AC38 205.12.
Mus musculus (Mouse).
 V SEGMENT.
D SEGMENT.
J SEGMENT.
BY SIMILARITY.
 PIR, A02040; MINGS8.
HSSP; P01789; 1MCP.
InterPro; 1PR007110; 1g-like.
InterPro; 1PR003006; 1g_MHC.
InterPro; 1PR003596; 1g_V.
Pfam; PR0047; 1g; 1.
PROSITE; SM0406; 1Gv; 1.
PROSITE; PS50839; 1G LIKE; 1.
 InterPro; IPR003596; IG_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
 Conservative
 STANDARD;
 118 AA;
 Local Similarity
 NCBI_TaxID=10090
 70;
 HV51 MOUSE
P06330;
 DISULFID
NON TER
SEQUENCE
 NON TER
SEQUENCE
 SEQUENCE
 DISULFID
 Query Match
 RESULT 5
HV51_MOUSE
DT 10-1734N
DT 01-1734N
DT 01-1734N
DT 01-1734N
DT 01-1734N
DT 01-1734N
DT 01-1734N
DE DE DE DE DE
RR MEDLINI
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 Matches
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'n
 61 EKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVYYGGSYYFDYWGQGTTLTVSS 120
 87
 1. BVQLQQSGPELVKPGASVKISCKASGYTFTDYYMNWVKQSHGKSLEWIGDINPNNGGTSY 60
 43
 9
 ---- 43
 61 NQKFKGKATLIVDKSSSATYMELRSLTSEDSAVYYCARGYGYDPFDVWGTGTTVTVSS 118
 1 vologsdaelvragssvrascrasgrrffsyginmvrorpgoglemigyinpgngytryn
 44 ----GKATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 2 IQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWI------
 Gaps
 Gaps
 44 ----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
 34;
31;
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI----
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Local Similarity
 NCBI_TaxID=10090;
 140 S 140
 87 S 87
 HV48 MOUSE
P03980;
 DOMAIN
 NON TER
SEQUENCE
 CHAIN
DOMAIN
NON TER
SEQUENCE
 Query Match
 Query Match
 CHAIN
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 120
 87
 44
 9
 61 NEKFKSKATLTVDKSSSATYMQLSTPTSEDSAVYXCARWDYEGDRYFDVWGTGTTVTVSS
 45 -----KATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------WGOGTTVTVSS
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG------
 Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.,
"A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523 (1984).
BIR, A02037; WHMS15.
HSSP; P01810; 2FBJ.
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1.11_TaxID=10090;
 33;
 71.1%; Score 318.5; DB 1; Length 120; 55.8%; Pred. No. 1.5e-29; Indels 33.
 STRAIN=A/J;
MEDLINE=82152818; PubMed=6801765;
Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
 "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain."; science 216:309-311(1982) -- SIMILARITY: Contains 1 immunoglobulin-like domain.
 13311 MW; 914453F426F09834 CRC64;
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
gheavy chain V region 93G7 precursor.
Mus musculus (Mouse)
 140 AA
 BY SIMILARITY,
 V SEGMENT.
D SEGMENT.
J SEGMENT.
 MEDLINE=84182519; PubMed=6201362;
 InterPro; IPPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003506; Ig_v.
Pfam; PP00047; ig; 1.
PROSITE; PS50835; IG_LKE; 1.
Immunoglobulin V region.
 EMBL; J00493; AAA38128.1;
 67; Conservative
 STANDARD;
 106 1
22
120 1
120 AA;
 PIR; A94264; HVMSG7
HSSP; P01810; 2FBJ.
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 MOUSE
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 Sims J.
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80 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSHYYGGSYDFDYWGQGTPLTVS 139
 79
 20 EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYINY
 44 -----GKATLIVDKSTSTAYMELSSLRSEDTAVYFCAR-------WGQGTTVTVS
 SEQUENCE FROM N.A.
MEDLINE=64248078; PubMed=6429663;
Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
 Gaps
 t
O
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 34;
 from C mu
 IG HEAVY CHAIN V REGION TEPC 1017.
 Length 138;
 COMPLEMENTARITY - DETERMINING - 1.
 Length 140;
 FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
 IG HEAVY CHAIN V REGION 93G7 IG-LIKE.
 70.3%; Score 315; DB 1; Length 14
54.5%; Pred. No. 4.4e-29;
ive 13; Mismatches 8; Indels
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWI
 15576 MW; 748157E4C6907B8E CRC64;
 20 139 IG-LIKE.
140 140
140 AA; 15514 MW; 25A4CBB31DA5CE8 CRC64;
 Tucker P.W.;
"Illegitimate recombination generates a class switch idelication in Ingo-secreting plasmacytoma.";
Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168 (1984).
PIR; A0203; HVMST7.
HSSP; P01810; 2FBU.
InterPro; IPR00110; Ig-like.
InterPro; IPR003206; Ig_NHC.
InterPro; IPR003296; Ig_NHC.
 DB 1;
 23-0CT-1986 (Rel. 02, Created)
23-0CT-1986 (Rel. 02, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
15-UUL-1999 (Rel. 38, Lest annotation update)
Mus musculus (Mouse)
 138 AA
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_W.
Pfam; PR00047; ig; 1.
SMART; SMO646; IGV, 1.
PROSTITE; RESG083; IG_LIKE; 1.
Immunoglobulin V region; Hybridoma; Signal.
 BY SIMILARITY
 Score 311;
 Pfam; PP00047; 1g; 1.
SMART; SM00406; 1gv; 1.
PROSITE; PS50835; 1G LIKE; 1.
Immunoglobulin V region; Signal.
 69.4%;
 66, Conservative
 STANDARD;
 139
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147 AA;
 SEQUENCE OF 20-147
 SEQUENCE FROM N.A.
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 a,
 61 NDNLKGKATLTADTSSSTAYIQLSSLTSEDSAIYHCARGIYYNSSPYFDSWGQGTTLTVS 120
 98
 44
 20 QVQLQQPGAELVKPGASVQLSCKASGHTFINYWIHWVKQRPGQGLBWIGEINPNDGRSNY 79
 80 NEKFKNKATLITVDKSSSTAYMQLSSLIPEEFAVYYCARSDGYYDWFVYWGQGTLVTFSA 138
 43
 9
 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS 87
 ------WGOGTTVTVS
 Zakut R., Cohen J., Givol D.,
Nucleic Acids Res. 94839-4840(1980).
-!- MISCELLANBOUS: THIS SECURNCE WAS TRANSLATED FROM AN MRNA ISOLATED
FROM A WYELOMA THAT SECRETES 1GG2B.
 1 OIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI--------
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----wvRQSPGKGLEWIG-------
 Gaps
 Gaps
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID=10090;
 SEQUENCE FROM N.A.
MEDLINE=81053741; PubMed=6253904;
Zakut R., Cohen J., Givol D.;
"Cloning and sequence of the CDNA corresponding to the variable region of immunoglobulin heavy chain MPC11.";
Nucleic Acids Res. 8:3591-3601(1980).
 34;
 32;
 Match
Local Similarity 52.1%; Pred. No. 5.3e-28;
Les 63; Conservative 14; Mismatches 10; Indels
 Indels
 -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A93708; GVMS11.
HSSP; PO1810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003506; Ig MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig/; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
 121 121
121 AA; 13135 MW; 227AEF3EC56EDOBF CRC64;
 44 -----GKATLIVDKSTSTAYMELSSLRSEDTAVYFCAR---
 Similarity 55.5%; Pred. No. 1.3e-28; 6; Conservative 12; Mismatches 9;
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SED-2003 (Rel. 42, Last annotation update)
119 heavy chain V region MPC 11.
Mus musculus (Mouse).
 147 AA.
 121 AA
 IG-LIKE.
 PRT;
 PRT;
 RESULT 11
HVIC_HUMAN STANDARD; 1
AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
 STANDARD;
 121
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 HV01 MOUSE
P01745;
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 Query Match
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Matches 6
 RESULT 10
HV01_MOUSE
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80 APRFQGRVIMTRDASFSTAYMDLRSLRSDDSAVFYCAKSDPFWSDYYNFDYSYTLDVWGQ 139
 43
 20 QTQLVQSGAEVRKPGASVRVSCKASGYTFIDSYIHWIRQAPGHGLEWVGWINPNSGGTNY 79
 79
 Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.; (In) Bach M.K. (eds.);
Immediate hypersensitivity; modern concepts and developments, pp.1-36, Marcel Dekker, New York (1978).
 Gaps
 MEDIINE=83065534; PubMed=6815656; Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J., Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J., Conld H.J.; Could H.J.; Coul
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 Marcel Dekker, New York (1978).
-!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA.
 41;
 ch 67.5%; Score 302.5; DB 1; Length 147; I Similarity 50.0%; Pred. No. 1.3e-27; 64; Conservative 13; Mismatches 10; Indels 41
 InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SN00406; IGv; 1.
PR0SITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
SIGNAL
 IG HEAVY CHAIN V-I REGION ND.
 1 QIQLVQSGGELVKPGASVRVSCXASGYSFT-----WVRQSPGKGLEWI
 IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID.
 44 ----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----
 16491 MW; 948F9F72A5366C20 CRC64;
 -!- SIMILARITY: Contains 1 immunoglobulin-like domain
16-OCT-2001 (Rel. 40, Last sequence update)
15-6EP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-I region ND precursor (Fragments).
 T -> V (IN REF. 2).
IH -> HI (IN REF. 2).
VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
 HSSP, P01789; IMCP.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0003823; P:antigen binding activity; NAS.

GO; GO:0005855; P:immune response; NAS.

InterPro; IPR007110; Ig-11ke.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003006; Ig_WHC.
 RESULT 12
HV05_MOUSE

ID HV05_MOUSE
STANDARD; PRT; 117 AA.

A P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FRB-2003 (Rel. 41, Last annotation update)
DF IGH-VUSES.
 GITVIVES 147
 80 GTTVTVSS 87
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HSSP; P01810; 2FBJ.
MGD; MGI:96486; IGh-VJSSB.
InterPro; IPR007110; IG-like.
InterPro; IPR003506; IG MHC.
InterPro; IPR003596; IG_V.
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
 EMBL; J00488; AAA38519.1; -. PIR; A02041; HVMS8A.
 Conservative
 STANDARD;
 PIR; A02032; HVMS02.
HSSP; P01810; 2FBJ.
 SEQUENCE FROM N.A.
 Similarity
 Baltimore D.;
 RESULT 14
HV06_MOUSE
ID HV06_MOUSE
AC POL750,9
DT 21-JUL-1986 (1)
 61;
 DOMAIN
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SEQUENCE
 Query Match
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its way muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 44
 20 QVQLQQPGAELVRPGSSVKLSCKASGYTFTSYMMDWVKQRPGQGLEWIGNIYPSDSETHY 79
 "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
 Gaps
 MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Baltimore D.;
 TGH-VDSS8.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteraca; Rodentia; Sciurognathi; Muridae; Musinse; Mus. NCBI_TaxID=10090;
 COLI CATANGO (LAZATION GENERALINE GENE BELONGS TO A SET OF CLOSELY MISCELLANEOUS; THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
 22;
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG----
 65.4%; Score 293; DB 1; Length 117; 60.2%; Pred. No. 1.2e-26; Indels 2; ive 12; Mismatches 5; Indels 2
 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
 COMPLEMENTARITY-DETERMINING-2.
 IG HEAVY CHAIN V REGION 3.
 13016 MW; 427C861C53975EDC CRC64;
 80 NOKFKDKATLIYDKSSSTAYMQLSSLTSEDSAVYXCAR 117
 76
 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last amnotation update)
1g heavy chain V region 108A precursor.
 SIMILARITY.
 SMART; SM00406, IGv; 1.
PROSITE; PS50835, IG_LIKE; 1.
Immunoglobulin V region; Signal.
 HSSP, POISIO, 2FBJ. VJ558.
MGD, MGI:96486, IGh. VJ558.
InterPro; IPR007110, IG-like.
InterPro; IPR00306, IG-MHC.
InterPro; IPR003596, IG-V.
 EMBL; J00536; AAA38605.1; -
 Unc., ...
Best Local Similar.,
w.r.hes 59; Conservative
 STANDARD;
 Pfam; PF00047; ig; 1.
 20
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117 AA;
 PIR; A02031; HVMS3.
 STRAIN=C57BL/6
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P01758;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed, usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
 ..
(7
 20 EVQLQQSGPELVKPGASVKISCKASGYTFIDYNMHWVKQSHGKSLEWIGYIYPYNGGTGY 79
 "Heavy chain variable region contribution to the NPD family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-637(1891).
-1- MISCELLANBOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
 Gaps
 STRAIN-C57BL/6;
MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
 22 :
SEQUENCE FROM N.A.
MEDLINE-81245215; PubMed=6789211;
Givol D., Zakut R., Effron K., Rechavi G., Ram D., Cohen J.B.;
"Diversity of germ-line immunoglobulin VH genes.";
"Divers 292:426-430(1981).
-i* SIMILARITY: Contains 1 immunoglobulin-like domain.
 65.4%; Score 293; DB 1; Length 117; 62.2%; Pred. No. 1.2e-26; ive 9; Mismatches 6; Indels
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG
 IG HEAVY CHAIN V REGION 108A. IG-LIKE.
 117 117
117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;
 80 NOKFKSKATLTVDNSSSTAYMELSSLTSEDSAVYYCAR 117
 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR 76
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
 Ź
 Ig heavy chain V region 102 precursor.
Mus musculus (Mouse).
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Search completed: January 13, 2004, 12:39:26
Job time : 4.79913 secs
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 ..
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 ----- 43
 21 VOLOOPGAELVKPCASVKVSCKASGYTFTSYWMHWVKORPGOGLEWIGRIHPSDSDTNYN 80
 Gaps
 SEGUENCE FROM N.A.
MEDLINE-83144028; PubMed=6298778;
MECHAVI G., Ram D., Glazer L., Zakut R., Givol D.;
"Evolutionary aspects of immunoglobulin heavy chain variable region (VH) gene subgroups.";
 Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 22;
 IG HEAVY CHAIN V-I REGION HG3. IG-LIKE.
 IG HEAVY CHAIN V REGION 102.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
 Length 117,
 FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
PRAMEWORK-3.
BY SIMILARITY.
 2 IQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWI---
 Score 292; DB 1; Length 11
Pred. No. 1.6e-26;
9; Mismatches 5; Indels
 roc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 12867 MW; 740A65DD851FCA8C CRC64;
 QKFKGKATLITVDKSSSTAYMQLSSLTSEDSAVYYCA 116
 HISP, POLT72; 2FB4.
HISP, POLT72; 2FB4.
GO; GO:0005825; F:antiquen binding activity; NAS.
GO; GO:0006825; F:antiquen binding activity; NAS.
GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like
InterPro; IPR003006; Ig-MHC.
THERPRO; IPR003596; Ig-V.
 44 ---- GKATLIVDKSTSTAYMELSSLRSEDTAVYFCA 75
 P01743;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-SEP-2003 (Rel. 42, Last annotation update)
1g heavy chain V-I region HG3 precursor.
 117 AA.
 Pfam, PF00047; ig; 1. 2-
SMARY; SM00406; IGv; 1.
SPSC1TE; PSSC035; IG LIKE; 1.
Immunoglobulin V region; Signal.
 NARET, SM00406, IGv. 1.
PROSITE, PS50835, IG LIKE, 1.
Emmunoglobulin V region, Signal.
 65.2%;
ilarity 62.5%;
Conservative
 EMBL; J00240; AAA52988.1; -.
 STANDARD;
 Homo sapiens (Human)
 A02024; HVHUHG.
 Query Match
Best Local Similarity
Matches 60; Conserv
 HV1B HUMAN
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3
 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFNSYYMHWYRQAPGQGLEWMGIINPSGGSTSY 79
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWI------- 43
 Gaps
 22;
 Length 117;
 Indels
 12946 MW; 2D3F92FC60CD1FE7 CRC64;
 80 AQKFQGRVIMTRDTSTSTVYMELSSLRSEDTAVYYCAR 117
 44 ----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR 76
 65.2%; Score 292; DB 1; L
60.2%; Pred. No. 1.6e-26;
Live 10; Mismatches 7;
 Local Similarity 60.2%
les 59; Conservative
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117 11
117 AA;
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QBvcx7 mus

Q921k1 mus musculu Q920e8 mus musculu

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SEQUENCE FROM N.A.

SEQUENCE STRAIN=CS1BL/6J; TISSUE=Pencreas;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Haza A., Fukunishi Y., Konno H., Adania J., Saito T., Okazaki Y., Golobori T., Sonno H., Kondo S., Yamanaka I.,

Asito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,

Radcta K., Matsuda H.A., Ashburner M., Barakawa T., Saito R.,

Radcta K., Matsuda H.A., Ashburner M., Baralov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fullta M., Maziacelli J., Mombaerts P.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Suzuki H., Toyo-oka K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nurabhiaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Napabhiaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
 "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001)
EMBL; AKO07918; BAB25349.1; --
HSSP; P01842; 7FAB.
 Q9D8L4;
01-JUN-2001 (TrEMBLrel. 17, C;
01-JUN-2001 (TrEMBLrel. 17, L;
01-MR-2003 (TrEMBLrel. 23, L;
1810060009Rik protein.
IGH-1 OR 1810060009RIK.
 PRELIMINARY;
 Mus musculus (Mouse)
 Hayashizaki Y.;
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 448
1 QIQLVQSGGELVKPGASVRV.....DIAVYFCARWGQGTTVTVSS 87
 Description
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0.9224468
 09d814
 Q924r6
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 830525 seqs, 258052604 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 0092400
0092400
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 BLOSUM62
Gapop 10.0 , Gapext 0.5
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 virus:*
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Match Length
 Title:
Perfect score:
 Scoring table:
 Minimum DB E
Maximum DB E
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 Sequence:
 Database
 Run on:
 Result
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Last sequence update) Last annotation update)

Created)

473 AA

ALI GNMENTS

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01-MAR-2003 (TrEMBLrel. 23, Las
V23-D-J-C mu protein (Fragment)
V23-D-J-C MU.
 Pfam; PF00047; ig
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 STRAIN=C57BL/6;
 NON_TER
NON_TER
SEQUENCE
 Query Match
 092404
 RESULT 4
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 8
 20 QVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRPGQGLEWIGKIGPGSGSTYY 79
 80 NEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARSGYDYDWFAYWGQGTLVTVSA 138
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI-------43
 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-------WGQGTTVTVSS 87
 1 OIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWIG------
 Gaps
 Gaps
 Kozono Y., Kozono H., Azuma T.;
Kozono Y., Kozono H., Azuma T.;

"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3 Nitrophenyl) Acetyl (NP).";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

Babels, ABO67783, Bab63268-1;

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003595; Ig_V.

Pfam; PF0047; ig; 1.

SWART; SM00406; IGV; 1.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARWDYWGQGTTLTVSS 112
 87
 25;
 32;
 75.8%; Score 339.5; DB 11; Length 137;
larity 62.5%; Pred. No. 2.8e-30;
Conservative 11; Mismatches 6; Indels 25;
 45 -----KATLIVDKSISTAYMELSELRSEDTAVYFCAR---WGQGTTVTVSS
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 6; Indels
 InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SWART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS502090; IG_MHC; 1.
SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
 137 AA; 15171 MW; 5C38D966DC6A4124 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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PROSITE; PS50835, IG_LIKE; 1.
 nate, mar. 19800110, ig-like.
InterPro; IPR003006; ig_MHC.
InterPro; IPR003596; ig_V.
 PRELIMINARY;
 Query Match
Best Local Similarity
 Mus musculus (Mouse)
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
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1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG------ 44
 61 NEKEKSKATLITVDKSSSTAYMQLSSLTSEDSAVYYCARGWEAMDYWGQGTSVTVSS 117
 Gaps
 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 SEQUENCE FROM N.A.
STRAIN=CSPB_/6;
STRAIN=CSPB_/6;
Kozono Y., Kozono H., Azuma T.;
Kozono Y., Kozono H., Azuma T.;
Moirect Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Mauuration of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NR).";
Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ABG67796; BBA63281.1;
InterPro; IPR003100; Ig_ANC.
InterPro; IPR003306; Ig_MC.
 Kozono Y., Kozono H., Azuma T.,
Kozono Y., Kozono H., Azuma T.,
Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of Bell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl) Agetyl (NR).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ABG69913, BAB63929.1;
InterPro; IPR007100, Ig-like.
InterPro; IPR0031006; Ig-MGC.
InterPro; IPR003506; Ig-V.
Pfam; PF00047; ig: I-V.
Pfam; PF00047; ig: I-V.
Pfam; PF00047; ig: I-V.
Pfam; PF000406; Ig-V.
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
WH186.2-D-U-C mu protein (Fragment).
Whis misculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
NCBI_TAXID=10090;
 Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 29;
 75.3%; Score 337.5; DB 11; Length 141; larity 60.3%; Pred. No. 4.9e-30; Conservative 11; Mismatches 6; Indels 29;
 Length 142;
 5; Indels
 141 141
141 AA; 15561 MW; DDD80482D66B76A0 CRC64;
 142 AA; 15622 MW; 24A265CE4EA4318B CRC64;
 / Match
Local Similarity 60.7%; Pred. No. 4.4e-30;
les 71; Conservative 11; Mismatches 5;
 PROSITE, PS50835, IG LIKE, 1.
 PROSITE; PS50835; IG_LIKE; 1
 PRELIMINARY;
 Local Similarity
nes 70; Conserval
(Mouse)
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Created) Last sequence update)

Q924Q1; 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,

PRELIMINARY;

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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
 EMBL, AB067799, BAB63275,1; -.
InterPro; IPR007110; IG-11ke.
InterPro; IPR00306; IG-NHC.
InterPro; IPR003596; IG-V.
SMART, SM00406; IGV; 1.
PR091TE; PS50835; IG_LIKE; 1.
 58.3%;
 Query Match
Best Local Similarity 58.3%
Matches 70; Conservative
 Best Local Similarity 59.3%
Matches 70; Conservative
 145 1
145 AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 NON TER
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Q924RB;
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Q924R8
ID Q924I
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 61 NEKFKSKATILTVDKFPSSTAYMQLSSLTSEDSAVYYCARDDYGRTFWGQGTTLTVSS 116
 Gaps
 61 NEKFKSKATLIVDKPSSTAYMQLSSLISEDSAVYXCARIYAGDYWGQGTSVIVSS 115
 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTTVTVSS 87
 Nozono Y., Kozono H., Azuma T.;

"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl) Acetyl (NR).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EmBL; ABG67788; BAB63273.1;
InterPro; IPR003006; Ig_MRC.
InterPro; IPR003006; Ig_MRC.
Pfam: PP0047; ig; 1.
SWART; SM00406; IGv; 1.
 Kozono Y., Kozono H., Azuma T., Direct Estimator Affinity by Flow Cytometry Reveals Affinity Maturation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP).";
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRC-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
WH186.2-D-J-C mu protein (Fragment).
Was musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutentais, Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 28;
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWIG----
 Match 75.2%; Score 337; DB 11; Length 140; Local Similarity 60.9%; Pred. No. 5.5e-30; Local 70; Conservative 11; Mismatches 6; Indels 2
 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWIG-
 140 140
140 AA; 15361 MW; 60739B790FC6AF24 CRC64;
 Last sequence update)
Last annotation update)
 01-DEC_2001 (TEMBLrel. 19, Created)
01-DEC-2001 (TEEMBLrel. 19, Last seq
01-MAR-2003 (TEEMBLrel. 23, Last ann
 7H186.2-D-J-C mu protein (Fragment)
 PRELIMINARY;
 PRELIMINARY;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 STRAIN=C57BL/6;
 NON TER
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 Q924R0
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44
 61 NEKFKSKATLIVUKPSSTAYMQLSSLTSEDSAVYYCARWDEDYAMDYWGQGTSVTVSS 118
 TRAIN-CSTEL/6;

A Kozono Y., Kozono H., Azuma T.; filnity by Flow Cytometry Reveals
A Kozono Y., Kozono H., Azuma T.;
T Direct Estimation of Relative Affinity by Flow Cytometry Reveals
IT Direct Estimation of Relative Affinity by Flow Cytometry Reveals
IT Hydroxy-3-Nitrophenyl) Acetyl (NP) ";
Hydroxy-3-Nitrophenyl) Acetyl (NP) ";
C Submitted (Aug-2001) to the EMBL/GenBank/DDBJ databases.

R MBL; ABG67793; BAB65278 1;
R InterPro; IPR003106; Ig-1ike.

InterPro; IPR00306; Ig-W.

InterPro; IPR00306; Ig-W.

DR Pfam; PR0047; ig; I.

RNART; SM0466; IGV; I.

PR RNART; SM0466; IGV; I.
 45 -----KATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG------
 45 -----KATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 Q924Q7 PRELIMINARY; PRT; 145 AA.
Q924Q7;
Q924Q7;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
WH186.2-D-J-C mu protein (Fragment).
Wh186.2-D-J-C mu protein (Fragment).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae;
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG----
 74.9%; Score 335.5; DB 11; Length 143; 59.3%; Pred. No. 8.4e-30; live 11; Mismatches 6; Indels 31;
 74.9%; Score 335.5; DB 11; Length 145; 58.3%; Pred. No. 8.5e-30; ive 11; Mismatches 6; Indels 33;
16141 MW; 55A59A7908B2CD6A CRC64;
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146 AA; 16023 MW; 4B0495991D49159 CRC64;
 Q924Q6;
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01-DEC-2001 (TrEMBLrel. 19, Last seq
 01-MAR-2003 (TrEMBLrel. 23, Last an VH186.2-D-J-C mu protein (Fragment)
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
 70; Conservative
 Conservative
 PRELIMINARY;
 Mus musculus (Mouse)
 145 AA;
 Query Match
Best Local Similarity
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les 70; Conserv
 SECUENCE FROM N.A.
 NCBI_TaxID=10090;
 121 S 121
 87 S 87
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 61 NEKFKSKATLIVDKPSSTAYMQLSSLISEDSAVYYCARSYYGSSLYYFDYWGQGTTLIVS 120
 9
 1 QVQLQQPGABLVKPGASVKLSCKASGYTFTSYMMHWVKQRPGRGLEWIGRIDPNSGGTKY
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWIG-----
 Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Affinity, Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitropheny) Azeryl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

Enterpro; IPR007100; Ig-1ike.
InterPro; IPR003106; Ig-Mtc.
InterPro; IPR00356; Ig-Mtc.
Defen: Defendance of the IPR0596; Ig-V.
 "Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Phytoxy.3-Nittophenyl)Acetyl (NP).";
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 Length 146;
 Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB067781, BAB63266.1; ...
InterPro; IPR003106; Ig-11ke.
InterPro; IPR003506; Ig-V.
Pfom; PF00047; ig; 1.
 146 AA; 16216 MW; 92460F1FDF1B7538 CRC64;
 Last sequence update)
Last annotation update)
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 74.8%; Score 335; DB 11;
57.9%; Pred. No. 9.8e-30;
 11; Mismatches
 01-DEC-2001 (TrEMBLrel 19, Last seq
01-MRA-2003 (TrEMBLrel 23, Last ann
VH186.2-D-J-C mu protein (Fragment)
Mus musculus (Mouse)
 Created)
 VH186.2-D-J-C mu protein (Fragment) Mus musculus (Mouse).
 Kozono Y., Kozono H., Azuma T.; "Direct Estimation of Relative D
 Ffam, PF00047; ig; 1. SMART; SMO0406; IGv; 1. PROSITE; PS50835; IG_LIKE; 1.
 Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
 01-DEC-2001 (TrEMBLrel. 19,
 Local Similarity 57.9 es 70; Conservative
 PRELIMINARY;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 NCBI_TaxID=10090
 STRAIN=C57BL/6;
 121 8 121
 Pfam; PF00047
SMART; SM0040
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61 NEKFKSKATLIVDKPSSTAYMQLSSLTSEDSAVYYCARSTLSHYYAMDYWGQGTSVTVSS 120
 61 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARTFITTVVAPFDYWGGGTTLTVS 120
 9
 45 -----KATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVS
 ----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG------
 Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
VH186.2-D-JC mu protein (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota, Metazoa; Chordata; Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 74.7%; Score 334.5; DB 11; Length 145; 58.3%; Pred. No. 1.1e-29; ive 11; Mismatches 6; Indels 33;
Length 146;
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG-
 IndelB
 Hydroxy-3 "Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB067794; BAB63279.1, -.
InterPro; IPR007110; Ig-like..
InterPro; IPR003066; Ig-WHC.
 145
16011 MW; 9BC0846D40DF97EA CRC64;
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Last annotation update)
74.8%; Score 335; DB 11; 57.9%; Pred. No. 9.8e-30; iive 11; Mismatches 6;
 145 AA
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---WGQGTTVTVSS 87
 145 AA; 16081 MW; ECDB1A135E05B8AA CRC64;
 Q924R4 PRELIMINARY; PRT; 145 AA. Q924R4; 100 CHEST CONTROL CON
 092403;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
VH186.2-J-J-C mu protein (Fragment).
 146 AA
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 PRELIMINARY;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 NCBI_TaxID=10090;
 STRAIN=C57BL/6;
 STRAIN-C57BL/6;
 NON TER
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Q924Q3
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 61 NEKFKSKATLIVDKPSSTAYMQLSSLISEDSAVYYCARSLITTYYAMDYWGQGTSVTVSS 120
 9
 87
 A KOZONO Y., KOZONO H., AZUMBA T.;

KOZONO Y., KOZONO H., AZUMBA T.;

"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
T Affinity Maturation Of B Cell Antigen Receptors in Response to (4-
THYDOXY-3-Witrophenyl) Acetyl (MP).";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; ABR067911 BAR3276.1;

R InterPro; IPR00710; Ig-like.

R InterPro; IPR003506; Ig-W.

R R InterPro; IPR003506; Ig-W.

R R PF0047; ig: 1.

R PROSITE; PS50815; IG-LIKB; 1.

T NON TER 145 145

C SEQUENCE 145 AA; 16001 MW; OF409BB09FA333D2 CRC64;
 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 Gaps
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 Kozono Y., Kozono H., Azuma T.;

"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl) Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

InterPro; IRR007109; 19—11ke.

InterPro; IRR003006; 19—11ke.

InterPro; IRR003006; 19—11ke.

InterPro; IRR003006; 19—11ke.
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
Wus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 33;
 33;
 Match 74.7%; Score 334.5; DB 11; Length 145; Local Similarity 58.3%; Pred. No. 1.1e-29; les 70; Conservative 11; Mismatches 6; Indels 33;
 Query Match

74.7%; Score 334.5; DB 11; Length 145;
Best Local Similarity 58.3%; Pred. No. 1.1e-29;
Matches 70; Conservative 11; Mismatches 6; Indels 33;
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG----
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWIG-
 145 145 145 145 MW; 0162D0A26C746C04 CRC64;
 PRT; 145 AA.
 Pfam; PP60047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
 PRELIMINARY;
 SEQUENCE FROM N.A.
 STRAIN=C57BL/6;
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 61 NEKFKSKATLITVDKPSSTAYMQLSSLTSEDSAVYYCARYDGSSFYAMDYWGQGTSVTVSS 120
 45 -----KATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS B7
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG------
 Query Match 74.7%; Score 334.5; DB 11; Length 145; Best Local Similarity 58.3%; Pred. No. 1.1e-29; Matches 70; Conservative 11; Mismatches 6; Indels 33; Gaps
 Kozono Y., Kozono H., Azuma T.;
"Direct Batimation of Relative Affinity by Flow Cytometry Reveals
"Direct Batimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl) Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EmBL; ABG67785; BAB63270.1;
InterPro; IPR007100; Ig_Nic.
InterPro; IPR003596; Ig_V.
Fran; PR0047; ig_1.
SMART; SM00406; igy, 1.
SMART; SM00406; igy, 1.
 Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Hydroxy.3-Witrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB067797; BAB63282.1;
Interpro; IPR00110; Ig-like.
Interpro; IPR003506; Ig-MC.
Interpro; IPR003596; Ig_W.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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61 NEKFKSKATLITUDKPSSTAYMQLSSLTSEDSAVYXCARSLYDYGDYAMDYWGQGTSVTVS 120
 1 QVQLQQPGABLVKPGASVKLSCKASGYTFTSVWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG------44
 45 -----KATLIVDKSTSTAYMELSSLRSEDTAVYFCAR-------WGQGTTVTVS 86
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWIG-------44
 45 -----KATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS 87
 Query Match 74.4%; Score 333.5; DB 11; Length 143; Best Local Similarity 59.3%; Pred. No. 1.4e-29; Matches 70; Conservative 10; Mismatches 7; Indels 31; Gaps
 Gaps
 Kozono Y., Kozono H., Azuma T.;

**Direct Estimation of Relative Affinity by Flow Cytometry Reveals

**Affinity Maturation of B Cell Antigen Receptors in Response to (4-

**Rydroxy-3-Nitrophenyl)Acetyl (NP).";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

**EmBL; ABRG7795; BAB62280.1; --

InterPro; IPR00110; Ig_-1ike.

InterPro; IPR003006; Ig_-MRC.

InterPro; IPR003065; Ig_-MRC.
 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
01-MR86.2-D-U-C mu procein (Fragment).
Mus musculus (Mouse).
Bukaryota, Metazca; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Muscul TaxID=10090;
 34;
 Query Match 74.6%; Score 334; DB 11; Length 146; Best Local Similarity 57.9%; Pred. No. 1.3e-29; Matches 70; Conservative 11; Mismatches 6; Indels 34
Pfam; PF00047; ig; 1.
SWART; SW00406; IGV; 1.
PROSITE; PS50815; IG_LIKE; 1.
NON TER 1 1 1 1
NON TER 146 146
SEQUENCE 146 AA; 16136 MW; CEABDD6E1955807F CRC64;
 143 AA; 15908 MW; 55A2372870F0D568 CRC64;
 (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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January 13, 2004, 12:18:44; Search time 20.2873 Seconds (without alignments) 680.681 Million cell updates/sec
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
 | SIDB1/gcgdata/genesed/genesedp_emb1/AA1992_DAT:
| SIDB1/gcgdata/genesed_genesedp_emb1/AA1992_DAT:
| SIDB1/gcgdata/genesed_genesedp_emb1/AA1993_DAT:
| SIDB1/gcgdata/genesed_genesedp_emb1/AA1995_DAT:
| SIDB1/gcgdata/genesed/genesedp_emb1/AA1995_DAT:
| SIDB1/gcddata/genesed/genesedp_emb1/AA1996_DAT:
| SIDB1/gcddata/genesed/genesedp_emb1/AA1999_DAT:
| SIDB1/gcddata/genesed/genesedp_emb1/AA1999_DAT:
| SIDB1/gcddata/genesed/genesedp_emb1/AA1999_DAT:
| SIDB1/gcgdata/genesed/genesedp_emb1/AA2000_DAT:
 448
1 QIQLVQSGGELVKPGASVRV......DTAVYFCARWGQGTTVTVSS 87
 1107863
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 /SIDS1/gcgdata/geneseq/geneseqp-embl.
/SIDS1/gcgdata/geneseq/geneseqp-embl.
 Total number of hits satisfying chosen parameters:
 1107863 seqs, 158726573 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 A_Geneseq_19Jun03:*
 seq length: 0
seq length: 200000000
 06-985-066-60-SD
 Title:
Perfect score:
 Scoring table:
 Minimum DB
Maximum DB
 Searched:
 Sequence:
 Database
 Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description                      | Homologous sequenc | Murine humanised M | Humanised HBV pre- | Homologous sequenc | Humanised anti-alp | A heavy chain vari | HuMc3 VH region. | Heavy chain variab | Humanised antibody |
|----------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------------|--------------------|--------------------|
| ΔΙ                               | AAR92991           | ABG74721           | AAB12168           | AAR93003           | AAW84097           | AAB07965           | AAW06442         | AAR28744           | AAY71548           |
| DB                               | 17                 | 24                 | 21                 | 17                 | 20                 | 21                 | 17               | 13                 | 21                 |
| %<br>Query<br>Match Length DB ID | 87                 | 87                 | 115                | 87                 | 117                | 135                | 136              | 121                | 136                |
| *<br>Query<br>Match              | 83.9               | 82.6               | 81.9               | 81.7               | 81.5               | 80.5               | 80.4             | 79.5               | 79.5               |
| Score                            | 376                | 370                | 367                | 366                | 365                | 360.5              | 360              | 356                | 356                |
| Result<br>No.                    |                    | N                  | m                  | 4                  | വ                  | 9                  | 7                | ω                  | Φ                  |

95BP-0201752

27-JUN-1995;

| Humanised anti-Fas | anis     | ≥.       | Variable heavy cha | puc-Rvh-1220d. Sy | Anti-human HM1.24 | Anti-human HM1.24 |          | ъ   | •   | 24 ant | I        | umanised | chain V | chain V | H chain V region v | chain V regi | reshaped | HM1.24 antibody he | Reshaped human AUK | 1220b. | Humanised anti-HM1 | Т   |     | ised | 425 a | anti-EGFR | anti- | sed anti-F | fied (prop) | in SEQ I | Cid      | J        | ent of | ised C   | Amino acid sequenc |  |
|--------------------|----------|----------|--------------------|-------------------|-------------------|-------------------|----------|-----|-----|--------|----------|----------|---------|---------|--------------------|--------------|----------|--------------------|--------------------|--------|--------------------|-----|-----|------|-------|-----------|-------|------------|-------------|----------|----------|----------|--------|----------|--------------------|--|
|                    |          |          |                    |                   |                   |                   |          |     |     |        |          |          |         |         |                    |              |          |                    |                    |        |                    |     |     |      |       |           |       |            |             |          |          |          |        |          |                    |  |
| AAW90935           | ABB74904 | AAR92218 | 769                | 901               | AAW65773          | 77                | AAW62205 | 20  | 77  | N      | AAY02575 | 57       | 548     | 48      | 35                 | 35           | ABG71946 | 29                 | 241                | - 1    | AAW62212           | 10  |     | 20   | 781   | 569       | 93    | 190        | 361         | AAW58510 | AAW49813 | AAR39267 | 981    | AAR39268 | AAW49818           |  |
|                    | 23       |          |                    | 13                | 13                | 19                | 19       | 13  | 20  | 20     | 20       | 20       | 20      | 50      | 23                 | 23           | 24       | 19                 | 18                 | 13     | 13                 | 20  | 20  | 23   | 23    | 23        | 21    | 23         | 14          | 13       | 13       | 14       | 19     | 14       | 19                 |  |
| 470                | 470      | _        | 116                | 135               | 139               | 139               | 139      | m   | m   | m      | C        | 3        | m       | 3       | ന                  | m            | C        | 4                  | н                  | ന      | m                  | m   | 139 | 4    | 121   | 121       | ~     | 470        | Н           | 116      | $\vdash$ | N        | N      | 3        | 3                  |  |
| 79.0               |          |          | Ψ.                 | ·                 | ά.                | w.                | m,       | m.  | w.  | m      | œ.       | w.       | m       | w.      | œ.                 | m.           | m.       | m.                 | w.                 | 'n.    | m.                 | m.  | ന   | m.   | œ.    | m.        | œ.    | ш,         | œ.          | œ.       | œ.       | œ.       | œ,     | ď        | œ.                 |  |
| 10                 | 354      | 53.      | 53.                | 53.               | 53.               | 53.               | 23       | 53. | 53. | 53.    | 53.      | 53.      | 53.     | 53.     | 53.                | 53.          | 53.      | 53.                | 52.                | 52.    | 522                | 52. |     | 52.  | ம     | ഥ         | ഥ     | ம          | 50.         |          | ഗ        | ഗ        | ഗ      | ഗ        | സ                  |  |
| 10                 | 11       | 12       | 13                 | 14                | 15                | 16                | 17       | 18  | 19  | 70     | 21       | 22       | 23      | 24      | 25                 | 56           | 27       | 28                 | 29                 | 30     | 31                 | 32  | 33  | 34   | 35    | 36        | 37    | 38         | 39          | 40       | 41       | 4        | 43     | 44       | 45                 |  |
|                    |          |          |                    |                   |                   |                   |          |     |     |        |          |          |         |         |                    |              |          |                    |                    |        |                    |     |     |      |       |           |       |            |             |          |          |          |        |          |                    |  |

## ALIGNMENTS

RESULT 1

```
IOR-R3; monoclonal antibody, human, mouse; heavy chain; homology; variable region; epidermal growth factor receptor; hybridoma; framework; cloning; computer; algorithm; immunogenicity; site-directed mutagenesis; T-lymphocyte epitope; tertiary structure; point mutation; antibody engineering; protein engineering; humanised antibody; antitumour; cancer; therapy.
 Homologous sequences to antibody IOR-R3 variable region heavy chain.
 6.30
note= "Amino acids involved in tertiary structure"
 /note= "Amino acid involved in tertiary structure"
 Location/Qualifiers
 AAR92991 standard; Protein; 87 AA
 (updated)
(first entry)
 Homo sapiens
 25-MAR-2003
18-MAY-1996
 EP699755-A2
 06-MAR-1996
 AAR92991;
 Key
Region
 Region
AAR92991
```

94CU-0000080

30-JUN-1994;

WPI; 1996-130770/14.

Rodriguez RP,

```
human interleukin (II)-labeta, and binds the same epitope on mature human II-labeta as mouse monoclonal antibody Mu007 or humanized antibody Hu007. The antibody of the invention have antithermatic, antiarthritic, antiantlambatory osteopathic, antiallergic, cerebroprotective, antiantendermatic, immunosuppressive and antibacterial activity and can be used in a vaccine. The antibody is useful for manufacturing a medicament for treating rheumatoid arthritis or useful for manufacturing an edicament for treating altergy, septic or endotoxic shock, septicaemia, stroke, asthma, gatefur versus host disease, crohr's disease, or inflammatory bowel disease. This sequence represents a protein associated with the humanised murine Mu007 antibody described in the disclosure of the
 This invention describes a novel antibody that specifically binds mature
 New IL-1beta antibodies, useful for treating allergy, septic or
endotoxic shock, septicemia, stroke, asthma, graft versus host disease,
Crohn's disease, or inflammatory bowel disease
 1 QIQLVQSGGELVKFGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME
 Humanised HBV pre-S1 antibody HKR127HC(I) heavy chain variable region.
 ;
0
 Tsurushita N;
 Length 87;
 10; Indels
 Humanised antibody; HBV surface antigen pre-51; mouse;
human; hepatitis B; liver cirrhosis; liver cancer.
 82.6%; Score 370; DB 24; 78.2%; Pred. No. 1.6e-27; iive 9; Mismatches 10;
 Manetta JV,
 (KOAD) KOREA ADV INST SCI & TECHNOLOGY. (GREC) KOREA GREEN CROSS CORP.
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 87
 61 LSSLRSEDTAVYYCATWGQGTLVTVSS
 AAB12168 standard; Protein; 115 AA
 Jia AY, Kuhstoss SA,
 Disclosure, Fig 2, 98pp, English.
26-JUL-2001; 2001US-307973P.
14-AUG-2001; 2001US-312278P.
 99WO-KR00699
 (first entry)
 Query Match
Best Local Similarity 78.2
Matches 68; Conservative
 sapiens
 WPI; 2003-248068/24.
 (ELIL) LILLY & CO
 87 AA;
 Chimeric - Homo
Chimeric - Mus s
 WO200031141-A1
 17-JAN-2001
 19-NOV-1999;
 19-NOV-1998;
 02-JUN-2000.
 Bright SW,
Vasquez MJ;
 AAB12168;
 invention
 Sequence
 RESULT 3
 쉱
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 à
 The sequence represents residues from a human immunoglobulin with homology to the heavy chain variable region from monoclonal antibody compounded by a mouse hybridoma. The sequence is partial, and produced by a mouse hybridoma. The sequence is partial, and complementarity determining regions are omitted. The sequence is isolated by comparison of human and mouse immunoglobulins and analysis for T-lymphocyte antigent sequences using a computer calgorithm. Residues not within a complementarity determining region, canonical structure or Vernier zone may be modified to reduce immunogenicity in humans (e.g. in sequence AAR929292). This method, which involves the introduction of only a few point mutations into T-cell epitope coding regions, is generally applicable in humanisation of mouse antibodies. The resulting humanised antibodies may be used e.g. as antitumour agents. They retain the antipen recognition of the original antibody, but are not immunogenic in humans. Cupianal antibody, but are not immunogenic in humans.
 QIQLVQSGGELVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
 1 SYQLVQSGAEVKKPGASVKVSCKASGYTFNWVRQAPGQGLEMMGRVTMTRDTSTSTVXME 60
 Murine; light chain; variable region; antibody; Crohn's disease; human interleukin (IL)-lbeta; antirheumatic; antiarthritic; humanised; antiinflammatory; osteopathic; antiallergic; cerebroprotective; antiasthmatic; immunosuppressive; antibacterial; vaccine; Mu007; rheumatoid arthritis; osteoarthritis; cartilage destruction; allergy; septic shock; endotoxic shock; septicaemia; stroke; asthma; graft versus host disease; inflammatory bowel disease; DP-5.
 0; Gaps
 Identifying interspecies differences in amino acid sequence of Igreal epitopes - by sequence comparison, also humanised antibodies contg. altered T-call epitopes, retaining antigen specificity but not immunogenicity, esp. for tumour treatment
 83.9%; Score 376; DB 17; Length 87; 79.3%; Pred. No. 4.3e-28; ive 10; Mismatches 8; Indels
 Valladares JL, Mateo De Acosta Del Rio CM;
 Murine humanised Mu007-associated protein DP-5.
 LSSLRSEDTAVYYCARWGQGTLVTVSS 87
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 (IMMU-) CENT IMMUNOLOGIA MOLECULAR
 ABG74721 standard; Protein; 87 AA
 Claim 14; Fig 2; 33pp; English.
```

Local Similarity 79.3

ò 유 à g

87 AA;

Sequence Query Match 18-JUL-2002; 2002WO-US21281

WO2003010282-A2

Unidentified

ABG74721 ABG74721 XX AC ABG AC ABG DT 10-XX XX XX XX XX XW MUL KW AUL CW AUL KW AUL CW AUL C

(first entry)

10-MAY-2003

; 0

Gaps

94CU-0000080

```
30-JUN-1994;
 15-MAR-1999
 AAW84097;
 Key
Region
 Region
 Region
 AAW84097
ID AAW8
 RESULT
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•
 Hepatitis B virus (HBV) is responsible for hepatitis infection in humans, which may progress to liver cirrhosis or cancer. One of HBV's surface antigens is pre-Si. Monoclonal antibodies specific for pre-Si antigen may efficiently neutralise HBV. The present invention relates to humanised antibodies specific for HBV surface antigen pre-Si. The humanised antibodies are useful for preventing HBV infection and for treating chronic hepatitis B. The Complementarity Determining Regions of mouse pre-Si antibody KR127 were grafted onto human antibody to produce the humanised antibodies of the present invention. The present sequence is the humanised pre-Si antibody HKR127HC(I) heavy chain variable region (VH). The coding sequence for the present sequence was produced from the coding sequence of the mouse pre-Si antibody VH sequence (AAA62115).
 43
 9
 Homologous sequences to antibody IOR-CEA-1 variable region heavy chain.
 Humanized antibody specific for hepatitis B virus surface antigen pre-S1. containing humanized heavy and light chain regions, useful for preventing hepatitis B virus (HBV) infection and for treating chronic hepatitis B -
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWI------
 1. QVQLVQSGAEVVKPGASVKVSCKASGYAFSSSWMYWVRQAPGQCLEWIGRIYPGDGDTNY
 variable region, framework; cloning; computer; algorithm; immunogenicity; site-directed mutagenesis; Tlymphocyte epitope; tertiary structure; point mutation; antibody engineering; protein engineering; humanised antibody; antitumour; cancer; therapy.
 Gaps
 61 AQKFQGKATLITADKSTSTAYMELSSLRSEDTAVYFCAREYDEAYWGQGTLVIVSS 115
 IOR-CEA-1; monoclonal antibody; human; mouse; heavy chain; homology;
 44 -----GKATLTVDXSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTTVTVSS 87
 /note= "Amino acid involved in tertiary structure"
76
 /note= "Amino acid involved in tertiary structure"
 /note= "Amino acid involved in tertiary structure"
 28;
 Match 81.9%; Score 367; DB 21; Length 115; Local Similarity 67.0%; Pred. No. 3.9e-27; les 77; Conservative 7; Mismatches 3; Indels 2:
 Location/Qualifiers
 AAR93003 standard; Protein; 87 AA.
 Claim 2; Fig 1; 61pp; English.
 95EP-0201752.
 (updated)
(first entry)
 Ryu CJ, Hur
 WPI; 2000-400048/34.
N-PSDB; AAA62118.
 Homo sapiens
 27-JUN-1995;
 25-MAR-2003
18-MAY-1996
 EP699755-A2
 06-MAR-1996
 Seguence
 AAR93003;
 Hong HJ,
 Query Match
 Region
 Region
 Region
 Best Loca
Matches
 RESULT 4
 g
```

```
The sequence represents residues from a human immunoglobulin with homology to the heavy chain variable region from mouse monoclonal antibody IOR-CER-1 (AAR39102). The sequence is partial, and complementarity determining regions are omitted. The sequence is complementarity determining regions are omitted. The sequence is isolated by comparison of human and mouse immunoglobulins and analysis for T-lymphocyte antigenic sequences using a computer algorithm. Residues not within a complementarity determining region, canonical structure or Vernier zone may be modified to reduce immunogenicity in humans (e.g. in sequence AAR93004). This method, which involves the introduction of only a few point mutations into T-cell epitope coding regions, is generally applicable in humanisation of mouse antibodies. The resulting humanised antibodies may be used e.g. as antitumour agents. They retain the antigen recognition of the criginal antibody, but are not immunogenic in humans.

(Updated on 25-MAR-2003 to correct PI field.)
 09
 9
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME
 Gaps
 Identifying interspecies differences in amino acid sequence of Ig T-cell epitopes - by sequence comparison, also humanised antibodies contg. altered T-cell epitopes, retaining antigen specificity but not immunogenicity, esp. for tumour treatment
 engineering;
 Humanised antibody, monoclonal antibody; MAb; antibody engineerin mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis; cancer; metastasis; rheumatoid arthritis; atherosclerosis; angiogenesis; diabetic retinopathy; inflammation; macular degeneration; osteoporosis; Paget's disease; hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
 ö
 Length 87;
 Mateo De Acosta Del Rio CM;
 Indels
 . 6
 Humanised anti-alpha-v beta-3 MAb D12HZHC 1-0 VH
 Query Match
81.7%; Score 366; DB 17;
Best Local Similarity 77.0%; Pred. No. 3.7e-27;
Matches 67; Conservative 12; Mismatches 8;
 87
 87
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS
 LSSLRSEDTAVYYCARWGEGTLVTVSS
 Location/Qualifiers
 AAW84097 standard; Protein; 117 AA
 Claim 22, Fig 9; 33pp; English.
 Valladares JL,
 31..35
/label= CDR1
 CDR2
 50..66
/label= (
99..106
 WPI; 1996-130770/14.
 Sequence 87 AA;
 Rodriquez RP,
 Homo sapiens
Synthetic.
(IMMU-) CENT
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Taylor AH;

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the Ammana) of indicate and anti-human alpha-versity are retained from the murine anti-human alpha-versity are retained. The humanised heavy chain can be expressed in host are retained. The humanised heavy chain can be expressed in host calls using nucleic acid molecules (see AAV17199) of the invention. Humanised DIV is also provided (see AAW41099) of the invention. The humanised antibodies can be used for passive immunotherapy of disorders antibodies can be used for passive immunotherapy of disorders antibodies can be alpha-v beta-3 receptor. e.g. cardiovascular or angionalized lasorders, such as angiogenesis associated with diabetic retinopathy, atherosolerosis and restences, chronic inflammatory disorders, macular degeneration, rheumatoid arthritis and cancer, e.g. solid tunnour metaerasis, and diseases where bone resorption is associated with pathology such as osteoporosis, hyperparathyroidism, paget's disease, hypercalcemia of malignancy,
 61 NQKFKGKATLIVDKSTSTAYMELSSLRSEDTAVYYCARQNYGSFAYWGQGTLVTVSS 117
 44 ----GKATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS 87
 hyperparathyroidism, Paget's disease, hypercalcemia of malignancy, osteolytic lesions produced by bone metastasis, bone loss due to immobilisation or sex hormone deficiency. They can also be used for targeted drug therapy, and for detection and diagnosis.
 New anti alpha v beta 3 vitronectin receptor antibodies - used for
immunotherapeutic treatment of e.g. diabetic retinopathy,
inflammatory disorders, atherosclerosis, restenosis, cancers or
 This is the amino acid sequence of the heavy chain variable region
 (VH) of humanised anti-alpha-v beta-3 vitromectin receptor monoclonal antibody D12HZHC 1-0. It is based on the VH sequence (see AAM84095) of human Kabat subgroup I VH, with complementarity
 1 QIQLVQSGGBLVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI-----
 A heavy chain variable region of humanised 3S1 antibody.
 AAB07965 standard; Protein; 135 AA
 Claim 1; Page 58; 97pp; English
 (SMIK) SMITHKLINE BEECHAM CORP
 /label= CDR3
 98WO-US04987.
 97US-0039609
 (first entry)
 77; Conservative
 Jonak ZL,
 Local Similarity
 WPI; 1999-034590/03.
N-PSDB; AAV71799.
 117 AA;
 Johanson KO,
 14-NOV-2000
 12-MAR-1998;
 12-MAR-1997;
 WO9840488-A1
 AAB07965;
 Sequence
 Query Match
 Matches
 RESULT 6
 AAB07965
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'n
 The present sequence represents the heavy chain variable region of the humanised murine antibody 3D1. The antibody has a binding specificity to B7 molecules. The antibody is used to construct humanised immunoglobulins, which comprise an antigen binding region of non-human origin and a portion of a human immunoglobulin. The humanized diseases, inflammatory derived for treating autoimmune diseases, infectious diseases, inflammatory dermatitis, systemic lupus erythemacosus, diabetes mellitus, insultis, asthma, arthritis, inflammatory benefits, and multiple sclerosis. The immunoglobulins are also useful for treating a transplant recipient or preventing transplant rejection in a transplant recipient, and treating proliferative disease thalassemia and aplastic ansemia), inborn errors of metabolism, congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
 43
 79
systemic lupus erythematosus; diabetes mellitus; insulitis; asthma; arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis; multiple sclerosis; transplant rejection; proliferative disease; leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia; aplastic anaemia; myeloid dysplasia syndrome.
 Humanized immunoglobulin having a binding specificity to B7-1 (derived from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules, modulates immune responses and can therefore treat e.g. autoimmune diseases, infectious diseases -
 20 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTDYAIQWVRQAPQQCLEWIGVINIYYDNTNY
 Gaps
 ----GKAILIVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTTVTVSS 87
 Celniker AC, Collins M, Goldman S;
Rup B, Veldman GM;
 29;
 DB 21, Length 135;
 note= "complementarity determining region 1"
 69.85
/note= "complementarity determining region 2"
 'note= "complementarity determining region 3"
 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWI
 3; Indels
 Score 360.5; DB 2:
Pred. No. 1.9e-26;
 9; Mismatches
 ..19
note= "aignal peptide"
 "mature protein"
 Location/Qualifiers
 Example 3; Fig 2A; 162pp; English.
 Vasquez M, Carreno B,
, Knight A, O'hara D,
 80.5%;
 09-FEB-2000; 2000WO-US03303.
 99US-0249011.
 (GEMY) GENETICS INST INC.
 Local Similarity 64.7
les 75; Conservative
 118..124
 20..135
 note=
 WPI; 2000-524532/47.
N-PSDB; AAA59694.
 WO200047625-A2
 12-FEB-1999;
24-JUN-1999;
 Mus sp.
Homo sapiens.
 17-AUG-2000
 synthetic.
 Sequence
 Gray GS,
 Query Match
 Key
Peptide
 Protein
 Region
 Region
 Region
 CO MS,
 Matches
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Gaps

30;

81.5%; Score 365; DB 20; Length 117; 65.8%; Pred. No. 6.2e-27; ive 7; Mismatches 3; Indels 30

Antibody 3D1, B7 molecule, B7, humanised immunoglobulin, autoimmune disease, infectious disease, inflammatory disorder,

A.

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AAR28744 standard; Protein; 121
 AAR28744;
 Chimeric.
 AAY71548
RESULT 8
 AAR28744
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 윱
 This sequence represents the variable heavy (VH) chain of the humanised murine antibody HuMC3 VH. The MC3 VH sequence was humanised using the burined residue modification technique, where important non-human framework residues are unaffected. The MC3 antibody binds to the BA46 antigen of the human milk fat globule (HMFG). The milk fat globule membrane is derived from the apical surface of the mammalian epithelial cell during lactation, and therefore is a source for breast membrane glycoproteins. The antibody can be used in an in vitro method to detect a HWFG antigen for antigen fragment), and to diagnose the presence of the antigen in a subject. The antibody containing a HWFG antigen. The antibody can also be used to deliver an agent to a target (within a subject sold), containing a HWFG antigen. The antibodies can also be used for diagnosis, prognosis, and therapeutic applications of breast cancer. As the humanised antibodies retain their high affinity binding to the antigen, they are useful for immunodiagnostic and immunotherapeutic applications in humans.
 ë.
 Humanised antibody, variable heavy region, buried residue modification, VH, HuMc3 VH, BA46 antigen, human, milk fat globule, HMFG, lactation, fat globule membrane, murine, mammal, epithelial cell, breast cancer, breast membrane glycoprotein, therapy, immunotherapy.
 80 NQKFQDKATLITVDKSTSTAYMELSSLRSEDTAVYFCARRWRYTMDYWGQGTLVTVSS 136
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWIG------
 -----KATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------MGOGTTVTVSS 87
 20 EVOLVOSGAEVKKPGASVKVSCKASGYSFTGYTMHWVKQSPGMNLEWIGLINPYNGGTVY
 80 NOKFKGKATMTVDKSTSTAYMELSSLRSEDTAVYYCARAAWYMDYWGQGTLVTVSS 135
 Gaps
 Recombinant Mc3 antibody which binds BA46 antigen of HMFG -comprises a modified heavy or light chain variable region, useful in the diagnosis and therapy of breast cancer
 5; Indels 30;
 Query Match 80.4%; Score 360; DB 17; Length 136; Best Local Similarity 65.8%; Pred. No. 2.1e-26; Matches 77; Conservative 5; Mismatches 5; Indels 3
 Do Couto FJR, Peterson JA;
 RES FUND CONTRA COSTA.
 Ā
 AAW06442 standard; Protein; 136
 Claim 13; Fig 18; 91pp; English
 95US-0487598,
94US-0307868,
 95WO-US11683
 (first entry)
 WPI; 1996-179941/18.
 136 AA;
 N-PSDB; AAT42717.
 HuMc3 VH region.
 (CANC-) CANCER
 WO9608565-A2.
 14-SEP-1995;
 17-JUN-1995;
 16-SEP-1994;
 Ceriani RI,
 04-FEB-1997
 Synthetic.
 Seguence
 AAW06442;
 RESULT 7
```

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61 NQKFKGKGTLTVDKSTSTAYMELSSLTSEDTAVYYCARSAFYNNYEYFDVWGQGTTVTVS 120
 This sequence is that of the heavy chain variable domain of a chimeric antibody to an epitope of human tumour necrosis factor. It is also known as hymri. Mouse CDRs were used at positions 26-35 (CDR1), 50-65 (CDR2), and 95-102 (CDR3). In addition mouse residues were used in the frameworks at postions 48, 67, 69, 71, 73, 76, 89, 91, 94 and 108. Comparison of the HTNI mouse and BU human heavy chain residues reveals that these are identical at positions 23, 24, 29, and 78. (Updated on 25-MAR-2003 to correct PN field.)
 1 OIQLVQSGGELVKPGASVRVSCKASGYSFT----wvRQSPGKGLEWI------
 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVS
 monoclonal antibody; humanised; chimeric; CDR; neoplastic therapy; shock; antilymphocyte therapy; endotoxin shock; septic shock; sepsis; cardiovascular shock; tumour necrosis factor alpha; multi-organ failure.
 Recombinant antibody specific for human TNF-alpha - for treatment of shock and immuno:regulatory and inflammatory disorders, also used in diagnosis
 79.5%; Score 356; DB 13; Length 121; 61.2%; Pred. No. 4.5e-26; tive 10; Mismatches 3; Indels 3
 Heavy chain variable domain of gEU humanised CDR grafted Ab
 Emtage JS;
 AAY71548 standard; Protein; 136 AA.
 Bodmer MW,
 Example 1; Fig 1; 57pp; English.
 91WO-GB02300
 90WO-GB02017.
(updated)
(first entry)
 Ouery Match
Best Local Similarity 61.22
Then 74; Conservative
 Adair JR, Athwal DS,
 (CLLT) CELLTECH LTD.
 WPI; 1992-250102/30.
 Sequence 121 AA;
 5 87
 121 S 121
 WO9211383-A1.
 20-DEC-1991;
 21-DEC-1990;
03-MAY-1991;
25-MAR-2003
11-JAN-1993
 09-JUL-1992
 RESULT 9
AAY71548
ID AAY7
XX
AX
AC AAY7
```

```
99WO-US28195
 98US-0110523
 like, Crohn's disease.
 WPI; 2000-412292/35.
 N-PSDB; AAD01348
 Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
 WO200032634-A1
 29-NOV-1999;
 01-DEC-1998;
 Region
 /note= "Corresponds to position 74 of mature HuZAF-VH, substituted with residue at equivalent position of mouse mature AF2 antibody heavy chain (VH)"
 /note= "Corresponds to position 30 of mature HuZAF-VH, substituted with residue at equivalent position of mouse mature AF2 antibody heavy chain (VH)"
 /note= "Corresponds to position 11 of mature HuZAF-VH, substituted with residue at equivalent position of mouse mature AF2 antibody heavy chain (VH)"
 /note= "Corresponds to position 27 of mature HuZAF-VH, substituted with residue at equivalent position of mouse mature AF2 antibody heavy chain (VH)"
 /note= "Corresponds to position 28 of mature HuZAF-VH, substituted with residue at equivalent position of mouse mature AF2 antibody heavy chain (VH)"
 /note= "Corresponds to position 38 of mature HuZAF-VH, substituted with residue at equivalent position of mouse mature AF2 antibody heavy chain (VH)"
 /note= "Corresponds to position 48 of mature HuZAF-VH, substituted with residue at equivalent position of mouse mature AF2 antibody heavy chain (VH)"
 /note= "Corresponds to position 67 of mature HuZAF-VH, substituted with residue at equivalent position of mouse mature AF2 antibody heavy chain (VH)"
 /note= "Corresponds to position 68 of mature HuZAF-VH, substituted with residue at equivalent position of mouse mature AF2 antibody heavy chain (VH)"
 /note= "Corresponds to position 70 of mature HuZAF-VH, substituted with residue at equivalent position of mouse mature AF2 antibody heavy chain (VH)"
 /note= "Corresponds to position 72 of mature HuZAF-VH, substituted with residue at equivalent position of mouse mature AF2 antibody heavy chain (VH)"
 Humanised antibody, HuZAF; mouse AF2 antibody; human EU antibody; VL, light chain variable region; VH; heavy chain variable region; HuZAF-VH; gamma-interferon; IFN, complementarity determining region; CDR, FR; framework region; immunosuppressive; antiinflammatory; antisolarotic; gastrointestinal; antidiabetic; antiarthritic; dermalogical; inhibitor; autoimmune disease; graft versus host disease; organ transplant; IgG1; multiple sclerosis; Type I diabetes; rheumatoid arthritis; psoriasis; systemic lupus erythematosus; SLB; Crohn's disease.
 /note= "Mature humanised antibody HuZAF heavy chain
variable region (HuZAF-VH)"
 Humanised antibody HuZAF, heavy chain variable region (HuZAF-VH).
 50..54
|Jabel= CDR
|note= "Complementarity determining region"
 note= "Complementarity determining region"
 1..19
/note= "N-terminal peptide"
 Location/Qualifiers
 69..85
/label= CDR
12-OCT-2000 (first entry)
 - Homo sapiens.
- Mus sp.
 20,.136
 Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
 Misc-difference
 Chimeric .
Chimeric .
 Peptide
 Protein
 Region
 Region
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Misc-difference

The present amino acid sequence is the humanised version of the mouse AF2 immunoglobulin, HuZAF heavy chain variable region (HuZAF-VH), of IgG1 isotype. The humanised HuZAF antibody comprises mouse AF2 antibody complementarity determining regions (CDR8), functionally joined to the human acceptor antibody EU framework regions (FR). Mature HuZAF-VH FR at positions il. 27, 28, 30, 38, 48, 67, 68, 70, 72, 74, 93, 95, 98, 107, 108, 109 and ill are occupied by residues present in the equivalent positions of the mouse mature AF2 heavy chain variable region (VH). HuZAF antibody specifically binds to and neutralises gamma-interferon (FR). They can also block the binding of mouse AF2 immunoglobulin to gamma-IFN. HuZAF does not contain sequences that are immunoglobulin to create its activity or circulating half-life. HuZAF may be administered to treat autoimmune diseases such as graft versus host disease following organ transplant, Type I diabetes, multiple sclerosis, rheumatoid arthitis, psoriasis, systemic lupus erythematosis, rheumatoid arthitis, psimary biliary cirrhosis and inflammatory bowel disease /note= "Corresponds to position 98 of mature HuZAF-VH, substituted with residue at equivalent position of mouse mature AF2 antibody heavy chain (VH)" 118..125 /label= CDR /note= "Corresponds to position 109 of mature HuZAF-VH, substituted with residue at equivalent position of mouse mature AF2 antibody heavy chain (VH)" /note= "Corresponds to position 107 of mature HuZAF-VH, substituted with residue at equivalent position of mouse mature AF2 antibody heavy chain (VH)" /note= "Corresponds to position 111 of mature HuZAF-VH, substituted with residue at equivalent position of mouse mature AF2 antibody heavy chain (VH)" substituted with residue at equivalent position of mouse mature AF2 antibody heavy chain (VH)" /note= "Corresponds to position 95 of mature HuZAF-VH, substituted with residue at equivalent position of mouse mature AF2 antibody heavy chain (VH)" /note= "Corresponds to position 108 of mature HuzAF-VH, substituted with residue at equivalent position of mouse mature AF2 antibody heavy chain (VH)" 'note= "Corresponds to position 93 of mature HuZAF-VH Humanized murine AF2 immunoglobulins, useful for inhibiting gamma-interferon for the treatment of autoimmune diseases, ( note= "Complementarity determining region" Queen CL; Vasquez M, Landolfi NF, Tsurushita N, multiple sclerosis and diabetes Claim 10; Fig 2B; 32pp; English. (PROT-) PROTEIN DESIGN LABS INC 136 AA; Sequence

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<u>ښ</u>
 anti-allergic; anti-athritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; artirheumatic; antirheumatic; antirheumatic; antirheumatic; antirhertality; neuroprotective; antirheumatic; antirhertality; neuroprotective; antirheumatical; apoptosis; systemic lupus erythematosus; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; since disease; rheumatoid arthritis; graft versus host disease; sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; goodpasture syndrome; cohn's disease; sterility; myasthenia gravis; unsulin dependent diabetes mellitus; arteriosolerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 This invention describes a novel humanized anti-Pas antibody-like molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell swiface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-andiabetic, anti-lalergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosupressive, thyronimetic, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antiarterioscleroric, cardiant and hepatropic activity. (1) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (1) are used to treat and/or prevent diseases associated with the Pas/Fas ligand system, especially systemic lugus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWIG------- 44
 20 QVQLVQSGAELKKPGSSVKVSCKASGYIFTSSWINWVKQAPGQGLEWIGRIDPSDGEVHY 79
 New humanized anti-Fàs antibody, useful for treating or preventing e.g.
inflammatory or autoimmune disease, induces apoptosis selectively in
cells with abnormal Fas-Fas ligand systems
 80 NQDFKDKATLTVDKSTNTAXMELSSLRSEDTAVYYCARGFLPWFADMGQGTLVTVSS 136
 87
 Gaps
 Fas, antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 45 -----KATLIVDKSISTAYMELSSLRSEDTAVYFCAR-----WGQGTTVTVSS
 30;
 Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 DB 21; Length 136;
 4; Indels
 Humanised anti-Fas designed heavy chain Heu 3 protein.
 5e-26;
 8; Mismatches
 Score 356;
 Pred. No.
 Claim 2; Page 180-182; 263pp; English.
 AAW90935 standard; Protein; 470 AA
Query Match
Best Local Similarity 64.1%;
Matches 75, Conservative 8
 99EP-0307711
 98JP-0276881
98JP-0276882
 (first entry)
 CO LID.
 WPI; 2000-258930/23.
 N-PSDB; AAA11646.
 (SANY) SANKYO
 29-SEP-1999;
 30-SEP-1998;
 08-AUG-2000
 EP990663-A2
 05-APR-2000
 Synthetic.
 AAW90935;
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'n
 disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, alleayy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulomephitis, hepatitis (fulminant, chromic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human auti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu 3 which is described in the method of the invention.
 80 NOKFKGKATLITVDISTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGQGTLVTVS 139
 44 -----GKATLITVDXSTSTAYMBLSSLRSEDTAVYFCAR-------WGQGTTVTVS 86
 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNY 79
 The invention relates to a preventive or treating agent for diseases caused by abnormality in Fas/Fas ligand system containing as the active component an antibody having as the light chain subunit a polypeptide containing residues 1-218 of one of 3, 239 residue amino acid sequences, or residues 1-451 of one of 3, 470 residue amino acid sequences, all fully defined in the specification and having an activity of combining
 1 OIOLVOSGGELVKPGASVRVSCKASGYSFT-----WVROSPGKGLEWI------
scleroderma, Goodpasture syndrome, Crohn's
 Gaps
 Drug containing humanised anti-Fas antibody, used for preventing and treating autoimmune diseases, allergy, and atopy -
 Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
light chain subunit; apoptosis; immunosuppressive; antiallergic;
autoimmune disease; allergy; atopic.
 34;
 Mouse humanised anti-Fas antibody related protein SEQ ID NO 9.
 Length 470;
 4; Indels
 Example 4 (Preparatory); Page 79-80; 194pp; Japanese.
 Query Match
Pest Local Similarity 62.0%; Pred. No. 2.6e-25;
Matches 75; Conservative 8; Mismatches 4;
 ABB74904 standard; Protein; 470 AA.
 29-MAR-2000; 2000JP-0090918.
 28-MAR-2001; 2001JP-0093106.
anemia, Addison's disease,
 entry)
 (SANY) SANKYO CO LID.
 (first
 WPI; 2002-145113/19.
 470 AA;
 N-PSDB; ABL45926.
 JP2001342148-A.
 S 140
 87 S 87
 Mus musculus.
 26-APR-2002
 11-DEC-2001
 ABB74904;
 Sequence
 140
 ABB74904
ID ABB7
8X888888888888X8
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14-APR-1998
 25-SEP-1997
 Hansen H,
 Chimeric
Chimeric
 Sequence
 AAW27698;
 AAW27698
 Query Match
 Key
Region
 Region
 Region
 Best Loc
Matches
 AAW27698
 RESULT
 888888888
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 Э,
 80 NOKFKGKATLIVDTSTSTAYMELSSIRSEDTAVYYCARNRDYSNNWYFDVWGQGTLVTVS 139
specifically with mammalian Fas and an activity of inducing apoptosis in a cell expressing Fas. The agent has immunosuppressive and antialleroic activity and is used for preventing and treating autoimmune diseases, allergy, atopy and others.
 43
 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVRQAPGQGLEWMGEIDPSDSYTNY 79
 86
 ----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVS
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI--------
 Gaps
 antibody; MAb; LL2; B-cell lymphoma; complementarity determining region;
 The complementarity determining regions (CDRs) of mouse monoclonal antibody (MAD) LL2 VK (AAR921215) and VH (AAR92216) regions were recombinantly linked to the framework sequences of human VK and VH regions, respectively, to give humanised LL2 VK (AAR92217) and VH
 conjugates
 79.0%; Score 354; DB 23; Length 470; 62.0%; Pred. No. 2.6e-25; ive 8; Mismatches 4; Indels 3:
 Chimeric and humanised LL2 antibodies - used to produce for the therapy and diagnosis of B-cell lymphoma(s) and
 Location/Qualifiers
 AAR92218 standard; Protein; 116 AA
 Claim 5; Page 39; 70pp; English.
 Humanised antibody; monoclonal leukaemia; therapy; diagnosis;
 50..66
/label= CDR2
99..105
/label= CDR3
 31..35
/label= CDR1
 95WO-US09641.
 94US-0289576.
 Humanised LL2 MAb VH region
 (first entry)
 CDR; antibody engineering
 Local Similaricy
 (IMMU-) IMMUNOMEDICS INC
 WPI; 1996-139454/14.
 Leung S;
 470 AA;
 N-PSDB; AAT15804
 140 S 140
 87
 leukaemia(s)
 WO9604925-A1
 11-AUG-1995;
 12-AUG-1994;
 28-MAY-1996
 22-FEB-1996
 87 S
 Hansen H,
 Synthetic
 44
 AAR92218;
 Sequence
 Query Match
 Region
 Region
 Region
 Best Loca
Matches
 8X8686
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ب
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 44
 1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYWLHWVRQAPGQGLEWIGYINPRNDYTEY
 61 NONFKDKATITADESTNTAYMELSSLRSEDTAFYFCARRDITTFYWGGGTTVTVSS 116
 Gaps
 87
(AAR92218). These were subsequently linked, respectively, to human kappa and IgG1 constant regions. A humanised MAb was obtd. that retained the B-lymphona and leukaemia cell targeting and internalisation characteristics of the parental LL2 MAb, and which exhibited a lowered HAMA reaction. It can be linked to e.g. a
 Monoclonal antibody engineered to contain glycosylation site - in non-Fc constant heavy or light chain region, useful to diagnose or treat B cell malignancies, e.g. non-Hodgkins lymphoma
 45 -----KATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------WGOGTTVTVSS
 The present sequence is the variable heavy chain of the bacil specific monoclonal antibody (MAb) hLL2. hLL2 is a highly specific anti-B cell lymphoma and anti-lymphocytic leukaemia cell humanised murine MAb. The MAb can be used to diagnose or treat B
 Variable heavy chain; B cell; monoclonal antibody; MAb; hLL2; B cell lymphona; lymphocytic leukaemia cell; murine; humanised; diagnosis; treatment; B cell malignancy; non-Hodgkins lymphoma; chronic lymphocytic leukaemia
 29;
 DB 17; Length 116;
 /note= "complementarity determining region 1"
 5
 region
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG-
 region
 4; Indels
 "complementarity determining
 "complementarity determining
 78.9%; Score 353.5; DB 1762.9%; Pred. No. 7.3e-26; ive 10; Mismatches 4;
 cytostatic agent for therapeutic appln
 Location/Qualifiers
 Ź
 Example 3; Fig 5B; 88pp; English.
 Variable heavy chain of MAb hLL2
 standard; Protein; 116
 96US-0013709
 ÿ
 (first entry)
 73; Conservative
 (IMMU-) IMMUNOMEDICS INC.
 99..105
/note= "c
 ಕ್ಷ
 - Mus sp.
- Homo sapiens.
 50..66
/note=
99..105
 WPI; 1997-479995/44
 Leung S,
 Local Similarity
 116 AA;
 N-PSDB; AAT88131.
 WO9734632-A1
 19-MAR-1997;
 20-MAR-1996;
```

3,

Gaps

29;

43

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The sequences given in AAR29016-17 are portions of monoclonal antibodies which were encoded by plasmids contained within the mouse hybridoma, AUK12-20. The DNA encoding the complementarity determining regions (CDR's) was isolated by polymerase chain reaction. These antibodies recognise human interleukin-6 receptor (IL-6R). The hybridoma cells were transformed with plasmids containing fragments of the antibody gene which caused the production of the antibody from the hybridoma
 The anti-human HM1,24 antibody is the preferred cytotoxic antibody to be used in the treatment of lymphocytic tumours, including T-cell tumours and B-cell tumours other than myeloma. The antibody is preferably monoclonal and has ADCC or CDC type cytotoxicity. It may be chimeric or
 20 QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYYIHWVRQAPGQGLEWIGYIDPFNGGTSY
 80 NOKFKGKVTMTVDTSTNTAYMELSSIRSEDTAVYYCARGGNRFAYWGQGTLVTVSS 135
 Treatment of lymphocytic tumours using cytotoxic antibody - binding to specific antigen such as HMI.24 and effective against T-cell tumours and B-cell tumours other than myeloma
 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 Cytotoxic antibody, anti-human HM1.24; lymphocytic tumours; pre-B lymphoma; Burkitt's lymphoma; T-cell tumour; B-cell tumour.
 Length 135;
 Indels
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI
 Anti-human HM1.24 antibody heavy chain variable region r.
 Score 353.5; DB 13;
Pred. No. 8.5e-26;
8; Mismatches 5;
 (Updated on 25-MAR-2003 to correct PN field.)
 Disclosure; Page 159-60; 207pp; Japanese.
 /note= "Signal peptide"
 "Mature peptide"
 Disclosure; Page 47-48; 82pp; Japanese.
 Location/Qualifiers
 AAW65773 standard; Protein; 139 AA.
 Query Match
Best Local Similarity 63.8%;
Matches 74; Conservative
 97JP-0041410
 Yoshimura Y;
 (first entry)
 (CHUS) CHUGAI SEIYAKU KK.
 20..139
./note= "1
 WPI; 1998-456869/39.
 135 AA;
 N-PSDB; AAV07581
 Koishihara Y,
 WO9835698-A1
 12-FEB-1998;
 12-FEB-1997;
 16-NOV-1998
 20-AUG-1998
 Sequence
 Synthetic
 AAW65773
 Peptide
 Peptide
 RESULT 15
 AAW65773
 8X000000000X8
 셤
 à
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 ë,
 9
 1 QVQLVQSGAEVKKFGSSVKVSCKASGYTFTSYWLHWVRQAPGQGLEWIGYINPRNDYTEY
 61 NONFKDKATITADESTNTAYMELSSLRSEDTAFYFCARRDITTFYWGQGTTVTVSS 116
 Gaps
 45 -----KATLIVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTTVTVSS 87
 Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse; complementarity determining region; monoclonal; hybridoma; PCR; plasmid; polymerase chain reaction; amplify.
 Reconstituted human antibody to human interleukin-6 receptor -has low antigenicity and contains mouse V-region complementarity determining regions
 29;
 18; Length 116;
 Tsuchiya M;
 4; Indels
cell malignancies, e.g. non-Hodgkins lymphoma or chronic
lymphocytic leukaemia.
 78.9%; Score 353.5; DB 1062.9%; Pred. No. 7.3e-26; iive 10; Mismatches 4
 Saldanha JW, Sato K,
 1..19
/note= "Leader peptide"
 Location/Qualifiers
 AAR29017 standard; Protein; 135 AA
 50..54
/label= CDR1
 69..85
/label= CDR2
 118..124
/label= CDR3
 20..49
/label= FR1
 86..117
/label= FR3
 92WO-JP00544
 91JP-0095476
92JP-0032084
 55..68
/label= FR2
 125..135
/label= FR4
 Query Match
Best Local Similarity 62.9*
Matches 73; Conservative
 (updated)
(first entry)
 (CHUS) CHUGAI SEIYAKU
 Jones ST,
 WPI; 1992-398882/48.
 116 AA;
 N-PSDB; AAQ31391.
 pUC-RVh-1220d
 25-APR-1991;
19-FEB-1992;
 W09219759-A1
 24-APR-1992;
 25-MAR-2003
30-MAR-1993
 12-NOV-1992
 Bendig MM,
 Synthetic
 AAR29017;
 Sequence
 Key
Peptide
 Region
 Region
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 Region
 Region
 Region
 cell
 RESULT 14
 AAR29017
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humanised, and preferably contains a human antibody constant region C gamma (such as C gamma 1 or C gamma 3). A preferred antibody is an anti-human HM1.24 antibody or an antibody which binds to an epitope recognising anti-human HM1.24 antibody. The cytotoxic antibody is useful in the treatment of lymphocytic tumnours such as acute or chronic B lymphocytic leukaemia, pre-B lymphoma, Burkitt's lymphoma, or acute or chronic T lymphocytic leukaemia.
```

Sequence 139 AA;

|                                        | 3,                                                  |                                               |                                                                    |                                                     | σı                                                                  |
|----------------------------------------|-----------------------------------------------------|-----------------------------------------------|--------------------------------------------------------------------|-----------------------------------------------------|---------------------------------------------------------------------|
|                                        |                                                     | 43                                            | 79                                                                 | 87                                                  | 13                                                                  |
|                                        | Gaps                                                | 43                                            | DGDTRY                                                             | WGOGTTVTVSS                                         | TVTVS                                                               |
| 139;                                   | 33;                                                 |                                               | SIFP                                                               | WGOGI                                               | WGOGT                                                               |
| 78.9%; Score 353.5; DB 19; Length 139; | Indels                                              | PGKGLEWI-                                     | PGQGLEWMO                                                          |                                                     | REGGYYFDY                                                           |
| DB 19;                                 | 3 4;                                                | WVRQSI                                        | HILL<br>MOWVROAI                                                   | YFCAR                                               | YYCARGL                                                             |
| 353.5;                                 | ol.8%; Fred. NO. 0.08-20;<br>live 10; Mismatches 4; | GYSFT                                         | :  <br>GYTFTPYV                                                    | GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR                   | LRSEDTA                                                             |
| Score                                  | 10, Mi                                              | RVSCKAS                                       | KVSCKAS                                                            | AYMELSS                                             | AYMELSS                                                             |
| 78.98;                                 | ive<br>ive                                          | KPGASV                                        | KPGASV                                                             | DKSTS1                                              | DKSTST                                                              |
|                                        | œ                                                   | 1 OIOLVOSGGELVKPGASVRVSCKASGYSFTWVRQSPGKGLEWI | 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTPYWNQWYRQAPGQGLEWMGSIFPGDGDTRY 79 | 44GKAILIVDKSTSTATAYMELSSLRSEDTAVYFCARWGQGTTVTVSS 87 | 80 SQKFKGRVIMTADKSTSTAYMELSSLRSEDTAVYYCARGLRRGGYYFDYWGQGTTVTVSS 139 |
| <u>.</u>                               | 73;                                                 | .O.~                                          | -6r                                                                | 4,                                                  | Š                                                                   |
| Query Match                            | Best Local Similarity<br>Matches 73; Conserv        | λα                                            | Db 2                                                               | Qy 4                                                | Db 8                                                                |

Search completed: January 13, 2004, 12:38:24 Job time : 21.2873 secs

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January 13, 2004, 12:43:20 ; Search time 13.9048 Seconds (without alignments) 1260.812 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Sequence Sequence 6
 Sequence
Sequence
 Sequence
Sequence
 Sequence
 Sequence
 Sequence
 Sequence
 Sequence
 Sequence
 1 QIQLVQSGGELVKPGASVRV......DIAVYFCARWGQGTTVTVSS
 FUDILIBRED. Applications. Ash.

1. (groz 6/ptodata2/pubpaa/USO7_PUBCOMB.pep:*

1. (groz 6/ptodata2/pubpaa/USO7_NEW_PUB.pep:*

3. (cgroz 6/ptodata2/pubpaa/USO6_PUBCOMB.pep:*

3. (cgroz 6/ptodata2/pubpaa/USO6_PUBCOMB.pep:*

3. (cgroz 6/ptodata2/pubpaa/USO7_NEW_PUB.pep:*

3. (cgroz 6/ptodata2/pubpaa/USO7_NEW_PUB.pep:*

3. (cgroz 6/ptodata2/pubpaa/USO8_NEW_PUB.pep:*

3. (cgroz 6/ptodata2/pubpaa/USO8_PUBCOMB.pep:*

3. (cgroz 6/ptodata2/pubpaa/USO8_PUBCOMB.pep:*

3. (cgroz 6/ptodata2/pubpaa/USO8_PUBCOMB.pep:*

3. (cgroz 6/ptodata2/pubpaa/USO8_PUBCOMB.pep:*

3. (cgroz 6/ptodata2/pubpaa/USO9_PUBCOMB.pep:*

4. (cgroz 6/ptodata2/pubpaa/USO8_PUBCOMB.pep:*

 747907
GenCore version 5.1.6
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 US-10-230-880-90
US-110-230-880-90
US-110-230-880-95
US-09-990-586-89
US-09-990-586-89
US-110-230-880-91
US-110-230-880-91
US-110-230-880-95
US-110-230-880-95
US-110-230-880-95
US-110-230-880-95
US-110-230-880-95
US-09-990-586-96
US-110-230-880-96
US-110-230-880-96
US-110-230-880-96
US-110-230-880-96
US-110-230-880-96
US-110-230-880-96
US-110-230-880-96
 Total number of hits satisfying chosen parameters:
 747907 segs, 201509753 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Published_Applications_AA:*
 - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 US-09-990-586-90
 Query
Match Length
 Title:
Perfect score:
 Scoring table:
 OM protein
 Sequence:
 Searched:
 Database
 Run on:
 Result
 No.
```

| 4 87.9 87 12 US-10-230 880-175 4 87.9 87 11 US-09-990-586-85 6 87.1 87 12 US-10-230 880-175 7 86.4 87 12 US-10-230 880-167 8 87.8 11 US-09-990-586-85 8 84.8 87 11 US-09-990-586-84 8 84.6 87 12 US-10-230-880-157 8 84.2 87 12 US-10-230-880-171 8 84.2 87 12 US-10-230-880-171 8 84.2 87 12 US-10-230-880-157 8 81.3 87 12 US-10-230-880-157 8 81.5 11 US-09-990-586-83 8 83.3 87 11 US-09-990-586-83 8 83.3 87 11 US-09-240-118-7 8 80.5 461 10 US-09-240-0118-24 8 80.5 135 10 US-09-256-2068-7 8 80.4 136 10 US-09-256-2068-7 8 80.4 136 10 US-09-565-2068-7 8 80.5 11 US-09-256-2068-7 8 80.4 136 10 US-09-565-2068-7 |  |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--|
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |  |
| 33333333333333333333333333333333333333                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |  |

## ALIGNMENTS

```
APPLICANT: JIAO, JIN.-AN
APPLICANT: JIAO, JIN.-AN
APPLICANT: JIAO, JIN.-AN
APPLICANT: WONG, HING C.
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
TITLE OF INVENTION: OF USE THEREOF
FILE REPERENCE: 71758/46943-CIP2
CURRENT APPLICATION NUMBER: US/09/990,586
CURRENT APPLICATION NUMBER: 09/293,854
PRIOR APPLICATION NUMBER: 09/293,854
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 99.
 1 OJOLVOSGGELVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
 Gaps
 ;
0
 Length
 0; Indels
 Query Match
100.0%; Score 448; DB 11;
Best Local Similarity 100.0%; Pred. No. 2.9e-37;
Matches 87; Conservative 0; Mismatches 0;
 61 LSSLRSBDTAVYFCARWGQGTTVTVSS 87
 61 LSSLRSEDTAVYFCARWGOGTTVTVSS 87
US-09-990-586-90

'Sequence 90', Application US/09990586

'Publication No. US20030109680Al

; GENERAL INFORMATION:
 ORGANISM: Homo sapiens US-09-990-586-90
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RESULT 2 US-10-230-880-90 ; Sequence 90, Application US/10230880

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RESULT 5
US-09-990-586-89
 US-09-990-586-89
 TYPE: PRT
ORGANISM:
 셤
 Sequence 95. Application US/09990586
Publication No. US20030109680A1
GENERAL INFORMATION
APPLICANT: JIAO, JIN-AN
APPLICANT: JIAO, JIN-AN
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
TITLE OF INVENTION: USE THEREOF
FILE REFERENCE: 71758/46943-CIP2
CURRENT APPLICATION NUMBER: US/09/990,586
CURRENT PILING DATE: 1090-00111-21
PRIOR FILING DATE: 1999-04-16
PRIOR FILING DATE: 1999-04-16
 1 QIQLVQSGPELVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
 1 ÓIÓLVÓSGGELVKÞGASVRVSCKASGYSFTWVRÓSÞGKGLEWIGKATLTVDKSTSTAYME 60
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME
 Gaps
Publication No. US20030190705A1
GENERAL INVORMATION:
APPLICANT: WONG, HING C.
APPLICANT: STINSON, JEFFREY L.
APPLICANT: STINSON, JEFFREY L.
TILLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
FILE REFERENCE: 17758/5806
CURRENT APPLICATION NUMBER: US/10/230,880
CURRENT APPLICATION NUMBER: 09/990,586
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-11-23
PRIOR FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/343,306
PRIOR APPLICATION NUMBER: 60/343,306
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 174
SOFFWARE: PALENTIN VET: 2.1
SEQ ID NO 90
LENGTH: 87
 .
0
 Query Match
Best Local Similarity 100.0%; Pred. No. 2.9e-37;
Matches 87; Conservative 0; Mismatches 0; Indels C
 98.2%; Score 440; DB 11; Length 87; 98.9%; Pred. No. 1.8e-36;
 0; Mismatches
 61 LSSLRSEDTAVYFCARWGOGTTVTVSS 87
 LSSLRSEDTAVFCARWGQGTTVTVSS 87
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 95
LENGTH: 87
 Query Match
Best Local Similarity 98.99
Matches 86; Conservative
 TYPE: PRT
CORGANISM: Homo sapiens
US-09-990-586-95
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-90
 RESULT 3
US-09-990-586-95
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 g
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RESULT 4 US-10-230-880-95

```
APPLICANT: JIAO, JIN-AN
APPLICANT: JIAO, JIN-AN
APPLICANT: JIAO, JIN-AN
APPLICANT: WONG, HING C.
TITLE OF INVENTION: ANTEDDIES FOR INHIBITING BLOOD COAGULATION AND METHODS
TITLE OF INVENTION: OF USE THEREOF
FILE REFERENCE: 71758/46943-CIP2
CURRENT APPLICATION NUMBER: US/09/990, S86
CURRENT FILING DATE: 1090-11-21
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PATCHIN VEY: 2.1
SEQ ID NO 89
LENGTH: 87
 1 OJOLYOSGGELYKPGASYRVSCKASGYSFTWYRQSPGKGLEWIGKATLIVDKSTSTAYME 60
 1 QIQLVQSGPELVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME
Sequence 95, Application US/10230880
| Publication No. US2030190705A1
| GENERAL INFORMATION NO. US2030190705A1
| APPLICATION NO. USCONDING HING C. APPLICANT: WONG, HING C. APPLICANT: WONG, HING C. APPLICANT: MONGUERA, LUIS A. TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES FILE REFERENCE: 71758/58066
| CURRENT APPLICATION NUMBER: US/10/230,880
| CURRENT FILING DATE: 2001-12-23
| PRIOR APPLICATION NUMBER: 09/290,586
| PRIOR FILING DATE: 2001-11-0-29
| PRIOR FILING DATE: 2001-11-0-29
| PRIOR FILING DATE: 2001-10-29
| PRIOR FILING DATE: 1999-04-16
| NUMBER OF SEQ ID NOS: 174
| SOFTHARE: PatentIN Ver. 2.1
| SEQ ID NO 95
 Length 87;
 Length 87;
 Indels
 Score 440; DB 12;
Pred. No. 1.8e-36;
0; Mismatches 1;
 ch 1 Similarity 97.7%; Pred. No. 2.3e-36; 85; Conservative 1; Mismatches 1;
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 61 LSSLRSEDTAVYFCARWGÓGTTVTVSS 87
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 Sequence 89, Application US/09990586
Publication No. US20030109680A1
GENERAL INFORMATION:
 ch 98.2%;
1 Similarity 98.9%;
86; Conservative
 Homo sapiens
 , ORGANISM: Homo sapiens
US-10-230-880-95
 Query Match
Best Local Similarity
Matches 85; Conserval
 Query Match
Best Local Similarity
Matches 86; Conserv
```

```
, ORGANISM: Homo sapiens
US-10-230-880-91
 HING C.
 ; ORGANISM: Homo sapiens
US-10-230-880-89
 US-10-230-880-91
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Squence 91, Application US/09990586

Squence 91, Application US/09990586

Publication No. US20030109680A1

GENERAL INFORMATION:

APPLICANT: JIAO, JUN-AN

TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS

TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS

TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS

TITLE OF INVENTION: OF USE TIEREOF

FILE REFERENCE: 71058/46643-GIP2

CURRENT APPLICATION NUMBER: US/09/990,586

CURRENT PILING DATE: 1999-04-16

NUMBER OF SEQ ID NOS: 102

SOFTWARE: PALENTION VOICE: 2.1

SEQ ID NO 91

LENGTH: 87
 genence 92, Application US/0990586

publication No. US20030109680A1

general information:

APPLICANT: JIAO, JUN-AN

TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS

TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS

TITLE OF INVENTION: OF USE THEREOF

TITLE OF INVENTION: OF USE THEREOF

FILE REFERENCE: 71758/46943-CIP2

CURRENT APPLICATION NUMBER: US/09/990,586

CURRENT FILING DATE: 2001-11-21

PRIOR APPLICATION NUMBER: 09/293,884

PRIOR APPLICATION NUMBER: 09/293,884

PRIOR FILING DATE: 1999-04-16

NUMBER OF SEQ ID NOS: 102

SEQ ID NO 92

LENGTH: 87
 ö
 ò
 1 ÓIÓLVÓSGGEVKKÞGASVRVSCKASGYSFTWVRÓSÞGKGLEWIGKATLTVDKSTSTAYME 60
 1 ÓLOLVÓSGGEVKKPGASVRVSCKASGYSFIWVRÓSPGKGLEWIGKATLTVDKSTSTAYME 60
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME
 Gaps
 ö
 Score 439; DB 11; Length 87; Pred. No. 2.3e-36; 1; Mismatches 1; Indels
 Length 87;
 1; Indels
 Query Match

Best Local Similarity 97.7%; Pred. No. 2.3e-36;
Matches 85; Conservative 1; Mismatches 1;
 61 LSSLRSEDTAVYFCARWGOGTTVTVSS 87
 61 LSSLRSEDTAVYFCARWGOGTTVTVSS 87
 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 issirsedtavyrcakwegertvivss 87
 Query Match
Best Local Similarity 97.7%;
Matches 85, Conservative 1
 TYPE: PRT
CRGANISM: Homo sapiens
US-09-990-586-92
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-91
 RESULT 8
US-10-230-880-89
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; Sequence 89, Application US/10230880 ; Publication No. US20030190705A1

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9
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
 1 OIQLVQSGGBLVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
 1 OMOLOGISGGELVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
 1 QIQLVQSGGBLVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME
 0; Gaps
 Sequence 91, Application US/10230880

Sequence 91, Application US/10230880

Publication No. US2000190705A1

GENERAL INVORMATION:

APPLICANT: WONG, HING C.

APPLICANT: STINSON, JEFREX L.

APPLICANT: MOSQUERA, LUIS A.

TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES

FILE REFERENCE: 71758/58066

CURRENT APPLICATION NUMBER: US/10/230,880

CURRENT FILING DATE: 2001-11-21

PRIOR APPLICATION NUMBER: 09/990,586

PRIOR APPLICATION NUMBER: 09/990,586

PRIOR APPLICATION NUMBER: 09/990,586

PRIOR PELING DATE: 2001-10-29

PRIOR PELING DATE: 2001-10-29

NUMBER OF SEQ ID NOS: 174

SOFTWARE: PATENTIN VONS: 174

SOFTWARE: PATENTIN VONS: 1.74
APPLICANT: WONG, HING C.
APPLICANT: STINGON, JEFFREY L.
APPLICANT: STINGON, JEFFREY L.
APPLICANT: STINGON, JEFFREY L.
TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
FILE REFERENCE: 7158/5806
CURRENT APPLICATION NUMBER: US/10/230,880
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: 60/390,586
PRIOR PLILING DATE: 2001-10-29
PRIOR PLILING DATE: 2001-10-29
PRIOR PLILING DATE: 2001-10-29
PRIOR PLILING DATE: 2001-10-29
PRIOR PLILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 174
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 89
 Query Match 98.0%; Score 439; DB 12; Length 87; Best Local Similarity 97.7%; Pred. No. 2.36-36; Matches 85; Conservative 1; Mismatches 1; Indels
 Length 87;
 Score 439; DB 12;
Pred. No. 2.3e-36;
1; Mismatches 1;
 87
 61 LSSLRSEDTAVYFCARWGOGTTVTVSS 87
 61 LSSLRSEDTAVYFCARWGOGTTVTVSS 87
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS
 Query Match
Best Local Similarity 97.7%;
Matches 85; Conservative 1
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RESULT 13
US-09-990-586-94
 SEQ ID NO 96
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 RESULT 11
US-09-90-586-96
| Sequence 96, Application US/09990586
| Publication No. US20030109680A1
| GENERAL INFORMATION:
| APPLICANT: UNFORMATION:
| APPLICANT: WONG, HING C.
| TITLE OF INVENTION: OF USE THEREOF
| TITLE OF INVENTION: AND UNBER: US/09/990,586
| CURRENT APPLICATION NUMBER: 09/293,854
| PRIOR APPLICATION NUMBER: 09/293,854
| PRIOR PILING DATE: 2001-11-21
| PRIOR FILING DATE: 199-04-16
| NUMBER OF SEQ ID NOS: 102
| SOFTWARE: Patentin Ver. 2.1
 9
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
 1 QIQLVQSGPEVVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME
 Gaps
 GENERAL INVOKATION:

APPLICANT: WONG, HING C.

APPLICANT: STINSON, JEFFREY L.

APPLICANT: STINSON, JEFFREY L.

APPLICANT: STINSON, JEFFREY L.

APPLICANT: STINSON, JEFFREY L.

TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES

CURRENT APPLICATION NUMBER: US/10/230,880

CURRENT APPLICATION NUMBER: 09/990,586

PRIOR APPLICATION NUMBER: 09/990,586

PRIOR FILING DATE: 2001-11-21

PRIOR APPLICATION NUMBER: 09/293,854

PRIOR FILING DATE: 2001-10-29

PRIOR FILING DATE: 1999-04-16

NUMBER OF SEQ ID NOS: 174

SEQ ID NOS: 174

SEQ ID NOS: 174

SEQ ID NOS: 174

SEQ ID NOS: 174

SEQ ID NOS: 174

SEQ ID NOS: 174

SEQ ID NOS: 174

SEQ ID NOS: 174

SEQ ID NOS: 174

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SEQ ID NOS: 174

SEQ ID NOS: 174

SEQ ID NOS: 174

SEQ ID NOS: 174

SEQ ID NOS: 1
 ö
 DB 11; Length 87; 3.6e-36;
 1; Indels
 Score 439; DB 12;
Pred. No. 2.3e-36;
1; Mismatches 1;
 1; Mismatches
 97.5%; Score 437; 97.7%; Pred. No. 3
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
Application US/10230880
o. US20030190705A1
 Query Match
Best Local Similarity 97.7%;
Matches 85; Conservative
 85; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
US-09-990-586-96
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-92
 Query Match
Best Local Similarity
Sequence 92, Ap
Publication No.
 SEQ ID NO 96
LENGIH: 87
 Matches
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Sequence 94, Application US/09990586
Fublication No. US20030109680A1
GENERAL INFORMATION:
APPLICANT: UIAO, JIN-AN
APPLICANT: UIAO, JIN-AN
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
TITLE OF INVENTION: OF USE THEREOF
FILE REPERBNCE: 7175846943-CIP2
CURRENT APPLICATION NUMBER: US/09/990,586
FURRENT FILING DATE: 1090-04-16
FRIOR APPLICATION NUMBER: 09/293,854
FRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 94
LENGTH: 87
 1 QIQLVQSGPEVVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
 1 QIQLVQSGGBLVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLIVDKSTSTAYME 60
 1 QIQLVQSGPELKKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME
 Gaps
 Gaps
 APPLICANT: WONG, HING C.
APPLICANT: WONG, HING C.
APPLICANT: WONG, HING C.
TITLE OF INVENTION: AETHER L.
TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
FILE REPRENCE: 71758/S806
CURRENT APPLICATION NUMBER: US/10/230,880
CURRENT APPLICATION NUMBER: 09/990,586
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-11-22
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 174
SOOTHWARE: PRECENTION UNDER: 201-16
 .
0
 Length 87;
 Length 87;
 1: Indels
 2; Indels
 Score 434; DB 11;
Pred. No. 7.2e-36;
0; Mismatches 2;
 Query Match
Best Local Similarity 97.7%; Pred. No. 3.6e-36;
Matches 85; Conservative 1; Mismatches 1;
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 61 LSSLRSEDTAVYFCARWGOGTTVTVSS 87
Sequence 96, Application US/10230880 Publication No. US20030190705A1 GENERAL INFORMATION:
 Query Match
Best Local Similarity 97.7%;
Matches 85; Conservative
 TYPE: PRT
CORGANISM: Homo sapiens
US-09-990-586-94
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-96
```

Search completed: January 13, 2004, 13:13:43 Job time :: 13.9048 secs

61 LSSLRSEDTAVYFCARWGQGTTVTVSS

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61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87

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US-US-JUL-SUB-JS

Sequence 93, Application US/08990586

Publication No. US20030109680A1

SEMERAL INFORMATION:
APPLICANT: UNOW, HING C.
TITLE OF INVENTION: OF USE THEREOF
FILE REFERENCE: 71758/46943-CIP2
CURRENT FILING DATE: 2001-11-21

PRIOR APPLICATION NUMBER: 09/293,854

PRIOR PILING DATE: 1999-04-16

NUMBER OF SEQ ID NOS: 102

SOFTWARE PATENTING PATE: 2.21

SEQ ID NO 93

LINGH NO 93

LINGTH: 87
 ö
 1 QIQLVQSGPEVKKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
 1 QIQLVQSGPBLKKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME
 0; Gaps
RESULT 14

US-10-20-80-94

Sequence 94, Application US/10230880

Sequence 94, Application US/10230880

Sequence 94, Application US/005A1

GENERAL INPORMATION:

APPLICANT: WONG, HING C

APPLICANT: WONG, JEFFRRY L.

APPLICANT: WOSQUERA, LUIS A.

TILE OF INVENTION: MINGER: US/10/230,880

CURRENT APPLICATION NUMBER: 09/990,586

PRIOR PILING DATE: 2001-11-22

PRIOR FILING DATE: 2001-11-21

PRIOR PILING DATE: 2001-11-21

PRIOR PILING DATE: 2001-11-2

PRIOR PILING DATE: 1999-04-16

NUMBER OF SEQ ID NOS: 174

SOFTWARE: PEACHTIN NUMBER: 09/293,854

PRIOR PILING DATE: 1999-04-16

NUMBER OF SEQ ID NOS: 174

SEQ ID NO 94

LENGTH: 87
 Query Match 96.2%; Score 431; DB 11; Length 87; Best Local Similarity 96.6%; Pred. No. 1.4e-35; Matches 84; Conservative 1; Mismatches 2; Indels
 96.9%; Score 434; DB 12; Length 87; 97.7%; Pred. No. 7.2e-36; Live 0; Mismatches 2; Indels
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 Query Match
Best Local Similarity 97.77
Matches 85; Conservative
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-94
 TYPE: PRT
CRGANISM: Homo sapiens
US-09-990-586-93
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DENGTH: 87 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
 Conservative
 TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
 Query Match
Best Local Similarity
Matches 69; Conserv
 US-08-497-312-16
 Sequence 16, Appl
Sequence 78, Appl
Sequence 63, Appl
Sequence 27, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
 102, App
102, App
7, Appli
8, Appli
41, Appl
 ; Search time 7.52227 Seconds (without alignments) 489.353 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Sequence 8,
Sequence 41,
Sequence 41,
 Sequence 1
Sequence 1
Sequence 7
 Sequence 1
Sequence 1
Sequence 2
 Sequence Negatives
 Sequence
Sequence
Sequence
 448
1 QIQLVQSGGELVKPGASVRV.....DTAVYFCARWGQGTTVTVSS
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
 US-08-497-312-16
US-08-525-539A-78
US-08-450-520A-63
US-08-497-312-27
US-08-690-102A-8
US-08-157-902-8
US-08-157-902-8
US-08-157-902-8
US-08-157-902-9
US-08-157-102-102
US-08-157-1170-102
US-08-137-1170-102
US-08-137-1170-102
US-08-136-1138-168
US-08-107-6890-54
 US-08-082-842A-54
US-08-839-765-168
US-09-136-389-168
 Total number of hits satisfying chosen parameters:
 328717 seqs, 42310858 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 January 13, 2004, 12:33:50
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Issued_Patents_AA:
 length: 0
length: 2000000000
 08-086-60-SU
 Length
 Query
 sed
 Title:
Perfect score:
 Scoring table:
 Minimum DB
Maximum DB
 Sequence:
 Searched:
 Database
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 Result
 Run
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83.9%; Score 376; DB 1; Length 79.3%; Pred. No. 1e-31; ive 10; Mismatches 8; Indel

```
APPLICANT: DO COUTO, FERNANDO J.R.
APPLICANT: DO COUTO, FERNANDO J.R.
APPLICANT: DO COUTO, FERNANDO J.R.
APPLICANT: CERIANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
TITLE OF INVENTION: METHODS OF WETHODS OF USE THEREOF, AND
TITLE OF INVENTION: METHODS OF HWANIZING ANTIBODY PEPTIDES
NUMBER OF SEQUENCES: 81
CORRESPONDRICE ADDRESS:
 1 QVQLVQSGAEVKKAPGASVKVSCKASGYTFNWVRQAPGQGLEWMGRVTMTRDTSTSTVYME 60
QIQLVQSGGELVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
 61 NOKFODKATLITVDKSTSTAYMELSSLRSEDTAVYFCARRWRYTMDYWGOGTLVTVSS 117
 1 EVOLVOSGABVKKPGASVKVSCKASGYSFTGYTMHMVKQSPGMNLEWIGLINPYNGGTVY
 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS 87
 Gaps
 80.4%; Score 360; DB 4; Length 117; 65.8%; Pred. No. 6.1e-30; Migmarches 5; Indels 30;
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWIG----
 COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATTONRY/AGENT INPORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REBERENCE/DOCKET NUMBER: 37,612
REBERENCE/DOCKET NUMBER: 27633-20001.21
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (415) 813-5600
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 LSSLRSEDTAVYYCARWGQGTLVTVSS 87
 US-08-525-539A-63
; Sequence 63, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION: PERMANDO I P
 Sequence 78, Application US/08525539A
Patent No. 6309636
 SEE: MORRISON & FOERSTER 1: 755 Page Mill Road Palo Alto
 TELEKAN (415) 45.
TELEKAN (614)
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
 Query Match
Best Local Similarity 65.8
Matches 77; Conservative
 US-08-525-539A-78
 RESULT 2
US-08-525-539A-78
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 STATE: C.
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DO COUTO, FERNANDO J.R. CERIANI, ROBERTO L.

APPLICANT: APPLICANT:

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ω
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 ----- 44
 20 BVQLVQSGAEVKKPGASVKVSCKASGYSFTGYTWHWVKQSPGMNLEWIGLINPYNGGTVY 79
 RECOMBINANT PEPTIDES DERIVED FROM THE MG3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND METHODS OF HUMANIZING ANTIBODY PEPTIDES
 80 NOKFODKATLIVDKSISIAYMELSSLRSEDTAVYFCARRWRYIMDYWGQGTLVTVSS 136
 45 -----KATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS 87
 30;
 80.4%; Score 360; DB 4; Length 136; 65.8%; Pred. No. 7.2e-30; 1ive 5; Mismatches 5; Indels 3
 APPLICANT: Vasquez, Maximiliano
APPLICANT: Vasquez, Maximiliano
APPLICANT: Landolfi, Nicholas F.
APPLICANT: Teurushita, Naoya
APPLICANT: Queen, Cary L.
APPLICANT: Protein Design Labs, Inc.
APPLICANT: Protein Design Labs, Inc.
APPLICANT: Protein Usergan Labs, Inc.
TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon
FILE REFERENCE: 011823-00811003
CURRENT APPLICATION NUMBER: US/09/450,520A
PRICA PLING DATE: 1999-11-29
PRICA FILING DATE: 1999-12-01
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG-
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-5EP-1995
CLASSIFICATION: 424
ATTCRNEY/AGRNT INFORMATION:
NAME: DYLAN, TYLEN
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 37,612
TELECOMMUNICATION INFORMATION:
TELEPRAK: (415) 813-5600
TELEFRAK: (415) 813-5600
TITLE OF INVENTION: RECOMBINANT P
TITLE OF INVENTION: MC3 ANT.-BA46
TITLE OF INVENTION: METHODS OF HUNNUMER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: MORISON & FORESTER
STREET: 755 Page Mill Road
CITY: Palo Alto
COUNTRY: USA
 Sequence 8, Application US/09450520A
Patent No. 6329511
 TELBEAX: (4.2,
TELBEAX: 706141
INTORNATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
"vpe: amino acid
"vpe: amino acid
 63:
 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
 NUMBER OF SEQ ID NOS: 13
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 136
 Best Local Similarity 65.8 Matches 77; Conservative
 GENERAL INFORMATION:
 ,
US-08-525-539A-63
 US-09-450-520A-8
 Query Match
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78.9%; Score 353.5; DB 1
62.9%; Pred. No. 2.8e-29;
vative 10; Mismatches 4
 APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/463/IMIN
TELECOMMUNICATION INFORMATION:
 E: Foley & Lardner
3000 K Street, N.W., Suite 500
 Foley & Lardner
3000 K Street, N.W., Suite 500
 60 LSSLRSEDTAVYYCARWGEGTLVTVSS 86
 Sequence 8, Application US/08690102A; Patent No. 5789554; GENERAL INFORMATION: APPLICANT: LEUNG, Shui-on APPLICANT: LEUNG, Shui-on TITLE OF INVENTION: IMMUNCCNUUGATE TITLE OF INVENTION: ANTIBODIES SPEC NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS: ADDRESSE: FOLSE: F
 : 116 amino acids
amino acid
 Query Match
Best Local Similarity 62.5.
These 73; Conservative
 (202) 672-5399
 TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 , MOLECULE TYPE: protein US-08-690-102A-8
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
 COUNTRY: USA
ZIP: 20007-5109
 TELEPHONE:
 TOPOLOGY:
 US-08-690-102A-8
 TELEFAX:
 RESULT 7
 RESULT 6
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 d
 Method for obtaining modified immunoglobulins with reduced immunoglobulins with reduced immunogenicity of murine antibody variable domains, compositions containing them.
 9
 80 NODFKDKATLIVDKSINIAYMELSSLRSEDIAVYYCARGFLPWFADWGQGTLVIVSS 136
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME
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 45 -----KATLIVDKSTSTAYMELSSIRSEDTAVYFCAR------WGQGTIVIVSS 87
 Gaps
CTHER INFORMATION: Description of Artificial Sequence:human-mouse; OTHER INFORMATION: transgenic construct HuZAF VH
US-09-450-520A-8
 30;
 Length 86;
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG-
 Length 136;
 Indels
 4; Indels
 GENERAL APPLICANT:
APPLICANT:
TITLE OF INVENTION: immunoglobulins with TITLE OF INVENTION: immunoglobulins with TITLE OF INVENTION: antibody variable domains, convented on SOUTHORS:
NUMBER OF SOUTHORS:
ADDRESSE: CENTRO DE INMUNOLOGIA MOLECULAR CAREET: 215 Y 15, ATABEY PLAYA
 DB 1;
 Query Match

79.5%; Score 356; DB 4;
Best Local Similarity 64.1%; Pred. No. 1.8e-29;
Matches 75; Conservative 8; Mismatches 4;
 Query Match 79.1%; Score 354.5; DB 1
Best Local Similarity 77.0%; Pred. No. 1.6e-29;
Matches 67; Conservative 11; Mismatches 8
 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 Sequence 27, Application US/08497312 Patent No. 5712120 GENERAL INFORMATION:
 unknown
) MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-497-312-27
 unknown
 TYPE: amino acid
STRANDEDNESS: un
 JS-08-497-312-27
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IMMUNOCONJUGATES AND HUMANIZED
ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
 1 QVQLVQSGABVKKPGSSVKVSCKASGYTFTSYWLHWVRQAPGQGLEWIGYINPRNDYTEY 60
 61 NONFKDKATITADESTNTAYMELSSLRSEDTAFYFCARRDITTFYWGQGTTVTVSS 116
 Gaps
 45 -----KATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS 87
 29;
 Length 116;
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG-
 Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,102A
FILING DATE: 01-JUL-1996
CLASSIFICATION: 424
 DB 1;
```

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45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-
 ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
 Sequence 8, Application PC/TUS9509641
GENERAL INFORMATION:
APPLICANT:
 COMPUTER READABLE FORM:
NEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
 : 116 amino acids
amino acid
 MOLECULE TYPE: protein
PCT-US95-09641-8
 linear
 20007-5109
 RESULT 10
US-08-137-117D-102
 TOPOLOGY:
 RESULT 9
PCT-US95-09641-8
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 8
 JOS-123-1, Josephication US/09155107

Patent No. 6254868

GENERAL INFORMATION

APPLICANT: HANSEN, Hans

APPLICANT: HANSEN, Hans

APPLICANT: DAINGEN, HANSEN, GU, ZORBENTATION: GIYCOSTLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES

TITLE OF INVENTION: G1YCOSTLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES

FILE REFERENCE: 19873/0879

CURRENT FILING DATE: 1998-11-19

EARLIER PILING DATE: 1998-11-19

EARLIER PILING DATE: 1997-03-19

EARLIER FILING DATE: 1996-03-20

NOTWHER OF SEQ ID NOS: 47

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8

LENGTH: 116
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 45 -----KATLIVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTTVTVSS
 29;
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWIG----
 78.9%; Score 353.5; DB 3; Length 116; 62.9%; Pred. No. 2.8e-29; tive 10; Mismatches 4; Indels 29
 DB 3; Length 116;
 Query Match 78.9%; Score 353.5; DB 3; Length Best Local Similarity 62.9%; Pred. No. 2.8e-29; Matches 73; Conservative 10; Mismatches 4; Indels
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,902
FILING DATE:
 PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/690,102
FILING DATE: 01-JUL-1996
APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/463/IMIN
TELECOMMUNICATION: INFORMATION:
 ZIP: 20007-5109
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 TELEX: 904136
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: TENTH: 116 amirr
 Query Match
Best Local Similarity 62.9
Matches 73; Conservative
Washington, D.C
) MOLECULE TYPE: protein US-09-127-902-8
 TYPE: PRT
ORGANISM: Homo sapiens
US-09-155-107-8
 COUNTRY: USA
ZIP: 20007-5
 TELEPHONE:
 US-09-155-107-8
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TITLE OF INVENTION: IMMUNOCONUUGATES AND HUMANIZED
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOWA AND LEUKEMIA CELLS;
NUMBER OF SEQUENCES: 21
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US95/09641
APPLICATION NUMBER: PCT/US95/09641
FILING DATE: 11-AUG-1995
RIOR APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994
INFORMATION FOR SEQ ID NO: 8
SECURENCE CHARACTER STICS:
LENGTH: 116 amino acids
 44
 ----- 44
 61 NONFKDKATITADESTIVTAYMELSSLRSEDTAFYFCARRDITTFYWGGGTTVTVSS 116
 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 29;
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG---
 Length 116;
 Query Match
78.9%; Score 353.5; DB 5; Length:
Best Local Similarity 62.9%; Pred. No. 2.8e-29;
Matches 73; Conservative 10; Mismatches 4; Indels
 Sequence 102, Application US/08137117D

Patent No. 5795965

GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: JONES, Steven
APPLICANT: WESHAPED HUMAN ANTIBODY TO HUMAN
ITILE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
```

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20 OVOLVOSGABVKKPGASVKVSCKASGYSFTSYYIHWVRQAPGQGLEWIGYIDPFNGGTSY 79
 80 NQKFKGKVTMTVDTSINTAYMELSSLRSEDTAVYYCARGGNRFAYWGQGTLVTVSS 135
 29; Gaps
 44 -----GKATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS 87
 PEATURE:
) OTHER INFORMATION: Description of Artificial Sequence: Amino acid
) OTHER INFORMATION: sequence of H chain V region version r of
) OTHER INFORMATION: humanized anti-HMI.24 antibody
US-09-355-925-7
 78.9%; Score 353.5; DB 4; Length 139; 60.8%; Pred. No. 3.4e-29; tive 10; Mismatches 4; Indels 33
 Score 353.5; DB 2; Length 135; Pred. No. 3.3e-29; 8; Mismatches 5; Indels 29
 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KOISHIHARA, YASUO
APPLICANT: VOSHIMURA, YASUO
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE REFERENCE: 053466/025
CURRENT APPLICATION NUMBER: US/09/355,925
CURRENT FILING DATE: 1999-08-11
PRIOR PILING DATE: 1999-08-12
PRIOR PILING DATE: 1997-02-12
PRIOR FILING DATE: 1997-02-12
PRIOR FILING DATE: 1997-02-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
 1 OIOLVOSGGELVKPGASVRVSCKASGYSFT----WVROSPGKGLEWI-
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: W0 PCT/JP92/00544
FILING DATE: 24-APR-1992
RIGHT DATE: 24-APR-1992
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
FILING DATE: 19-FEB-1992
RIGHT APPLICATION NUMBER: JP 78-1991
ATTORNEY/AGENT INFORMATION:
AMME: WEGNER, HAIOLI C.
REGISTRATION NUMBER: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HAIOLI C.
REGISTRATION NUMBER: 25-258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEBORHONE: (2029/52-5300)
 Sequence 7, Application US/09355925
Patent No. 6503510
 78.98;
 TYPE: PRT
ORGANISM: Artificial Sequence
 (202) 672-5300
(202) 672-5399
 : 135 amino acide amino acide
 Query Match
Best Local Similarity 60.8$
Matches 73; Conservative
 Query Match
Best Local Similarity 63.5.
-hos 74; Conservative
 TELEX: 904136
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acid
 MOLECULE TYPE: protein US-08-436-717-102
 TELEFAX:
 LENGTH: 139
 US-09-355-925-7
 ď
 20 QVQLVQSGAEVKKPGASVKVSCKASGXSFTSYXIHWVRQAPGQGLEWIGYIDPFNGGTSY 79
 80 NOKFKGKVIMIVDISINIAYMELSSIRSEDIAVYYCARGGNRFAYWGOGTLVIVSS 135
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT----WVRQSPGKGLEWI-----
 78.9%; Score 353.5; DB 1; Length 135; 63.8%; Pred. No. 3.3e-29; Live 8; Mismatches 5; Indels 29
 APPLICANT: TSUCHLYA, MASAYUKI APPLICANT: SATO, Koh APPLICANT: SATO, Koh APPLICANT: SATO, Koh APPLICANT: SATO, MASAYUKI APPLICANT: SALDANA, JOSE SEVEN APPLICANT: SALDANA, JOSE TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRES
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILNG DATE: 20-DEC-1993
CLASSIFICATION NUMBER: US/08/137,117D
FILNG APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILNG APPLICATION DATA:
APPLICATION NUMBER: 24-APR-1952
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 19-FEB-1992
FILNG DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: 25,258
FILING DATE: 25-APR-1991
ATFORNEY/AGENT INPORMATION:
NAME: WECKET MUMBER: 25,258
REGISTRATION NUMBER: 25,258
REFERRNCE/DOCKET NUMBER: 25,258
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/436,717
 Sequence 102, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
 OPERATING SYSTEM: PC-DOS/MS-DOS
 TELEX: 904136
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
 : 135 amino acids
amino acid
 Query Match
Best Local Similarity 63.0.
Best Local 74; Conservative
 , MOLECULE TYPE: protein US-08-137-117D-102
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SEQUENCE CHARACTERISTICS
 CLASSIFICATION:
PRIOR APPLICATION DATA:
 , MOLECULE TYPE: protein US-08-561-521-41
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 TYPE: amino acid
STRANDEDNESS: single
 CITY: San Francisco
STATE: California
COUNTRY: USA
 linear
 94105
 요
 ò
 80 SQKFKGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGLRRGCYYFDYWGQGTTVTVSS 139
 80 SQKFKGRVTMTADKSTSTAYMELSSLRSEDTAVYYCARGLRRGGYYFDYWGQGTTVTVSS 139
20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTPYWMQWVRQAPGQGLEWMGSIFPGDGDTRY 79
 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 Gaps
 OTHER INFORMATION: Description of Artificial Sequence: Amino acid OTHER INFORMATION: sequence H chain V region version s of OTHER INFORMATION: anti-HM1.24 antibody
 APPLICANT: KOISHIHARA, YASUO
APPLICANT: YOSHIMURA, YASUO
APPLICANT: YOSHIMURA, YASUO
APPLICANT: YOSHIMURA, YASUO
FILE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
FILE REPERENCE: 053466/0255
CURRENT FILING DATE: 1999-08-11
FRIOR APPLICATION NUMBER: PCT/JP98/00568
PRIOR PELING DATE: 1999-02-12
PRIOR FILING DATE: 1999-02-12
PRIOR FILING DATE: 1999-02-12
PRIOR FILING DATE: 1999-02-12
PRIOR FILING DATE: 1997-02-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE PREDETIN VET: 2.1
SEQ ID: NO 8
LENGTH: 139
 4; Indels 33;
 78.9%; Score 353.5; DB 4; Length 139; 60.8%; Pred. No. 3.4e-29; iive 10; Mismatches 4; Indels 33
 APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
 1 QIQLVQSGGELVKPGASVRVSCXASGYSFT----WVRQSPGKGLEWI
 NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
GTY: San Francisco
STATE: California
COUNTRY: USA
 Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
 Sequence 41, Application US/08561521 Patent No. 5840299 GENERAL INFORMATION:
 Sequence 8, Application US/09355925 Patent No. 6503510
 COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatibl
 TYPE: PRT
ORGANISM: Artificial Sequence
 GENERAL INFORMATION:
APPLICANT: KOISHIH
APPLICANT: YOSHIMU
 94105
 US-09-355-925-8
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1 QVOLVQSGAEVKKPGASVKVSCKASGYSFTSYXIHWVRQAPGQGLEWVGYIDPFNGGTSY 60
 61 NOKFKGKVTWTVDTSTNTAYMELSSLRSEDTAVYYCARGGNRFAYWGQGTLVTVSS 116
 Gaps
 44 -----GKATLIVDKSISTAYMELSSLRSEDIAVYFCAR------WGQGTTVTVSS 87
 Length 116;
 APPLICANT: Bending, Mary M.
APPLICANT: Bending, Mary M.
APPLICANT: Bending, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
 1 QIQLVQSGGELVKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI
 Indels
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ACHIECATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
 .5e-29;
 9; Mismatches
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
 APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
 Sequence 41, Application PC/TUS9501219 GENERAL INFORMATION:
 NAME: Smith, William L. REGIGSTRATION NUMBER: 30,223 REFERENCE/DOCKET WUMBER: 15 TELECOMMUNICATION INFORMATION: 415-543-9600
 TELEPHONE: 415-543-9600
TELEPAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 41
SEQUENCE CHARACTERISTICS:
 Query Match
Best Local Similarity 62.9%;
Matches 73; Conservative
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Search completed: January 13, 2004, 12:46:32 Job time : 7.52227 secs

us-09-990-586-91.rpr

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C)Species: none suplems (mail)
C)Species: none suplems (mail)
C)Accession: PHO958
R)Martin, T. 'Duffy, S.F.' Carson, D.A.; Kipps, T.J.
R)Martin, T. 'Duffy, S.F.' Carson, D.A.; Kipps, T.J.
A)Exp. Med. 175, 983-991, 1992
A)Title: Evidence for somatic selection of natural autoantibodies.
A)Reference number: PH0952; MUID:92202880; PMID:1552291
A)Accession: PH0958
A)Accession: PH0958
A)Status: nucleic acid sequence not shown
A)Anolecule type: DMA
A)Anolecule type: DMA
A)Accession: 1-122 cMAR
C)Superfamily: immunoglobulin V region; immunoglobulin homology
 g gamma-2a chain
g heavy chain V r
heavy chain r
 heavy chain V r
heavy chain V r
heavy chain V r
heavy chain V r
heavy chain V r
heavy chain V r
heavy chain V r
heavy chain V r
heavy chain V r
heavy chain V r
heavy chain V r
heavy chain V r
heavy chain V-1
heavy chain precur
 Ig heavy chain V r ig heavy chain Drecur ig heavy chain Drecur ig heavy chain V r chain pre
chain pre
chain V r
 ; Search time 6.30655 Seconds (without alignments) 1326.664 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 449
1 QIQLVQSGGEVKKPGASVRV.....DTAVYFCARWGQGTTVTVSS 87
 Description
 283308
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 283308 segs, 96168682 residues
 SUMMARIES
 Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
 OM protein - protein search, using sw model
 January 13, 2004, 12:22:35
 A33548
S20783
S36260
S37483
PH0957
 10958
10958
10959
10962
10962
10952
10955
 19665
21810
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 length: 0
length: 2000000000
 US-09-990-586-91
 Query
Match Length DB
 PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
 Minimum DB seq
Maximum DB seq
 9344.5

9440.9

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 Scoring table:
 Score
 Perfect score:
 Sequence:
 Searched:
 Database
 Run on:
 Result
No.
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| 30                               | ω.                                | ۳.                         | 136                             | (7         | 831600                                                         | chain V                                         |
|----------------------------------|-----------------------------------|----------------------------|---------------------------------|------------|----------------------------------------------------------------|-------------------------------------------------|
| 31                               | 28.                               | ۳.                         | 141                             | N          | JL0076                                                         | chain pr                                        |
| 32                               | 32                                | m ,                        | 116                             | (1)        | 855542                                                         | chain v                                         |
| 93                               |                                   | N (                        | 120                             | N C        | 541394                                                         | chain v                                         |
| 34                               |                                   | N C                        | 1 to 0                          | N C        | PS0024                                                         | chain pr                                        |
| 0 Y                              | 1 C                               | , N                        | 135                             | N (V       | 240333<br>PH0953                                               | Id heavy chain V r                              |
| 3.7                              | l (A                              | 'n                         | 160                             | N          | PL0105                                                         | erythr                                          |
| 38                               | 26.                               | ď                          | 116                             | N          | 853751                                                         | Fab Je                                          |
| 33                               | •                                 | 'n                         | 139                             | -          | MHMS18                                                         | chain                                           |
| 40                               | 56                                | ni.                        | 287                             | 4.         | PC4402                                                         | B leader/19                                     |
| 41                               | 32                                | ni o                       | 123                             | <b>7</b>   | D33548                                                         | neavy chain                                     |
| 42                               | ٠                                 | ni o                       | 119                             | N (        | F30502                                                         | neavy chain                                     |
| 43                               | 4.                                | , i                        | 9 6                             | <b>N</b> ( | C30560                                                         | heavy Chain                                     |
| 4. 4.<br>4. 10                   | 323.5                             | 72.2                       | 115                             | N 10       | S20640<br>A54378                                               | Ig heavy chain v r                              |
|                                  |                                   |                            |                                 |            | ALIGNMENTS                                                     |                                                 |
| RESULT                           | н                                 |                            |                                 |            |                                                                |                                                 |
| Ig heav                          | y chain                           | V regio                    | +95) u                          | T-L33)     | 33) - human (fragment)                                         |                                                 |
| C;Species: Hom<br>C;Date: 17-Apr | ;Species: Homo<br>;Date: 17-Apr-  | sapie<br>1993 #            | ns (man)<br>sequence            |            | revision 17-Apr-1993 #text                                     | _change 16-Aug-1996                             |
| C, Acces<br>R, Marti             | Bion: Pi                          | H0961<br>Duffv, S          | U                               | arson,     | n, D.A.; Kipps, T.J.                                           |                                                 |
| J. Exp.                          | Med. 175,                         | , 0, 4                     | rd *r                           | 992        | otion of natural                                               | t i bodi es                                     |
| A;Refer                          | ence nur                          | 1                          |                                 | _          | :92202880; PMID:155                                            | 2291                                            |
| A; Accessic                      | ដ្ឋធ                              | HO961<br>Bic acid          | segnence                        |            | not shown                                                      |                                                 |
| A, Molecule                      | ule type                          |                            |                                 |            |                                                                |                                                 |
| A; kesid<br>C; Super             | ; Kesidues: 1-1<br>; Superfamily: | inwunoglobul               |                                 | ><br>d.    | mmunoglobulin                                                  | homology                                        |
| C; Keywo                         | ords: het                         | Keywords: heterotetramer;  |                                 | תשת        | noglobulin                                                     |                                                 |
| F;15-98                          | 5-98/Domain:                      | immuno.                    | globul                          | d ai       | omology                                                        |                                                 |
| 33                               | /Region                           |                            | complementarity-<br>framework 2 | tty.       | determin                                                       |                                                 |
| 8-1-6                            | 57/Region:<br>98/Region:          |                            | complementarity<br>framework 3  | ity-       | determining 2                                                  |                                                 |
| 66                               | 7/Regio                           | 0                          | omplementari                    | rity       | -determining 3                                                 |                                                 |
| Query  <br>Best L<br>Matche      | Match<br>Local                    | Similarity<br>1; Conservat | 59                              | .3%;       | Score 347; DB 2; Le<br>Pred. No. 4.3e-27;<br>12; Mismatches 4; | Length 119;<br>Indels 32; Gaps 3                |
| ò                                | 7                                 | SÖZZÖ                      | GGEVKKPGAS                      | SASV       | SCKASGYSFTWVRQSPC                                              | KGLEWI 43                                       |
| đ                                | -0                                | :     <br>  SOOTOOSE       | GAEVKKPGSSVKV                   | 3887       | <br>SCKASGGTFSSYAI                                             | :    :  :    :<br>SWVRQAPGQGLEWMGGIIPIFGTANY 60 |
| Š                                | 44                                | GKA                        | -GKATLTVDKSTSTAYMELS            | STST       | AYMELSSLRSEDTAVYFCAR                                           | WGQGTTVTVSS 87                                  |
| qq                               | 61 7                              | :  :   :<br>AQKFQGRVTITADE | :   :<br>TITADE                 | STST       |                                                                |                                                 |
| RESULT                           | N                                 |                            |                                 |            |                                                                |                                                 |
| PH0958<br>Ig heavy o             | -5                                | V region                   |                                 | Į.         | CLL-HUR) - human (fragment)                                    |                                                 |
| C;Speci                          | es: Homo                          | o sapien                   | s (man)                         | -          | ## COO F 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                   | ,                                               |

Length 116;

Indels

87

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Deavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
C;Dates: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
C;Accession: A12483
R;Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck, Biochhys. Res. Commun. 160, 1250-1256, 1989
A;Title: Rapid coloning of rearranged immunoglobulin genes from human hybridoma cells us A;Title: Rapid cloning of rearranged immunoglobulin genes
 61 AQKRQGRVTITADKSTSTAVMELSSLRSEDTAVYYCARGRTRVSVSTLYDSSGYYDFSGY 120
 C;Species: Homo sapiens (man)
C;Detcies: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0960
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0960
A;Accession: PH0960
 61 AQKFQCRVTITADESTSTAYMELSSLRSEDTAVYYCARGDNWFDPWGQGTLVTVSS 116
 44 ----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTTVTVSS
 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
 1 OIQLVQSGGEVKKPGASVRVSCKASG----YSFTWVRQSPGKGLEWI
 1 QIQLVQSGGEVKKPGASVRVSCKASG----YSFTWVRQSPGKGLEWI
 44 -----GKATLIVDKSTSTAYMELSSLRSEDTAVYFCAR-----
 4
 DB 2;
 DB 2;
 'n
 Score 342.5; DB 2
Pred. No. 1.4e-26;
 Query Match 76.3%; Score 342.5; DB 2 Best Local Similarity 60.3%; Pred. No. 1.2e-26; Matches 70; Conservative 12; Mismatches 5
 11; Mismatches
 F)15-98/Domain: immunoglobulin homology <IMM>F)31-35/Region: complementarity-determining 1
F)36-50/Region: framework 2
F)51-67/Region: complementarity-determining 2
F)51-67/Region: complementarity-determining 2
F)99-104/Region: complementarity-determining 3
 F,99-124/Region: complementarity-determining 3
 31-35/Region: complementarity-determining 1
;36-50/Region: framework 2
;51-67/Region: complementarity-determining 2
;68-98/Region: framework 3
heterotetramer; immunoglobulin
 A;Status: nucleicod
A;Molecule type: DNA
A;Residues: 1-136 <MAR>
 :1-30/Region: framework 1
:15-98/Domain: immunoglobulin homology
 121 YGMDVWGQGTTVTVSS 136
 76.3%;
52.9%;
 Query Match
Best Local Similarity 52.9[†]
Matches 72, Conservative
 RESULT 6
 A32483
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 Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)

C;Species: Home sapiens (man)

C;Species: Home sapiens (man)

C;Date: 03.Peb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999

C;Accession: 536265

R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. A;Title: Human anti-eelf antibodies with high specificity from phage display libraries.

A;Reference number: 536265, MuID:93178448; PMID:7679990

A;Accession: S36265

A;Accession
 43
 9
 82
 61 AQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDFLSGYLDYWGQGTLVTVSS 118
 RESULT 4
PH0959
PH0959
Cypecies: Homo sapiens (Man)
Cypecies: Homo sapiens (Man)
Cypecies: Homo sapiens (Man)
Cypecies: Homo sapiens (Man)
Cypecies: T7-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
Cyaccession: PH0959
F.Martin, T.; Duffry, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
Ayritle: Svidence for somatic selection of natural autoantibodies.
Ayreference number: PH0952; MUID:92202880; PMID:1552291
AyAccession: PH0959
AyStatus: nucleic acid sequence not shown
 A;Cross-references: EMBL:Z18846; NID:g33121; PIDN:CAA79298.1; PID:g939900 C.Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin P;15-98/Domain: immunoglobulin homology <IMM>
 Gaps
 35;
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI----
 76.7%; Score 344.5; DB 2; Length 118; 61.0%; Pred. No. 7.6e-27; ive 9; Mismatches 6; Indels 31
 DB 2; Length 122;
 A,Residues: 1-116 <MAR>
C,Superfamily: immunoglobulin V region; immunoglobulin homology
 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR;------
 Indels
 Query Match 76.9%; Score 345.5; DB 2; Best Local Similarity 58.2%; Pred. No. 6.2e-27; Matches 71; Conservative 12; Mismatches 4;
 F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;69-98/Region: framework 3
F;99-110/Region: complementarity-determining 3
C; Keywords: heterotetramer; immunoglobulin F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
 Local Similarity 61.0
nes 72; Conservative
 121 SS 122
 86 SS 87
 A, Molecule type:
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 Query Match
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Gaps

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 61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGGVAGRPHFDYWGQGTLVTVSS 120
 71 AQKFQGRVTMTRDISTSTVYMELSSLRSEDTAVYYCAREKLATTIFGVLIITGMDYWGQG 130
 9
 43
 80
 70
 Tild heavy chain V region (G6+ CLL-SMI) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Dacession: P40952
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Tille: Evidence for somatic selection of natural autoantibodies.
A;Reference number: P40952; MUID:92202880; PMID:1552291
 "Theavy chain V region (G6+ T-142) - human (fragment)
Species: Homo sapiens (man)
Mattin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
Exp. Med. 117, 983-991, 1992
T.J. Exp. Med. 117, 983-991, 1992
T.J. Exp. Med. 117, 19052; MUD:92202880; PMID:1552291
 11 QVQLVQSGAEVKKPGASVKVSCKASGYTPTNYYMHWVRQAPGQGLEWMGIINPSGNSTNY
 1 QIQLVQSGGEVKKPGASVRVSCKASG----YSFTWVRQSPGKGLEWI------
 Gaps
 40;
 75.8%; Score 340.5; DB 2; Length 120; 58.3%; Pred. No. 1.9e-26;
 44 ----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR--------
 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;25-108/Domain: immunoglobulin homology <IMM>
 Length 142,
 Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWI
 6; Indels
 Indels
 44 ----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-
 Query Match 75.9%; Score 341; DB 2; Best Local Similarity 56.7%; Pred. No. 2e-26; Matches 72; Conservative 9; Mismatches 6
 12; Mismatches
 F;99-108/Region: complementarity-determining 3
 51-67/Region: complementarity-determining 2 68-98/Region: framework 3
 15-98/Domain: immunoglobulin homology < IMM> 31-35/Region: complementarity-determining 1
 Status: nucleic acid sequence not shown Molecule type: DNA
 Query Match 75.8%
Best Local Similarity 58.3%
Matches 70; Conservative:
A,Molecule type: mRNA
A,Residues: 1-142 <LAR>
A,Cross-references: GB:M26463
 TLVTVSS 137
 81 TTVTVSS 87
 .-30/Region: framework
 Residues: 1-120 <MAR>
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61 AQKFQGRVTITADESTSTAXMELSSLRSEDTAVYYCARPHASIDDFWSGYYPNYYYGMD 120
 61 AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGGNYDYIWGSYRSNDAFDIWGQ 120
 43
 1 QVQLVQSGABVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60
 C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0954
R;Martin, T.; Duffky, S.F.; Carson, D.A.; Kipps, T.J.
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
 Gaps
 Query Match
75.8%; Score 340.5; DB 2; Length 132;
Best Local Similarity 53.8%; Pred. No. 2.1e-26;
Matches 71; Conservative 12; Mismatches 4; Indels 45
 Length 128;
 A/Status: nucleic acid sequence not shown
A,Molecule type: DMP
A,Residues: 1-132 <MAR>
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: hererotetramer; immunoglobulin
 1 QIQLVQSGGEVKKPGASVRVSCKASG----YSFTWVRQSPGKGLEWI
 1 QIQLVQSGGEVKKPGASVRVSCKASG----YSFTWVRQSPGKGLEWI
 Indels
 44 -----GKATLIVDKSISTAYMELSSLRSEDTAVYFCAR-------
 Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
 44 ----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR---
 75.8%; Score 340.5; DB 2; 55.5%; Pred. No. 2e-26;
 5,
 11; Mismatches
 F,99-120/Region: complementarity-determining 3
 15-98/Domain: immunoglobulin homology <IMM>
 51-67/Region: complementarity-determining 2
A;Status: nucleic acid sequence not shown A;Molecule type: DNA
 Query Match
Best Local Similarity 55.5%
Marches 71, Conservative
 121 VWGQGTTVTVSS 132
 68-98/Region: framework 3
 121 GTMVTVSS 128
 80 GITVIVSS 87
 1-30/Region: framework
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form of the human IgM heavy chain
 ų,
 80 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAKTGILGPYSSGWYPNSDYYYYGM 139
 43
 63
 43
 79
 Tig heavy chain precursor V region (VMU-3.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999
 #text_change 23-Jul-1999
 4 QYQLQQSGPELVKPGASVKISCKASGYAFSSSWMNWVKQRPGKGLEWIGRIYPGDGDTNY
 20 QVQLVQSGABVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY
 Gaps
 87
 Gaps
 A;Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin; membrane protein
P;1-15/Domain: signal sequence #status predicted <SIG>
F;16-627/Product: Ig um chain #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
 <MAT>
 A; Residues: 1-119 < Willy A; Cross-references: GB:X03088; NID:g52378; FIDN:CAA26881.1; PID:g773578 A; Cross-references: GB:X03088; NID:g52378; FIDN:CAA26881.1; PID:g773578 A; Note: this sequence was determined from the germline gene C; Superfamily: immunoglobulin v region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F;4-119/Product: Ig heavy chain V region VMU-3.2 #status predicted <MAT: F;4-119/Product: immunoglobulin homology <IMM>
 44 ----GKATLIVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTTVTVSS
 29;
 46;
 Length 119;
 Length 627;
 1 OIOLVOSGGEVKKPGASVRVSCKASG----YSFTWVRQSPGKGLEWI-
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWI
 Indels
 Indels
 ----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR----
 membrane-bound (clone 201) - human
 ig mu chain precursor, membrane-bound (clone 201) - human (species: Homo sapiens (man) C;pacies: Homo sapiens (man) C;pacies: None 214683; 808047 (Accession: 814683; 81990 (Accession: 814683; MUID:90332450; PMID:2115996 (A;Reference number: 814683; MUID:90332450; PMID:2115996
 C, Accession: A.4672
R, Winter, E.; Radbruch, A.; Krawinkel, U.
EMBO J. 4, 2861-2867, 1985
A, Reference number: A91022; MUID:86055722; PMID:2998759
 74.9%; Score 336.5; DB 2;
60.3%; Pred. No. 4.6e-26;
iive 11; Mismatches 6;
 Score 337; DB 2;
Pred. No. 2.1e-25;
 Query Match
75.1%; Score 337; DB
Best Local Similarity 52.6%; Pred. No. 2.1e
Matches 70; Conservative 13; Mismatches
 140 DVWGQGTTVTVSS 152
121 DVWGQGTTVTVSS 133
 87
 Local Similarity 60.3
hes 70; Conservative
 --WGOGTTVTVSS
 A; Molecule type: mRNA
A; Residues: 1-627 <FRI>
 A; Molecule type: DNA
 A; Accession: S14683
 A;Accession: A24672
 44
 17
 Query Match
 Best Loca
Matches
 RESULT 14
 RESULT 13
 S14683
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 A) Experimental source: the sequence was determined from the differentiated gene C) Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;IS-98/Domain: immunoglobulin homology < IMM>
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 61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYCARVSIFGVVQHYYYYYMDVWGKG 120
 43
 9
 76
 80
 43
 9
 PH0955
Ig heavy chain V region (G6+ CLL-AND) - human (fragment)
C;Decies: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0955
C;Accession: PH0955
J; Exp. Med: 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
 OVOLVOSGAEVKKPGSSVKVSCKASGGTFSSYAISWVROAPGOGLEWMGGIIPIFGTANY
 Gaps
 Gaps
 46;
 40;
 75.1%; Score 337; DB 2; Length 133; 52.6%; Pred. No. 4.6e-26; ive 13; Mismatches 4; Indels 4
 Length 127;
 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin F;1-30/Region: framework 1
 1 QIQLVQSGGEVKKPGASVRVSCKASG----YSFTWVRQSPGKGLEWI
 Indels
 1 QIQLVQSGGEVKKPGASVRVSCKASG----YSFTWVRQSPGKGLEW
 ----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----
 44 ----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR--
 75.5%; Score 339; DB 2;
55.1%; Pred. No. 2.8e-26;
tive 13; Mismatches 4;
 F,99-115/Region: complementarity-determining 3
 F.15-98/Domain: immunoglobulin homology <INM>F.31-35/Region: complementarity-determining 1 F.36-50/Region: framework 2
 F;51-67/Region: complementarity-determining 2 F;68-98/Region: framework 3
 A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-127 <MAR>
 -- WGOGTTVTVSS 87
 Best Local Similarity 55.1
Matches 70; Conservative
 Conservative
 TTVTVSS 127
 TIVIVSS 87
 Similarity
 Query Match
Best Local Simi
Matches 70;
 44
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 121
 Query Match
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Ig heavy chain V-1 region (AND) - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996 C;Accession: B33549 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996 C;Accession: B33549 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996 R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A. Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1999 #Title: Developmentally restricted immunoglobulin heavy chain variable region gene expx A;Reference number: A33548; MUID:89348575; PMID:2503826
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
 R.Mahmoudi, M.; Edwards, J.; Cairns, B.; Bell, D. submitted to the EMBL Data Library, October 1994
A; Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: $48797
 A;Residues: 1-126 <KIP>
A;Residues: 1-126 <KIP>
A;Experimental source: the sequence was determined from the differentiated gene C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
 .
Н
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 43
 20 OVOLVOSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY 79
 anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C;Accession: S49530
 A;Status: preliminary
A;Molecule type: mENA
A;Rosidues: 1-13 < MAH>
A;Rosidues: 1-13 < MAH>
A;Cross-references: EMBi:Z46348; NID:g560839; PIDN:CAA86467.1; PID:g560840
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI-------
 80 AQKFQGRVTWIRDISISIAYMELSRLRSDDIAVYYCARARIGYNYWGQGTLVIVSS 135
 29; Gaps
 ----GKATLIVDKSISIAYMELSSLRSEDTAVYFCAR-----WGQGTTVTVSS 87
 Gaps
 39;
 74.9%; Score 336.5; DB 2; Length 135; ilarity 60.3%; Pred. No. 5.2e-26; Conservative 10; Mismatches 7; Indels 29
 Length 126;
 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------
 Indels
 1 OIQLVQSGGEVKKPGASVRVSCKASG----YSFTWVRQSPGKGLEWI
 Query Match 74.9%; Score 336.5; DB 2; Best Local Similarity 55.6%; Pred. No. 4.9e-26; Matches 70; Conservative 12; Mismatches 5;
 Search completed: January 13, 2004, 12:44:41
Job time : 7.30655 secs
 TVTVSS 126
 Query Match
Best Local Similarity
Matches 70; Conserv
 82 TVTVSS 87
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15419 MW; 1B57DD4FD0C9F465 CRC64;
 139 AA;
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 January 13, 2004, 12:19:34 ; Search time 3.79913 Seconds (without alignments) 1076.912 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 1 QIQLVQSGGEVKKPGASVRV......DTAVYFCARWGQGTTVTVSS 87
 Description
 P06330
P01744 P01744 P06329
P01746 P01746 P01746 P01743 P01743 P01743 P01745 P01745 P01745 P01745 P01765 P01760 P01760
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 127863 segs, 47026705 residues
 SUMMARIES
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HUMAN
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 HUMAN
 - protein search, using sw model
 Gapop 10.0 , Gapext 0.5
 seq length: 0
seq length: 200000000
 US-09-990-586-91
 Query
Match Length DB
 SwissProt_41:*
 BLOSUM62
 326.5
322.5
322.5
320.5
320.5
310.5
309.5
306.5
 Title:
Perfect score:
 Scoring table:
 Minimum DB s
Maximum DB s
 OM protein
 Database :
 Sequence:
 Searched:
 Run on:
 Result
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P01772 homo sapien
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| 268.5 59.8 126 1 HV3K HUMAN P01772 homo sapien 267.5 59.6 120 1 HV3H HUMAN P007421 homo sapien 267.5 59.6 120 1 HV3H HUMAN P01762 homo sapien 260.5 58.5 122 1 HV3B HUMAN P01762 homo sapien 260.5 58.5 119 1 HV3B HUMAN P01808 mus musculu 258.5 57.3 119 1 HV3F HUMAN P01807 mus musculu 255.5 56.9 136 1 HV3E HUMAN P01807 mus musculu 254.5 56.7 114 1 HV01_CANFA P01779 mus musculu 254.5 56.7 119 1 HV40_MOUSE P01783 mus musculu 255.5 56.1 119 1 HV40_MOUSE P01811 mus musculu 255.5 56.1 142 1 HV41_MOUSE P01810 mus musculu 251.5 56.0 122 1 HV21_MOUSE P01790 mus musculu 251.5 56.0 122 1 HV21_MOUSE P01790 mus musculu | THOUSE STANDARD, PRT; 1139 AA.  PROTOUGES  THOUSE STANDARD, PRT; 1139 AA.  101-51. PRO15-2.  101-52. PRO15-2.  11-101-102-15-2.  11-101-102-15-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-102-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-101-2.  11-10 |
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QIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG------ 44
 NEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVYYCARYRLGRYFDYWGQGTTLTVSS 137
 "Complete amino acid sequence of a mouse mu chain: homology among heavy chain constant region domains."; Biochemistry 21:5415-5424(1982).
-!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
 45 -----KATLIVDKSISIAYMELSSLRSEDIAVYFCAR------WGQGITVIVSS 87
 61 NQKFKGKATLIVDKSSSTAYMQLNSLTSEDSAVYXCARDYDWYFDVWGAGTIVTVSS 117
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWI------
 20 OVOLOOPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNORPGRGLEWIGRIDPNSGGTTY
 44 -----GKATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1g heavy chain V region J559.
In Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 MEDLINE=83075344; PubMed=6816276; Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H., Hood L.E.;
 30;
 IG-LIKE.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (COMPLEX)
 Length 117;
 th 71.3%; Score 320; DB 1; Length 117 Similarity 58.1%; Pred. No. 5.1e-30; 68; Conservative 12; Mismatches 7; Indels
 12983 MW; 3CFBACE4BE447E41 CRC64;
 -i- SIMILARITY: Contains 1 immunoglobulin-like domain. PIR; A02039; MHMS4E. HSSP; P01799; HMCP. InterPro; IPR007110; Ig-like. InterPro; IPR007106; Ig_MHC. InterPro; IPR003006; Ig_MHC.
 SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
 -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annocation update)
Ig heavy chain V region MOPC 104E.
 117 AA
 pfam; PF00047; ig; i. SMARY; SM04067; ig; i. SMARY; SM0406; iGv; i. IKB; i. PROSITE; PS50835; iG LiKB; i. Immunoglobulin V region; Glycoprotein.
 STANDARD;
 STANDARD;
 22
55
117 1
 Mus musculus (Mouse)
 NCBI_TaxID=10090;
 HV13 MOUSE
 MOUSE
 Query Match
Best Local S:
Matches 68,
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 'n
 80 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDYYGSSYFDYWGQGTTLTVSS 139
 44
 79
 87
 "Heary chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; cell 24:625-637(1981).
-!- MISCELLANBOUS: THE GAMMA-2A CHAIN MENA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
 20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYMMHWVKQRPGRGLEWIGRIDPNSGGTKX
 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG-----
 Gaps
 Gaps
 SEQUENCE FROM N.A.
MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1998 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 haavy chain V region S43 precursor.
19 haavy chain (Mouse).
Eukaryota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinee; Mus.
 31;
 33;
 71.8%; Score 322.5; DB 1; Length 137; 56.8%; Pred. No. 3.1e-30; ... 11; Mismatches 9; Indels 31
 Length 139;
 COMPLEMENTARITY-DETERMINING-1
 COMPLEMENTARITY - DETERMINING - 2
 IG HEAVY CHAIN V REGION S43.
FRAMEWORK-1.
 72.7%; Score 326.5; DB 1; Length 56.7%; Pred. No. 1.1e-30; cive 12; Mismatches 7; Indels
 15200 MW; ADD5881BF44B8EC9 CRC64;
 137 AA.
 BY SIMILARITY.
 FRAMEWORK-3.
D SEGMENT.
 SMART; SM00406; ĬĠv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
 EMBL, J00539; AAA38172.1; -. PIR, A02038; G2MS43. HSSP, PO1810; 2FBJ. InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_WHC.
 Conservative
 Query Match
Best Local Similarity 56.77
Matches 68; Conservative
 STANDARD;
 (NPB ANTIBODIES).
 137 1
137 AA;
 Similarity
67; Conserv
 Pfam; PF00047; ig;
 NCBI_TaxID=10090;
 Baltimore D.;
 MOUSE
 DISULFID
NON TER
SEQUENCE
 Query Match
Best Local S
Matches 67
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 SIGNAL
 DOMAIN
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Gaps

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Length 118;
 10;
 HSSP, P01789; IMCP.
GO: GO: 1005576; C: extracellular; NAS.
GO: 0003823; F: entigen binding activity; NAS.
GO: GO: 1003825; F: entigen binding activity; NAS.
GO: GO: 1006955; P: immune response; NAS.
InterPro: IPR001710; Ig-like.
InterPro: IPR001596; Ig-MC.
InterPro: IPR003596; Ig-V.
 69.8%; Score 313.5; DB 1
56.8%; Pred. No. 2.9e-29;
tive 10; Mismatches 10
 Query Match
Best Local Similarity 56.84
Matches 67; Conservative
 STANDARD;
 Homo sapiens (Human)
 SEQUENCE OF 20-147.
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 HV1C HUMAN P01744;
 CONFLICT
NON TER
SEQUENCE
 CHAIN
DOMAIN
MOD RES
DISULFID
 RESULT 6
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 9
 61 NOKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRYWYFDVWGAGTTVTVSS 117
 MEDLINE-84182519; PubMed-6201362;
Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
"A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523 (1984).
PIR; A02040; MHMS38.
N [1]

SEQUENCE.

MEDLINE=80078170; PubMed=6765983;
A Schilling J., Clevinger B., Davie J.M., Hood L.;
Schilling J., Clevinger B., Davie J.M., Hood L.;
Tamino acid sequence of homogeneous antibodies to dextran and DNA rearrangements in heavy chain V-region gene segments.";
Nature 283:35-40 (1980).
C -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN THE D AND J SEGMENTS.
C -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
C -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A26242; MHMSJG.
 1 OLOLVOSGGEVKKPGASVRVSCKASGYSFT----WVROSPGKGLEWI-------
 1 EVOLOGSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY
 44 ----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS 87
 01-JAN'1988 (Rel. 06, Created)
01-JAN'1988 (Rel. 06, Last sequence update)
15-JUL-1998 (Rel. 38, Last semocation update)
15 Heavy chain V region AC38 205.12.
19 Heavy chain V region AC38 Cof.12.
19 Heavy ctain Worse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae
 30;
 71.3%; Score 320; DB 1; Length 11 58.1%; Pred. No. 5.1e-30; cive 12; Mismatches 7; Indels
 117 117
117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;
 12934 MW; 94F7BEE4C762A018 CRC64;
 V SEGMENT.
D SEGMENT.
J SEGMENT.
BY SIMILARITY.
 IG-LIKE.
BY SIMILARITY.
 HSSP, P01789; 1MCP.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_WHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
PR031TE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
 HSSP, P01789, IMCP.
InterPro, IPR007110; Ig-like.
InterPro, IPR003006; Ig_MHC.
InterPro, IPR003596; Ig_V.
 Pfam; PF00047; ig; 1.
SMART; SMO466; IGv. 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
 Conservative
 STANDARD;
 Local Similarity
 NCBI_TaxID=10090;
 HV51 MOUSE
P06330;
 68
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61 NQKFKGKATLIYUDKSSSATYMELRSLTSEDSAVYYCARGYGYDPFDVWGTGTTVTVS 118
 Immediate hypersensitivity: modern concepts and developments, pp.1-36, Marcel Dekker, New York (1978)
-:- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYSLOMA
 20 QTQLVQSGAEVRKPGASVRVSCKASGYTFIDSYIHWIRQAPGHGLEWVGWINPNSGGTNY
Gaps
 44 ----GKATLITVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 MEDLINE-83065234; PubMed-6815656; Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney Bell L.O., Gould H.J.; "Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line."; proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
31;
 41;
 69.2%; Score 310.5; DB 1; Length 147; S0.8%; Pred. No. 8.2e-29; Indels 41; tive 13; Mismatches 9; Indels 41;
 Pram; Proco47; ig; 1.
SMAR; SMO0406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
 IG HEAVY CHAIN V-I REGION ND. IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID.
 1 OIQLVQSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI
Indels
 Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
(In) Bach M.K. (eds.);
 16491 MW; 948F9F72A5366C20 CRC64;
 -! - SIMILARITY: Contains 1 immunoglobulin-like domain
 21-JUL-1986 (Rel. 01, Created)
1-CCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15 heavy chain V-I region ND precursor (Fragments).
 T -> V (IN REF. 2).
IH -> HI (IN REF. 2).
VG -> GV (IN REF. 2).
MISSING (IN REF. 2).
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Capra J.D.;
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 EKFKGKTTLIVDKSSSTAYMQLRSLTSEDSAVYFCARSVYYGGSYYFDYWGQGTTLIVSS 120
 80 APRFQGRVTMTRDASPSTAYMDLRSLRSDDSAVFYCAKSDPFWSDYYNFDYSYTLDVWGQ 139
 43
 9
 87
 79
 MEDLINE=81131846; PubMed=6186498; Siekevitz M., Gefter M.L., Brodeur P., Riblet R., Marshak-Rothstein A.L., Brodeur P., Riblet R., Marshak-Rothstein A.L., Brodeur P., Riblet R., Marshak-Rothstein A. T. Immunol. 121023-1032[1982].

Fur. J. Immunol. 12:1023-1032[1982].

IDTFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J SEGMENT, JHZ.
 1 VOLOQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYTKYN
 44 ----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-------WGQGTTVTVSS
 Gaps
 01.JAN-1988 (Rel. 06, Created)
01.JAN-1988 (Rel. 06, Last sequence update)
01.JAN-1988 (Rel. 38, Last annotation update)
15.JUL-1999 (Rel. 38, Last annotation update)
15 mesculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Wertebrata; Euteleostomi;
NCBI_TaxID=10090;
 2 IQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWI------
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 34;
 Length 120;
 69.0%; Score 310; DB 1; Length 12
54.2%; Pred. No. 7.5e-29;
tive 13; Mismatches 8; Indels
 120 AA; 13307 MW; FF04E4A167B654AF CRC64;
 -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
HSSP; P01789; 1MCP.
 , Last sequence update)
 Pfan; Pro0047; ig; 1. 2. 28MART; SMO0406; IGV; 1. PROSITE; PS50835; IG LIKE; 1. Immunoglobulin V region; Hybridoma.
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequis-
15-SEP-2003 (Rel. 42, Last anno
1g heavy chain V region 36-65.
Mus musculus (Mouse).
 InterPro; IPR007110; IG-like.
InterPro; IPR003006; IG_MHC.
InterPro; IPR003596; IG_V.
 Conservative
 STANDARD;
 140 GTTVTVSS 147
 Query Match
Best Local Similarity
 80 GTTVTVSS 87
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 HV03 MOUSE
P01747;
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 HV50_MOUSE
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 9
 87
 Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
"A V region determinant (idiotope) expressed at high frequency in B lymphocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-528 (1984).
PIR; A02037, MHMS15.
PIRSP, PO1810, 2.FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
Pfan. PP00A47.
 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-------WGQGTTVTVSS
 Gaps
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG------
 -INCOSED STANDARD; PRT; 140 AA.
P01746;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16 heavy chain V region 9307 precursor.
In heavy chain (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
 33;
 68.9%; Score 309.5; DB 1; Length 120; 54.2%; Pred. No. 8.5e-29; ive 12; Mismatches 10; Indels 33
 MEDLINE-82152818; PubMed-6801765;
Sime J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
 "Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain."; science 216:309-311(1982) ... SIMILARITY: Contains 1 immunoglobulin-like domain.
 13311 MW; 914453F426F09834 CRC64;
 V SEGMENT.
D SEGMENT.
J SEGMENT.
BY SIMILARITY.
LINE-84182519; PubMed-6201362;
 Pfam, PF00047, ig; 1.
SMART, SM00406, ig; 1.
RROSITE, PS50835, ig Like; 1.
Immunoglobulin V region. V DOMAIN 198 V P
 EMBL, JO0493; AAA38128.1; -.
PIR, A94264; HVWSG7.
HSSP, PO1810; 2FBJ.
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v
 65; Conservative
 99 1
106 1
22
120 1
 SEQUENCE FROM N.A.
 Similarity
 NCBI_TaxID=10090;
 PHETERSOCOCOURAGE SERVICE CONTROL SERVICE SERV
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Gaps

43

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20 QVQLVQSGAEVKKPGASVKVSCKASGYTFNSYYMHWVRQAPGQGLEWMGIINPSGGSTSY 79
 20 QVQLQQPGAELVKPGASVQLSCKASGHTFINYMIHWVKQRPQQGLEMIGEINPNDGRSNY 79
 80 NEKFKNKATLITUDKSSSTAYMQLSSLIPEEFAVYYCARSDGYYDWFVYWGQGTLVTFSA 138
 45 -----KATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 SEQUENCE FROM N.A.
MEDILNE-84248078; PubMed-6429663;
Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
Tucker P.W.;
 "Illegitimate recombination generates a class switch from C mu to C delte in an IngD-secreting plasmacytoma.";
Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168 (1984).
PIR, A02033; HVMST7.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
 22;
 HEAVY CHAIN V REGION TEPC 1017.
 32;
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWIG----
 Length 117;
 COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
 FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
 Length 138;
 COMPLEMENTARITY-DETERMINING-2.
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWI
 67.3%; Score 302; DB 1; Length 11 ilarity 62.2%; Pred. No. 6.1e-28; Conservative 9; Mismatches 6; Indels
 10; Indels
 15576 MW; 748157E4C6907B8E CRC64;
 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR 117
 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR 76
 67.3%; Score 302; DB 1;
53.8%; Pred. No. 7.3e-28;
 23-OCT-1986 (Rel. 02, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region TEPC 1017 precursor.
Mus musculus (Mouse).
 Ą
 ; Pred. No. 7.3e-
13; Mismatches
 BY SIMILARITY.
 121
 PRT;
 MART, SM00406, IGv, 1.
ROSITE, PSSO835, IG LIKE, 1.
mmunoglobulin V region, Signal.
 ij
 Created)
 HSSP, PO1810, 2FBJ.
INTERFOO, IPR007110, IG-like.
INTERPOO, IPR003006, IG_MHC.
InterPoo, IPR003596, IG_V.
Pfam, PF00047, Ig_1.
 Local Similarity 53.89 tos 64; Conservative
 STANDARD;
 STANDARD;
 41
138
138 AA;
 Similarity
 23-OCT-1986 (Rel.
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Matches 61;
 HV48 MOUSE
P03980;
 HV01 MOUSE
P01745;
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HV01 MOUSE
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HV48 MOUSE
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 the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensegieb-sib.ch).
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 80 NEKFKGKTTLTVDKSSSTAYMOLRSLTSEDSAVYFCARSHYYGGSYDFDYWGQGTPLIVS 139
 43
 79
 96
 20 EVOLOQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKORPGOGLEWIGYINPGNGYINY
 44 ----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVS
 Gaps
 SEQUENCE FROM N.A.
PUDDLINE=81144028; PubMed=6298778; R., Givol D.;
Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
"Evolutionary aspects of immunoglobulin heavy chain variable region
 Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
 34;
 Length 140;
 IG HEAVY CHAIN V-I REGION HG3. IG-LIKE.
 IG HEAVY CHAIN V REGION 93G7 IG-LIKE.
 68.2%; Score 306; DB 1; Length 14
52.9%; Pred. No. 2.6e-28;
ive 14; Mismatches 9; Indels
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI
 15514 MW; 25A4CBBE31DA5CE8 CRC64;
 (VH) gene subgroups.";
Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 12946 MW; 2D3F92FC60CD1FE7 CRC64;
 HSSP, PO1772; 2FE4.

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; P:antigen binding activity; NAS.
GO; GO:0005825; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-Per-2003 (Rel. 42, Last annotation update)
Homo sapiens (Human).
 117 AA.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Hybridoma; Signal.
 MART; SM00406; ĪGv; 1.
ROSITE; PS50835; IG LIKE; 1.
mmunoglobulin V region; Signal.
 EMBL; J00240; AAA52988.1; -.
PIR; A02024; HVHUHG.
 Best Local Similarity 52.98
Matches 64; Conservative
 STANDARD;
 139
139
140
 140 AA;
 117 AA;
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 87 S 87
 HV1B HUMAN
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HSSP; P01772; 2FB4
 HV1D HUMAN
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 61 NDNLKGKATLTADTSSSTAYIQLSSLTSEDSAIYHCARGIYYNSSPYFDSWGQGTTLTVS 120
 43
 9
 96
 Zakut R., Cohen J., Givol D., Nuclear Res. 814839-4840(1980).
Nuclear Acids Res. 814839-4840(1980).
-!- MISCELLANBOUS: THIS SECUENCE MAS TRANSLATED FROM AN MENA ISOLATED FROM A MYELOMA THAT SECRETES 1GG2B.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR, A93708; GWMS11.
HSSP; P01810; ZFBJ.
 Cunningham B.A., Rutishauser U., Gall W.B., Gottlieb P.D., Waxdal M.J., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
[2]
 44 -----GKATLIVDKSTSTAYMELSSLRSEDTAVYFCAR-------WGQGTTVTVS
 Gaps
21-JUL-1986 (Rel. 01, Created)
15-SEP-2003 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16 heavy chain V region MPC 11.
19 heavy chain (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
 MEDLINE=81053741; PubMed=6253904;
Zakut R., Cohen J., Givol D.;
"Cloning and sequence of the cDNA corresponding to the variable
region of immunoglobulin heavy chain MPC11.";
Nucleic Acids Res. 8:3591-3601(1980).
 65.9%; Score 296; DB 1; Length 121; 50.4%; Pred. No. 3.1e-27; ive 15; Mismatches 11; Indels
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI
 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 heavy chain V-I region EU.
Homo sapiens (Human)
 117 AA
 IG-LIKE.
 MEDLINE=71064024; PubMed=5489771;
 Interpro; IPR007110; 1g-11ke.
Interpro; IPR003006; 1g wHC.
Interpro; IPR003596; 1g-v.
Pfam; PF00047; 1g; 1.
PR051TE; PS5035; 1G LIKE; 1.
Immunoglobulin, V region.
 61; Conservative
 STANDARD;
 Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090,
 s 121
 S 87
 HV1A_HUMAN
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1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWI------43
 group.";
Biochemistry 20:5822-5830(1981).
Biochemistry 20:5822-5830(1981).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GIOBULIN ACTIVITY.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02043; MHHUWL.
 1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSRSAIIWVRQAPGQGLEWMGGIVPMFGPPNY
 Andrews D.W., Capra J.D., and a regions of heavy chains from two "Amino acid sequence of the variable regions of heavy cross-reactive human IgM anti-gamma-globulins of the Wa
 Gaps
 44 -----GKATLIVDKSISTAYMBLSSLRSBDTAVYFCA-RWG------QGTTVTVSS
 P01760.
21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16 heavy chain V-I region WOL.
19 heavy chain V-I region Wol.
19 heavy chain Suthman).
19 heavy chain (Auman).
19 heavy chain Suthman).
19 Nammalia; Butheras, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
DISULFIDE BOND.

MEDLINE-17064027, PubMed-4923144;

MEDLINE-17064027, PubMed-4923144;

MEDLINE-17064027, PubMed-4923144;

MED covalent structure of a human gamma G-immunoglobulin.

"The covalent structure of a human gamma G-immunoglobulin.

Intrachain disulfide bonds.";

Biochemistry 9:13189-3196(1970).

-I- MISCELLANBOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.

-I- SIMILARITY: Contains 1 immunoglobulin-like domain.
 Length 117;
 65.7%; Score 295; DB 1; Length 11
55.6%; Pred. No. 3.9e-27; Pred. No. 3.9e-27;
 SMART; SMO406; Ig_v.

SMART; SM0406; Ig_v.

DR PROSITE; PS08135; IG LIKE; 1.

KW Immunoglobulin V region; Pyrrolidone carboxylic acid.

FT DOMAIN

T I 12 IG_LIKE.

FT NOD RIS

T NON TER 117 117

SEQUENCE 117 117
 IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID.
 GO; GO:0005576; C:extracellular; NAS.
GO; GO:000383; F:antigen binding activity; NAS.
GO; GO:0006955; P:immine response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-MGC.
InterPro; IPR003006; Ig-MC.
 MEDLINE=82046599; PubMed=7028111;
 Local Similarity 55.6
es 65; Conservative
 STANDARD;
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 ä
 82
 44
 1 QVQLMQSGAEVKKPGSSVRVSCKTSGGTFVDYKGLWVRQAPGKGLEWVGQIPLRFNGEVK 60
 Gaps
 SEQUENCE FROM N.A.
MEDLINE=88296408; PubMed=2841108;
Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
Ohno H., Fukuhara S., Honjo T.;
"Dispersed localization of D segments in the human immunoglobulin
heavy-chain locus.";
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 35;
 64.7%; Score 290.5; DB 1; Length 124; 50.8%; Pred. No. 1.4e-26; tive 14; Mismatches 11; Indels 35.
 IG HEAVY CHAIN V-I REGION V35. IG-LIKE.
 1 OIQLVQSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWIG-
 PYRROLIDONE CARBOXYLIC ACID.
 117 117
117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;
 124 AA; 13684 MW; CB98F365D004EC8B CRC64;
 MBO J. 7:1047-1051 (1988).
!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 mmunoglobulin V region; Pyrrolidone carboxylic acid.
 HSSP, P01772; 2FB4.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0003823; F:antigen binding activity; NAS.

GO; GO:0006955; P:immune response; NAS.

InterPro; IPR003100; Ig-like.

InterPro; IPR003596; Ig_MHC.
 HVIG HUMAN STANDARD; PRT; 117 AA. 123083.
12080.
1100V-1991 (Rel. 20, Last sequence update) 15-SEP-2003 (Rel. 22, Last annotation update) 15-BP-2003 (Rel. 42, Last annotation update) Homo sapiens (Human)
 EMBL; X07448; -; NOT_ANNOTATED_CDS.
PIR; S00476; HVHU35.
 Pfam: PF00047; ig; 1.
SMART; SM00406; IGy: 1.
Immunoglobulin V region; Signal.
PS50835; IG_LIKE; 1.
 Conservative
 112
 Best Local Similarity
Matches 62; Conserv
 SS 122
 86 SS 87
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PROSITE;
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Search completed: January 13, 2004, 12:39:26 Job time : 3.79913 secs

292465 mus musculu 094195 homo sapien 0948772 mus musculu 0948772 mus musculu 094877 mus musculu 09583 mus musculu 095846 mus musculu 095447 mus musculu 095447 mus musculu 095447 mus musculu 095445 mus musculu 09546 mus musculu 095466 
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Schistosoma japonicum (Blood fluke).

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatoidea; Schistosoma.
 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Monoclonal anti-idiotypic antibody NP30 heavy chain variable region
 SEQUENCE FROM N.A.

SONG X.T., Feng Z.Q., Guan X.H.;

SONG X.T., Feng Z.Q., Guan X.H.;

Mamplification, cloning and sequence analysis of the heavy chain variable region gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma japonicum.";

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

HSSP, P01772; ZFB4.

InterPro; IPR007110; Ig-like.

InterPro; IPR003006; Ig_MIC.

InterPro; IPR003596; Ig_WIC.
 Match 75.1%; Score 337; DB 5; Length 119; Local Similarity 58.8%; Pred. No. 1.3e-30; nes 70; Conservative 10; Mismatches 7; Indels 32;
 1 ÇIÇLVQSGGBVKKPGASYRVSÇKASGYSFT----WVRQSPGKGLEWIG----
 119 AA; 13567 MW; BA893873FD5FA6AB CRC64;
 119 AA
 ALIGNMENTS
0924R4
0924R3
0924R3
0924R3
0902F3
0901D95
091D95
0925R3
0925R3
0925R3
0925R3
0925R3
0924P3
 PRT;
 Pfam; PF00047; ig; 1. --
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
 PRELIMINARY;
 113
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 January 13, 2004, 12:20:44 ; Search time 15.5764 Seconds (without alignments) 1441.318 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
 Description
 US-09-990-586-91
449
1 QIQLVQSGGEVKKPGASVRV.....DTAVYFCARWGQGTTVTVSS
 830525
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 830525 segs, 258052604 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 09GYZZ
09ULJ94
09ULJ94
09DL14
0924R6
0924Q1
0924Q1
0924Q7
0924Q7
0924Q0
0924Q0
0924Q0
0924Q0
 SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_tungi:*
4: sp_tungi:*
5: sp_tunetebrate:*
5: sp_mammal:*
5: sp_mammal:*
5: sp_mammal:*
5: sp_mammal:*
5: sp_phage:*
5: sp_phage:*
5: sp_nian:*
 Gapop 10.0 , Gapext 0.5
 sp_vertebrate:*
sp_unclassified:*
 sp_rvirus:*
sp_bacteriap:*
 length: 0
length: 2000000000
 sp_archeap:*
 sp_plant:*
sp_rodent:*
 Query
Match Length DB
 virus:*
 BLOSUM62
 Title:
Perfect score:
 Minimum DB seq
Maximum DB seq
 337
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332.5
330.5
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 Scoring table:
 Sequence:
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Gaps

Indels

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C STRAIN-CSTBL/63. TISSUB-Pancreas;

WE SHOURNE'S KNOW N. N. TS STBE-Pancreas;

WE MEDLINE-2108560, PubMed=11217851;

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Eukunishi Y., Komon H., Adachi J., Fukuda S.,

A Arakawa T., Hara A., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,

Rubil P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonako M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Nordone P., Narchionni L., Mashima J., Mazzarelli J., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.,

"Functional annocation of a full-length mouse cDNA collection.";
 61 AQKFQGRVTMTRDTSTSTV7MBLSSLRSEDTAVYYCARGLYVVVPAAFSRFDYWGQGTLV 120
 ::|||:|| ||||||||||:|||||||:||:
1 EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYMHWVRQAPGQGLEMMGIINPSGGSTSY
 Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 74.1%; Score 332.5; DB 4; Length 124; 55.6%; Pred. No. 4.6e-30;
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWI
 13580 MW; 1BAAACBD96ACD2A2 CRC64;
 Last sequence update)
Last annotation update)
 Score 332.0,
Pred. No. 4.6e-30;
 12; Mismatches
 Created)
 Nature 409:685-690(2001).
EMBL; AK007918; BAB25349.1; -.
HSSP; P01842; 7FAB.
 MGD; MGI:96443; Igh-1.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP00047; ig; 4.
 InterPro; IPR00110; Ig-like.
InterPro; IPR033006; Ig_MHC.
InterPro; IPR003506; Ig_V.
Pfam; PR00047; Ig; 1.
SMART; SM00406; IGv; 1.
 Pfam, PF00047; ig; 1.
SMART; SM00406; iGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
 Q9D8L4;
Q9D8L4;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
EMBL; AF035022; AAD56258.1;
HSSP; P01772; 2FB4.
 69; Conservative
 01-JUN-2001 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel.
 1810060009Rik protein.
IGH-1 OR 1810060009RIK.
 124 1
124 AA;
 Similarity
 SEQUENCE FROM N.A.
 121 TVSS 124
 NCBI TaxID=10090;
 TVSS 87
 NON TER
NON TER
SEQUENCE
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 Q9D8L4
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 43
 61 AQKFQGKVTMTKDTSISTAYMELSRLRSDDTAVYYCARGGGRGLWFDFWGQGTLVTVSS 119
 61 NQKFKDRVTWTTDKSFSTAYMDLRSLRSADSAVYYCARYYDDHYCLDYWGQGTTVTVSS 119
 44 ----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS 87
 ----WGQGTTVTVSS 87
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI------
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
 "Myosin-reactive autoantibodies in rheumatic carditis and normal
 "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus ";
 32;
 SEQUENCE FROM N.A.
MEDINES-98277139; PubMed=9614934;
Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
 MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
 74.2%; Score 333; DB 4; Length 119; 58.0%; Pred. No. 3.8e-30; Live 11; Mismatches 7; Indels
 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;
 (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
 Clin. Immunol. Immunopathol. 87:184-192 (1998).
EMBL; AF035020; AAD56256.1; -.
HSSP; PO1810; 2FBG.
InterPro; IPR007110; Ig-like.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_V.
 Immunol. Immunopathol. 87:184-192(1998)
 124 AA
 119 AA.
 PRT;
 (Fragment).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Primates; (
NCBI_TaxID=9606;
 Conservative
 PRELIMINARY;
 PRELIMINARY;
 Homo sapiens (Human)
 Local Similarity
les 69; Conserv
 SEQUENCE FROM N.A.
 NCBI TaxID=9606;
 01-MAY-2000
01-MAY-2000
 Fragment)
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V23-D-J-C mu protein (Fragment).
 PRELIMINARY;
 140 GOGTTVTVSS 149
 78 GQGTTVTVSS 87
 Mus musculus (Mouse)
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 NCBI_TaxID=9606;
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 20 QVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRPGQGLEWIGKIGPGSGSTYY 79
 80 NEKFRŒKATLTADKSSTAYMQLSSLTSEDSAVYFCARSGYDYDWFAYWGQGTLVTVSA 138
 44
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT-----40RQSPGKGLEWI------43
 44 ----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS 87
 1 OIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG-----
 Gaps
 Gaps
 Kozono Y., Kozono H., Azuma T.;

"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Mitrophenyl) Acetyl (MP).",
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

Embl., ABG07783, BAB63268.1;
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
PF0047; ig; I.
SWART; SM00406; IGv; I.
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 23, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
Whus musculus (Mouse).
Eukarjota (Motaca). Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Sciurognathi; Musidae; Muridae; Musinae; M
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 61 NEKFKSKATLIVDKPSSTAYMQLSSLTSEDSAVYYCARWDYWGQGTTLIVUSS 112
 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR---WGQGTTVTVSS 87
 32;
 25;
 Query Match
Pest Local Similarity 60.7%; Pred. No. 8.7e-30;
Matches 68; Conservative 12; Mismatches 7; Indels 25;
 Query Match 73.7%; Score 331; DB 11; Length 473; Best Local Similarity 58.0%; Pred. No. 3.5e-29; Matches 69; Conservative 11; Mismatches 7; Indels 3;
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 473 AA; 51699 NW; 9DED57AS14475FBB_CRC64;
 137 137 137 15171 MW; 5C38D966DC6A4124 CRC64;
 , Last sequence update)
, Last annotation update)
 137 AA
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence
01-MAR-2003 (TrEMBLrel. 23, Last annotation
Putative matrix cell adhesion molecule-3.
 PRT;
 PRT;
 PRELIMINARY;
 PRELIMINARY;
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 STRAIN=C57BL/6;
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 80 SQKFQGRLIMTRDISISTVYMDLSSLRSDDTAVYFCAREMEITFGGAVSKGFYYYGMDVW 139
 44
 77 W-----
 20 QVQLVQSGABVKKPGASVKVSCKASGYTFSNYYMNWVRQAPGQGPEWMGVINPSGGSARY 79
 STAIN=CSTBL/6;

A Kozono Y. Kozono H., Azuma T.;

A Kozono Y. Kozono H., Azuma T.;

A Kozono Y. Kozono Of Relative Affinity by Flow Cytometry Reveals

T Affinity Maturation of B Cell Antigen Receptors in Response to (4-

T Hydroxy 3-Nitropheny1) Acetyl (NP).";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; AB069913; BAB63929-1;

R InterPro; IPR001016; Ig_MHC.

R InterPro; IPR003596; Ig_WHC.

R Pfam; PF00047; ig; I.

R Pfam; PF00047; ig; I.

R Pfam; PR004106; IGV; I.

R PR05ITE; PS50835; IG_IKE; I.
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG------
 Gaps
"Homo sapiens putative microfibrillar protein with Ig-like domain 3 mRNA (Matrix Cell Adhesion Molecule-3, Mat-CAM 3).";
Submitted (JUN-201) to the EMBL/GenBank/DDBJ databases.
EMBL, AY039025, AAK82649.1; -..
Interpro; IPR003106; Ig-like.
Interpro; IPR003106; Ig-MHC.
Interpro; IPR003106; Ig-W.
Pfam; PF00047; ig; 1.
SMART; SMO466; IG-V.
BERGUENCE 159 AA; I7497 MM; 5D29537E88IFAF02 CRC64;
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 43;
 30;
 Query Match 73.6%; Score 330.5; DB 4; Length 159; Best Local Similarity 53.8%; Pred. No. 1e-29; Matches 70; Conservative 11; Mismatches 6; Indels 43
 Query Match 73.3%; Score 329; DB 11; Length 142; Best Local Similarity 59.0%; Pred. No. 1.3e-29; Matches 69; Conservative 12; Mismatches 6; Indels 3
 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-------
 1 OIQLVOSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI
 142 AA; 15622 MW; 24A265CE4EA4318B CRC64;
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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SEQUENCE FROM N.A.
 NCBI_TaxID=10090
 STRAIN=C57BL/6;
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NON TER
SEQUENCE
 Query Match
 Query Match
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 9
 61 NEKFKSKATLITVDKSSSTAYMQLSSLISEDSAVYYCARRGWEAMDYWGQGTSVTVSS 117
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG-----
 61 NEKFKSKATLIVDKPSSTAYMQLSSLTSEDSAVYYCARDDYGRTFWGQGTTLIVSS 116
 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTTVTVSS 87
 Kozono Y., Kozono H., Azuma T.,
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl) Accepyl (RP).",
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB067788; BAB62273.1, --
Interpro; IPR00710; Ig-like.
Interpro; IPR003065; Ig-WHC.
 Kozono Y., Kozono H., Azuma T.;

Kozono Y., Kozono H., Azuma T.;

"Direct Estimation of Relative Affinity by Flow Cytometry Reveals

"Direct Estimation of Relative Affinity by Flow Cytometry Reveals

"Bitinty Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl) Acetyl (NP).";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

BMBL, AB067796; BAB63281.1;

InterPro; IPR003106; Ig-like.

InterPro; IPR003106; Ig-MHC.
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Mus.
NCBI_TaxID=10090;
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 Match 73.2%; Score 328.5; DB 11; Length 141; Local Similarity 58.6%; Pred. No. 1.5e-29; es 68; Conservative 12; Mismatches 7; Indels 29;
 141 AA; 15561 MW; DDD80482D66B76A0 CRC64;
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
 140 AA.
 141 AA
 Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
 PRELIMINARY;
 PRELIMINARY;
 SEQUENCE FROM N.A.
STRAIN=C57BL/6;
 SEQUENCE FROM N.A. STRAIN=C57BL/6;
 NCBI_TaxID=10090;
 45
 Query Match
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 44
 61 NEKFKSKATLITVDKPSSTAYMQLSSLTSEDSAVYYCARWDEDYAMDYWGQGTSVIVSS 118
 Gaps
 61 NEKFKSKATLITUDKPSSTAYMQLSSLTSEDSAVYYCARIYAGDYWGQGTSVTVSS 115
 45 -----KATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 Kozono Y., Kozono H., Azuma T.;
Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antique Receptors in Response to (4-
Affinity Maturation of B Cell Antique Receptors in Response to (4-
Hydroxy-3-Nitropheny) Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EmBL; ABG07790; BAB63275.1;
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003596; Ig_NHC.
Pfam; PF00047; ig; 1.
SMO0406; IGV;
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
VH186.2-D-J-C mu protein (Fragment).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTTVTVSS
 31;
 DB 11; Length 143;
 Length 140;
 1 OIQLVQSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWIG-
 1 OIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG
 72.7%; Score 326.5; DB 11; Length 57.6%; Pred. No. 2.6e-29; Indels tive 12; Mismatches 7; Indels
 7; Indels
 143 143
143 AA; 15868 MW; 139B2E966B81E07F CRC64;
 140 140
140 AA; 15361 MW; 60739B790FC6AF24 CRC64;
 0924Q7;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
VH186.2-D-J-C mu protein (Fragment)
 Pfam; PF00047; ig; 1.
SMART; SM0406; IGv; 1.
PROSITE; PSC0835; IG_LIKE; 1.
NON_TER 140 140
SEQUENCE 140 AA; 15361 MW;
 SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
 Local Similarity 57.6 tes 68; Conservative
 PRELIMINARY;
 PRELIMINARY;
 RESULT 11
092407
ID 09240
AC 09240
DT 01-DE
DT 01-DE
DT 01-MA
DE VH186
OS MUB m
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us-09-990-586-91.rspt

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45 -----KATLIYDKSISIAYMELSSLRSEDTAVYFCAR-------WGQGTIVIVS 86
 A KOZONO Y., KOZONO H., Azuma T.;

KOZONO Y., KOZONO H., Azuma T.;

KOZONO Y., KOZONO H., Azuma T.;

KOZONO Y., KOZONO H., Azuma T.;

KOZONO Y., KOZONO H., Azuma T.;

KOZONO Y., KOZONO H., Azuma T.;

TOTICECT BELIMATION OF BCELL ANTIGEN RECEPTORS IN RESPONSE tO (4-

HYDIOXY-3-Nitrophenyl)Acetyl (NP).";

KHYDICXY-3-Nitrophenyl)Acetyl (NP).";

SUDMITCE (AUG-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; AB067792; BAB63277.1;

R INTERPRO; IPRO03006; IG_MHC.

R INTERPRO; IPRO03506; IG_WHC.

R FRONTER; SM00406; IGY; 1.

R SMART; SM00406; IGY; 1.
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWIG------
 Match 72.6%; Score 326; DB 11; Length 146; Local Similarity 56.2%; Pred. No. 3.1e-29; les 68; Conservative 12; Mismatches 7; Indels 34; Gaps
 092408 PRELIMINARY; PRT; 146 AA.
092408.
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
Buks musculus (Mouse).
Buksayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
11 TaxID=10090;
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
VH186.2-D-J-C um protein (Fragment).
Whis musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae; Murinae; Mus.
VOLE_TaxID=10090;
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 PRELIMINARY;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
STRAIN=C57BL/6;
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 121 S 121
 87 $ 87
 87 S 87
 Query Match
 0924Q6
0924Q6;
 RESULT 14
Q924Q6
 Matches
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 1 SVQLQQPGAELVKPGASVKLSCKASGYTFTSYMMHWVKQRPGRGLEWIGRIDPNSGGTKY
 45 -----KATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG-----
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG-----
 Gaps
 Kozono Y., Kozono H., Azuma T., "Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl) Acetyl (MP).",
 Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of Bela Antigen Receptors in Response to (4-
Alfinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy.3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090,
 33;
 34;
 DB 11; Length 145;
 72.6%; Score 326; DB 11; Length 146; llarity 56.2%; Pred. No. 3.18-29; Conservative 12; Mismatches 7; Indels 3
 Hydroxy-3 "Mitrophenyll Acetyl Milly in New-Prolation Phydroxy-3 "Mitrophenyll Acetyl Milly", Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067793; BAB63278-1; -.
EINTER-Pro; IPR001100; Ig—11ke.
Inter-Pro; IPR001306; Ig—11ke.
INTER-IPR001306; Ig—11ke.
Inter-Pro; IPR001306; Ig—11ke.
INTER-IPR001306; Ig—IPR001306; Ig—
 Query Match 72.7%; Score 326.5; DB 11; Length Best Local Similarity 56.7%; Pred. No. 2.7e-29; Matches 68; Conservative 12; Mismatches 7; Indels
 146 146 146 MW; 92460F1FDF1B7538 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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 EMBL; AB067781; BAB63266.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
Pfam; PF00047; ig; 1.
 SMART; SM00406; IGv, 1.
PROSITE; PS50835; IG_LIKE; 1.
 PRELIMINARY;
 SEQUENCE FROM N.A.
 L Similarity
68; Conserv
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
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 Query Match
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61 NEKFKSKATLIVDKPSSTAYMQLSSLTSEDSAVYYCARSLITTYYAMDYWGOGTSVTVSS 120
 45 -----KATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS 87
 1 CVQLQQPGABLVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 60
 45 -----KATLIVDKSTSTAYMELSSLRSEDTAVYFCAR-------WGQGTTVTVSS 87
 1 OIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG------44
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG------
 72.5%; Score 325.5; DB 11; Length 145;
56.7%; Pred. No. 3.5e-29;
tive 12; Mismatches 7; Indels 33; Gaps
 Gaps
 Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Kozono Y., Kozono H., Azuma T.;
Joirect Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).",
Bydroxy-3-Nitrophenyl)Acetyl (NP).",
EMBL; AB067794; BAB65279-1; -
InterPro; IPR007110; Ig-like.
InterPro; IPR003506; Ig-MHC.
InterPro; IPR003596; Ig-V.
Proson Proson Proson Proson Proson Property Property InterPro; IPR00479; Ig-V.
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
Mus musculus (Mouse)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae; Mus
 Query Match 72.5%; Score 325.5; DB 11; Length 145; Best Local Similarity 56.7%; Pred. No. 3.5e-29; Matches 68; Conservative 12; Mismatches 7; Indels 33;
 Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067791; BAB63276.1; -.
 145 AA; 16001 MW; 0F409EB09FA333D2 CRC64;
 145 AA; 16011 MW; 9BC0846D40DF97BA CRC64;
 145 AA
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PROSITE; PS50835; IG_LIKE; 1.
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PROSITE; PS50835; IG LIKE; 1.
 InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig v.
 Query Match
Best Local Similarity 56.74
Matches 68; Conservative
 PRELIMINARY;
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
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Search completed: January 13, 2004, 12:43:07 Job time: 16:5764 secs

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 January 13, 2004, 12:18:44; Search time 20.2873 Seconds (without alignments) 680.681 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 US-09-990-586-91
449
1 QIQLVQSGGEVKKPGASVRV......DTAVYFCARWGQGTTVTVSS 87
 Description
 1107863
 | SIDSI/gcgdata/geneseq/geneseqp-embl/A
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 /SIDS1/gcgdata/geneseq/geneseqp-emb
 Total number of hits satisfying chosen parameters:
 1107863 segs, 158726573 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - protein search, using sw model
 ABG74721
AAR93003
AAW84097
AAB07965
AAW06442
AAB12168
AAW90935
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 A_Geneseq_19Jun03:
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 Query
Match Length DB
 Title:
Perfect score:
Sequence:
 Scoring table:
 OM protein
 Database :
 Searched:
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| Humanised LL2 MAD<br>Variable heavy cha<br>pUC-RVH-1220d. Sy<br>Anti-human HM1.24 | human HM1<br>hised anti<br>hised anti-<br>HM1.24 an | HM1.24 hised H hised H hised H hised H | chain<br>chain<br>uman re<br>Mi.24 a    | 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7        | Fragment of humani<br>Humanised C4G1 Ig<br>Amino acid sequenc<br>Completely humanis<br>Amino acid sequenc<br>Humanised Wr regio<br>Humanised anti-Tac<br>Protein SEQ ID NO:<br>Humanised anti-Tac |
|-----------------------------------------------------------------------------------|-----------------------------------------------------|----------------------------------------|-----------------------------------------|----------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| AAR92218<br>AAW27698<br>AAR29017<br>AAW65773                                      | 5220                                                | 002577<br>002577<br>00557              | 2233<br>71233<br>71235<br>71235         | 22 23 25 25 25 25 25 25 25 25 25 25 25 25 25 | AAW49817<br>AAR39268<br>AAW49818<br>AAR43339<br>AAW49816<br>AAW37815<br>AAW37812<br>AAW3785514                                                                                                    |
| 7 8 E G                                                                           | 00000                                               | 00000                                  | 1222111                                 | 448222444<br>80048644                        | 0 4 0 4 0 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                           |
|                                                                                   | . m m m r                                           | <b>~~~~~~</b>                          | <b>66641</b>                            | 0 W W W C C H W W                            | 2 2 2 2 4 4 4 1 1 1 1 1 1 1 1 1 1 1 1 1                                                                                                                                                           |
| 4444                                                                              |                                                     |                                        | 888888                                  |                                              | 000000000000000000000000000000000000000                                                                                                                                                           |
| 633.                                                                              | 9999                                                |                                        |                                         | $\cdots$                                     |                                                                                                                                                                                                   |
| 0111                                                                              | 4006                                                | 20000<br>20000<br>20000                | 1 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | 7                                            | <b>ままます は は は は は は な な な な な な は は は は は は は </b>                                                                                                                                                |

## ALIGNMENTS

us-09-990-586-91.rag

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The sequence represents residues from a human immunoglobulin with homology to the heavy chain variable region from monoclonal antibody composed to the heavy chain variable region from monoclonal antibody 10x83 (AAR82990), specific for epidermal growth factor receptor, produced by a mouse hybridoma. The sequence is partial, and complementarity determining regions are omitted. The sequence is isolated by comparison of human and mouse immunoglobulins and analysis for T-lymphocyte antigenic sequences using a computer algorithm. Residues not within a complementarity determining region, canonical structure or Vernier zone may be modified to reduce immunogenicity in humans (e.g. in sequence AAR92992). This method, which involves the introduction of only a few point mutations into 7 reell epitope coding regions, is generally applicable in humanisation of mouse antibodies. The resulting humanised antibodies may be used of mouse antibodies. They retain the antipen recognition of the original antibody, but are not immunogenic in humans. Cupdated on 25-MAR-2003 to correct PI field.)
 human interleukin (IL)-lbeca; antirheumatic; antiarthritic; humanised; antiinflammatory; osteopathic; antiallergic; cerebroprotective; antianthmatic; immunosuppressive; antibacterial; vaccine; Mu007; rheumatoid arthritis; osteoarthritis; cartilage destruction; allergy; septic shock; endoroxic shock; septicaemia; stroke; asthma; graft versus host disease; inflammatory bowel disease; DP-5.
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME
 Identifying interspecies differences in amino acid sequence of Ig T-cell epitopes - by sequence comparison, also humanised antibodies contg. altered T-cell epitopes, retaining antigen specificity but not immunogenicity, esp. for tumour treatment
 Murine, light chain, variable region, antibody, Crohn's disease,
 Mateo De Acosta Del Rio CM;
 86.0%; Score 386; DB 17; Length 8 81.6%; Pred. No. 3.9e-29; tive 9; Mismatches 7; Indels
 Murine humanised Mu007-associated protein DP-5
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
 ABG74721 standard; Protein; 87
 Claim 14; Fig 2; 33pp; English
 Valladares JL,
 18-JUL-2002; 2002WO-US21281.
94CU-0000080
 (first entry)
 Query Match
Best Local Similarity 81.0
Best Local 71; Conservative
 4PI; 1996-130770/14.
 87 AA;
 WO2003010282-A2.
 Rodriquez RP,
30-JUN-1994;
 10-MAY-2003
 Sequence
 ABG74721;
 RESULT 2
 ABG74723
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This invention describes a novel antibody that specifically binds mature human interleukin (II)-lbeta, and binds the same epitope on mature human II-lbeta as mouse monoclonal antibody Mu017 or humanized antibody Hu007. The antibody of the invention have antirheumatic, antiarthritic, antiatlargic, careborporcective, antiatlarmator, immunosuppressiv, antiallargic, careborporcective, antiatlargic, immunosuppressiv, antiallargic, acteborporcective, antiating them a vaccine. The antibody is useful for manufacturing a medicament for treating rhemmatoid archiritis or osteoarthritis, or for inhibiting cartilage destruction in a subject. The antibody is also useful for treating allergy, septic or endotoxic shock, septicaemia, stroke, asthma, gairf versus host disease, Crohn's disease, or inflammancy bowel disease. This sequence represents a protein associated with the humanised murine Mu007 antibody described in the disclosure of the
 9
 Homologous sequences to antibody IOR-CEA-1 variable region heavy chain.
 New IL-1beta antibodies, useful for treating allergy, septic or
endotoxic shock, septicemia, stroke, asthma, graft versus host disease,
Crohn's disease, or inflammatory bowel disease
 1 Ololvosegevkkpgasvrvsckasgysftwyrospekglewigkatlivdkststaywe
 IOR-CEA-1; monoclonal antibody; human; mouse; heavy chain; homology; variable region; framework; cloning; computer; algorithm; immunogenicity; site-directed mutagenesis; T-lymphocyte epitope; tertiary structure; point mutation; antibody engineering; protein engineering; humanised antibody; antitumour; cancer; therapy.
 Gaps
 6..30
note= "Amino acid involved in tertiary structure"
 structure"
 ô
 Manetta JV, Tsurushita N;
 Length 87,
 84.6%; Score 380; DB 24; Length 8 80.5%; Pred. No. 1.46-28; ive 8; Mismatches 9; Indels
 "Amino acid involved in tertiary
 /note= "Amino acid involved in tertiary
 87
 87
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS
 61 LSSLRSEDTAVYYCATWGQGTLVTVSS
 Location/Qualifiers
 Jia AY, Kuhstoss SA,
 AAR93003 standard; Protein; 87 AA
 Disclosure, Fig 2; 98pp; English.
26-JJL-2001; 2001US-307973P.
14-AUG-2001; 2001US-312278P.
 (updated)
(first entry)
 Query Match
Best Local Similarity 80.5-
Local 70; Conservative
 note=
 WPI; 2003-248068/24.
 (EFIL) LILLY & CO
 87 AA;
 Homo sapiens
 25-MAR-2003
18-MAY-1996
 Bright SW,
Vasquez MJ;
 AAR93003;
 Sequence
 Region
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 Region
 RESULT 3
 AAR93003
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Gaps

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Length 87;

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EP699755-A2

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complementarity detain variable region from mouse monocload antibody to the heavy chain variable region from mouse monocload antibody to R-CEA-1 (AAR93002). The sequence is partial, and complementarity determining regions are omitted. The sequence is isolated by comparison of human and mouse immunoglobulins and analysis for T-lymphocyte antigenic sequences using a computer clannical structure or Vernier zone may be modified to reduce immunogenicity in humans (e.g. in sequence AAR93004). This method, which involves the introduction of only a few point mutations into complement epitope coding regions, is generally applicable in humanisation of mouse antibodies. The resulting humanised antibodies may be used e.g. as antitumour agents. They retain the antigen recognition of the criginal antibody, but are not immunogenic in humans.

(Updated on 25-MAR-2003 to correct PI field.)
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME
 Identifying interspecies differences in amino acid sequence of Ig
recal epitopes - by sequence comparison, also humanised antibodies
contg. altered T-cell epitopes, retaining antigen specificity but
not immunogenicity, esp. for tumour treatment
 Humanised antibody, monoclonal antibody, MAD, antibody engineering, mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis; cancer; metastesis; rheumatoid arthritis; atherosclerosis; angiogenesis; diabetic retinopathy; inflammation; macular degeneration; osteoporosis; Paget's disease;
 The sequence represents residues from a human immunoglobulin with homology to the heavy chain variable region from mouse monoclonal
 hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
 83.7%; Score 376; DB 17; Length 87; 79.3%; Pred. No. 3.4e-28; Ative 11; Mismatches 7; Indels
 Valladares JL, Mateo De Acosta Del Rio CM;
 Humanised anti-alpha-v beta-3 MAb D12HZHC 1-0 VH.
 87
 61 LSSLRSEDTAVYFCARWGOGTTVTVSS
 LSSLRSEDTAVYYCARWGEGTLVTVSS
 (IMMU-) CENT IMMUNOLOGIA MOLECULAR
 AAW84097 standard; Protein; 117 AA
 Claim 22, Fig 9; 33pp; English.
 95EP-0201752
 94CU-0000080
 Local Similarry
hes 69; Conservative
 15-MAR-1999 (first entry)
 WPI; 1996-130770/14.
 87 AA;
 Rodriquez RP,
 Homo sapiens
Synthetic.
 27-JUN-1995;
 30-JUN-1994;
 36-MAR-1996
 D12HZHC-10
 AAW84097;
 Sequence
 Query Match
 Best Loc
Matches
 RESULT 4
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This is the amino acid sequence of the heavy chain variable region (VH) of humanised anti-alpha-v beta-3 vitronectin receptor monoclonal antibody DizHZHC 1-0. It is based on the VH sequence (see AAW84095) of human Kabat subgroup I VH, with complementarity determining regions (CDRs) from the murine anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody DI2 (see AAW84033).

7 Murine framework residues (24, 48, 70, 72 and 74) are retained. The humanised heavy chain can be expressed in host are retained. The humanised heavy chain can be expressed in host cells using nucleic acid molecules (see AAW84098)). The humanised antibodies can be used for passive immunotherapy of disorders antibodies can be used for passive immunotherapy of disorders andiogenic related disorders, such as angiogenesis associated with diabetic retinopathy, atherosclerosis and restenosis, chronic with diabetic retinopathy, atherosclerosis and restenosis, chronic and cancer, e.g. solid tumour metastasis, and diseases where bone resorption is associated with pathology such as osteoporosis, opereolytic lesions produced by bone metastasis, bone loss due to immobilisation or sex hormone deficiency. They can also be used for targeted drug therapy, and for detection and diagnosis.
 1 gvolvosgaevkkegasvkvsckasgvaersvnnymvkoaeggelemigyideyngdrey 60
 61 NQKFKGKATLITVDKSTSTAYMELSSLRSEDTAVYYCARQNYGSFAYWGQGTLVTVSS 117
 87
 Gaps
 44 ----GKATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 New anti alpha v beta 3 vitronectin receptor antibodies - used immunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory disorders, atherosclerosis, restenosis, cancers or
 Query Match
Best Local Similarity 67.5%; Pred. No. 5.6e-28;
Matches 79; Conservative 6; Mismatches 2; Indels 30
 1 QIQLVQSGGEVKKPGASVRVSCXASGYSFT-----WVRQSPGKGLEWI
Location/Qualifiers
 (SMIK) SMITHKLINE BEECHAM CORP.
 Claim 1; Page 58; 97pp; English.
 CDR2
 CDR1
 CDR3
 97US-0039609.
 98WO-US04987
 50..66
/label=
99..106
/label=
 31..35
/label=
 Jonak ZL,
 WPI; 1999-034590/03.
N-PSDB; AAV71799.
 117 AA;
 Johanson KO,
 WO9840488-A1
 osteoporosis
 17-SEP-1998,
 Sequence
 Key
Region
 Region
 Region
 RESULT 5
 g
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AAB07965 standard, Protein, 135 AA.

AAB07965

AAB07965 ID AAB0 XX AC AAB0 XX

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The present sequence represents the heavy chain variable region of the humanised murine antibody 3D1. The antibody has a binding specificity to 87 molecules. The antibody is used to construct humanized immunoglobulins, which comprise an antigen binding region of non-human origin and a portion of a human immunoglobulin. The humanized immunoglobulins are useful for treating autoimmune diseases, inflammatory diseases, inflammatory diseases, inflammatory diseases, inflammatory dermatitis, arthritis, inflammatory bowel disease, inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are also useful for treating a transplant recipient or preventing transplant rejection in a transplant recipient, and treating proliferative disease (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia).
 Antibody 3D1, B7 molecule; B7; humanised immunoglobulin; autoimmune disease; inflammatory disorder; autoimmune disease; inflammatory disorder; systemic lupus erythematosus; diabetes mellitus; insulitis; asthma; arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis; multiple sclerosis; transplant rejection; proliferative disease; leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia; aplastic.anaemia; myeloid dysplasia syndrome.
 a and aplastic anaemia), inborn errors of metabolism, immunodeficiency diseases, and myeloid dysplasia syndrome
 Humanized immunoglobulin having a binding specificity to B7-1 (derive from ATCC PTA-163), or B7-2 (derived from ATCC CRL-12524) molecules, modulates immune responses and can therefore treat e.g. autoimmune
 "complementarity determining region 2"
 118..124
/note= "complementarity determining region 3"
 Celniker AC, Collins M, Rup B, Veldman GM;
 A heavy chain variable region of humanised 3S1 antibody.
 50..54
/note= "complementarity determining
 ch 82.5%; Score 370.5; DB 21; I Similarity 66.4%; Pred. No. 1.7e-27; 77; Conservative 8; Mismatches 2; 1
 /note= "signal peptide"
 "mature protein"
 Location/Qualifiers
 thalassemia and aplastic anaemia),
 Example 3; Fig 2A; 162pp; English.
 Carreno B,
O'hara D,
 infectious diseases
 09-FEB-2000; 2000WO-US03303
 99US-0249011.
(first entry)
 (GEMY) GENETICS INST INC
 /note=
 /note=
 69..85
 WPI; 2000-524532/47.
 Vasquez M,
Knight A,
 Query Match
Best Local Similarity
Matches 77; Conserv
 135 AA;
 N-PSDB; AAA59694.
 WO200047625-A2
 12-FEB-1999;
24-JUN-1999;
 Mus sp.
Homo sapiens.
 14-NOV-2000
 17-AUG-2000.
 congenital
 o MS,
 Synthetic.
 diseases,
 Sequence
 Peptide
 Protein
 Region
 Region
 Region
 Gray
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,
 This sequence represents the variable heavy (VH) chain of the humanised murine antibody HuMc3 VH. The Mc3 VH sequence was humanised using the buried residue modification technique, where important non-human framework residues are unaffected. The Mc3 antibody binds to the Antibody can titled of the human milk fat globule (HMFG). The milk fat globule membrane is derived from the apical surface of the mammalian epithelial edil during lactation, and therefore is a source for breast membrane glycoproteins. The antibody can be used in an in vitro method to detect a HMFG antigen (or antigen fragment), and to diagnose the presence of the antipon in a subject. The antibody can also be used to deliver an agent to a target (within a subjects body), containing a HMFG antigen. The antibodies can also be used for diagnosis, prognosis, and therapeutic high affinity hindian to the house of the hindian the high affinity hindian the h
 SYQLYQSGABYKKPGASYKVSCKASGXSFTGYTMHWVKQSPGMNLEWIGLINPYNGGTVY 79
43
 Humanised antibody; variable heavy region; buried residue modification; VH; HuMc3 VH; BA46 antigen; human; milk fat globule; HMFG; lactation; fat globule membrane; murine; mammal; epithelial cell; breast cancer; breast membrane glycoprotein; therapy; immunotherapy.
 Gaps
 87
 Recombinant MG3 antibody which binds BA46 antigen of HMFG -comprises a modified heavy or light chain variable region, useful the diagnosis and therapy of breast cancer
 80 NQKFKGKATMTVDKSTSTAYMELSSLRSEDTAVYYCARAAWYMDYWGQGTLVTVSS
 ----GKATLIVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTTVTVSS
 30;
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG---
 high affinity binding to the antigen, they are useful for immunodiagnostic and immunotherapeutic applications in humans
 Length 136
 4; Indels
1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI
 Score 370; DB 17;
Pred. No. 1.9e-27;
4; Mismatches 4;
 Do Couto FJR, Peterson JA;
 (CANC-) CANCER RES FUND CONTRA COSTA
 Ą.
 Claim 13; Fig 18; 91pp; English
 AAW06442 standard, Protein; 136
 Query Match
Best Local Similarity 67.5%;
Matches 79; Conservative 4
 95US-0487598
94US-0307868
 95WO-US11683
 (first entry)
 WPI; 1996-179941/18.
 136 AA;
 N-PSDB; AAT42717
 HuMc3 VH region.
 14-SEP-1995;
 07-JUN-1995;
16-SEP-1994;
 WO9608565-A2
 21-MAR-1996.
 Ceriani RI,
 04-FEB-1997
 Synthetic.
 20
 AAW06442;
 Sequence
 20
 44
 RESULT 6
 AAW06442
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(derived

Goldman S;

Gaps

9

Indels

Length 135;

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RESULT 8
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 Hepatitis B virus (HBV) is responsible for hepatitis infection in humans, which may progress to liver cirrhosis or cancer. One of HBV's surface antigens is pre-S1. Monoclonal antibodies specific for pre-S1 antigen may efficiently neutralise HBV. The present invention relates to humanised antibodies specific for HBV surface antigen pre-S1. The humanised antibodies are useful for preventing HBV infection and for treating chronic hepatitis B. The Complementarity Determining Regions of mouse pre-S1 antibody KR127 were graffed onto human antibody to produce the humanised antibodies of the present invention. The present sequence is the humanised pre-S1 antibody HKR127HC(I) heavy chain variable region (VH). The coding sequence for the present sequence was produced from the coding sequence for the present sequence (AAA62115).
 43
 for
 80 NQKEQDKATLITVDKSTSTAYMELSSLRSEDTAVYFCARRWRYTMDYWGQGTLVIVSS 136
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWI-------
 Humanized antibody specific for hepatitis B virus surface antigen
pre-S1, containing humanized heavy and light chain regions, useful for
preventing hepatitis B virus (HBV) infection and for treating chronic
 Humanised HBV pre-S1 antibody HKR127HC(I) heavy chain variable region.
 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS 87
 Gaps
 28;
 81.1%; Score 364; DB 21; Length 115; 67.0%; Pred. No. 6e-27; ive 6; Mismatches 4; Indels 26
 Humanised antibody, HBV surface antigen pre-S1, mouse, human; hepatitis B, liver cirrhosis, liver cancer.
 (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
(GREC) KOREA GREEN CROSS CORP.
 AAB12168 standard; Protein; 115 AA
 Claim 2; Fig 1; 61pp; English.
 99WO-KR00699
 98KR-0049663.
 17-JAN-2001 (first entry)
 Hong HJ, Ryu CJ, Hur H;
 Conservative
 Chimeric - Homo sapiens.
Chimeric - Mus sp.
 WPI; 2000-400048/34.
 Local Similarity
es 77; Conserv
 115 AA;
 N-PSDB; AAA62118
 WO200031141-A1
 hepatitis B -
 19-NOV-1999;
 19-NOV-1998;
 02-JUN-2000.
 Sequence
 AAB12168;
 Query Match
 Matches
 RESULT
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This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents capprosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-dabetic, anti-allergic, anti-arthritic, antivaral, immunosuppressive, thyromimetic, anti-arteriosclearctic, antidabetic, antiffertility, neuroprotective, antidabetic, antiffertility, neuroprotective, antidateriosclearctic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent capptosis by binding to cell surface Fas or inhibit it by competitive inhibit solutions. Hashimoto disease, rheumatoid arthritis, graft versus host disease, Slorgen's syndrome, pernicious or hypoplastic versus host disease, Slorgen's syndrome, pernicious or hypoplastic canemia, Addison's disease, rheumatoid arthritis, graft corent and allergy, allergy, arteriosclerosis, myocarditis, dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis (bulminat, chronic, viral (B, C or D) or alcoholic, and transplant rejection. (I) selectively induce it in abnormal cells They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic murine disease models. (I) act on the active site of Fas, i.e. they mimic cultive light on the induce liver disease, and have reduced in murine disease models. (I) act on the active site of Fas, i.e. they mimic murine disease, and have reduced in the method of the invention.
 antiallergic; antiarthritic; antiviral; immunomodulatory; cardiant; dermatological; antiarthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antinfertility; neuroprotective; antiarteriosolerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; hheumatola arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Cohn's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosolerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 New humanized anti-Fas antibody, useful for treating or preventing e.g.
inflammatory or autoimmune disease, induces apoptosis selectively in
cells with abnormal Fas-Fas ligand systems
 Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 Takahashi T;
 Humanised anti-Fas designed heavy chain Heu 3 protein.
 Tamaki I,
 Serizawa N, Haruyama H, Nakahara K,
 Claim 2; Page 180-182; 263pp; English.
 Ą
 AAW90935 standard; Protein; 470
 98JP-0276881.
98JP-0276882.
 08-AUG-2000 (first entry)
 (SANY) SANKYO CO LTD.
 WPI; 2000-258930/23.
 N-PSDB; AAA11646
 30-SEP-1998;
30-SEP-1998;
 29-SEP-1999;
 EP990663-A2
 05-APR-2000
 Synthetic.
 AAW90935;
AAW90935
```

1 OVOLVOSGAEVVKPGASVKVSCKASGYAFSSSWMNWVROAPGOGLEWIGRIYPGDGDTNY

61 AQKFQGKATLIADKSTSTAYMELSSLRSEDTAVYFCAREYDEAYWGQGTLVTVSS 115 ----GKATLIVDKSISTAYMELSSLRSEDTAVYFCAR-----WGQGTTVTVSS 87

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80 NOKFKGKATLIVDISTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGQGTLVTVS 139
20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNY 79
 The complementarity determining regions (CDRs) of mouse monoclonal antibody (Whb. Li2 VK (AAR2215) and VH (AAR3226) regions were recombinantly linked to the framework sequences of human VK and VH regions, respectively, to give humanised LL2 VK (AAR3218). And VH (AAR3218). These were subsequently linked, respectively, to human veappa and IgG1 constant regions. A humanised MAb was obtd. that retained the B-lymphoma and leukaemia cell targeting and internalisation characteristics of the parental LL2 MAb, and which cytostatic agent for therapeutic appln. It can be linked to e.g. a
 Humanised antibody; monoclonal antibody; MAb; LL2; B-oell lymphoma; leukaemia; therapy; diagnosis; complementarity determining region; CDR; antibody engineering.
 81.0%; Score 363.5; DB 17; Length 116; larity 64.7%; Pred. No. 6.7e-27; Conservative 9; Mismatches 3; Indels 29;
 Chimeric and humanised LL2 antibodies - used to produce for the therapy and diagnosis of B-cell lymphoma(s) and
 ----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR
 Location/Qualifiers
 AAR92218 standard; Protein; 116 AA.
 Claim 5; Page 39; 70pp; English.
 99..105
/label= CDR3
 11..35
/label= CDR1
 95WO-US09641.
 94US-0289576.
 Humanised LL2 MAb VH region
 (first entry)
 50..66
/label= (
 (IMMU-) IMMUNOMEDICS INC
 WPI; 1996-139454/14.
N-PSDB; AAT15804.
 Hansen H, Leung S;
 Query Match
Best Local Similarity
Matches 75; Conserv
 116 AA;
 140 S 140
 $ 87
 11-AUG-1995;
 12-AUG-1994;
 28-MAY-1996
 409604925-A1
 or the ther
 22-FEB-1996.
 Synthetic
 AAR92218;
 Sequence
 44
 Key
Region
 Region
 Region
 RESULT 10
 요
 셤
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 'n
 80 NOKFKGKATLIVDISISIAYMELSSLRSEDIAVYYCARNRDYSNNWYFDVWGQGTLVIVS 139
 The invention relates to a preventive or treating agent for diseases caused by abnormality in Fas/Fas ligand system containing as the active component an antibody having as the light chain subunit a polypeptide containing residues 1-218 of one of 3, 239 residue amino acid sequences, or residues 1-451 of one of 3, 470 residue amino acid sequences, all fully defined in the specification and having an activity of combining specifically with mammalian Fas and an activity of inducing apoptosis antiallergic activity and is used for preventing and treating autoimmune diseases, allergy, atopy and others.
 43
 43
 79
 44 ----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVS 86
 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVRQAPGQGLEWMGEIDPSDSYTNY
 Gaps
 Gaps
 Drug containing humanised anti-Fas antibody, used for preventing and treating autoimmune diseases, allergy, and atopy -
 Human, mouse, humanised anti-Fas antibody, Fas/Fas ligand,
light chain subunit; apoptosis; immunosuppressive; antiallergic;
autoimmune disease; allergy; atopic.
 34;
 34;
 ο,
 81.1%; Score 364; DB 23; Length 470; 63.6%; Pred. No. 2.3e-26; ive 7; Mismatches 3; Indels 3
 Length 470;
 Mouse humanised anti-Fas antibody related protein SEQ ID NO
 1 QIQLVQSGGEVXKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI-
 3; Indels
 3xample 4 (Preparatory); Page 79-80; 194pp; Japanese.
 Score 364; DB 21;
Pred. No. 2.3e-26;
7; Mismatches 3;
 ABB74904 standard; Protein; 470 AA
 81.1%;
ilarity 63.6%;
Conservative
 28-MAR-2001; 2001JP-0093106.
 29-MAR-2000; 2000JP-0090918.
 (first entry)
 Query Match
Best Local Similarity 63.0%
Best Local 77; Conservative
 (SANY) SANKYC CO LTD
 Query Match
Best Local Similarity
The 77; Conserve
 WPI; 2002-145113/19.
N-PSDB; ABL45926.
 470 AA;
 470 AA;
 JP2001342148-A.
 S 140
 S 87
 Mus musculus
 26-APR-2002
 11-DEC-2001.
 ABB74904;
 Sequence
 Sequence
 140
 87
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ABB74904 RESULT

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Gaps

29;

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The sequences given in AAR29016-17 are portions of monoclonal antibodies which were encoded by plasmids contained within the mouse hybridoma, AUK12-20. The DNA encoding the complementarity determining regions (CDR's) was isolated by polymerase chain reaction. These antibodies recognise human interleukin-6 receptor (IL-6R). The hybridoma cells were transformed with plasmids containing fragments of the antibody gene which caused the production of the antibody from the hybridoma
 Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse; complementarity determining region; monoclonal; hybridoma; PCR; plasmid; polymerase chain reaction; amplify.
 Reconstituted human antibody to human interleukin-6 receptor has low antigenicity and contains mouse V-region complementarity determining regions
 Tsuchiya M;
45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR--
 (Updated on 25-MAR-2003 to correct PN field.)
 χ,
 Sato
 Disclosure; Page 159-60; 207pp; Japanese.
 note= "Leader peptide"
 Saldanha JW,
 location/Qualifiers
 AAR29017 standard; Protein; 135 AA
 69..85
/label= CDR2
86..117
/label= FR3
 5..68
label= FR2
 118..124
/label= CDR3
 |= CDR1
 92WO-JP00544
 91JP-0095476.
 0..49
label= FR1
 125..135
/label= FR4
 (updated)
(first entry)
 CHUS) CHUGAI SEIYAKU KK
 0..54
label=
 Bendig MM, Jones ST,
 WPI; 1992-398882/48.
 À;
 N-PSDB; AAQ31391.
 135
 puc-RVh-1220d.
 24-APR-1992;
 25-APR-1991;
 WO9219759-A1
 19-FEB-1992;
 25-MAR-2003
30-MAR-1993
 12-NOV-1992
 Synthetic
 AAR29017;
 Sequence
 Peptide
 Region
 Region
 Region
 Region
 Region
 Region
 Region
 RESULT 12
 AAR2901
 'n
 44
 9
 9
 44
 116
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG-----
 87
 Gaps
 Monoclonal antibody engineered to contain glycosylation site - in non-Fc constant heavy or light chain region, useful to diagnose or treat B cell malignancies, e.g. non-Hodgkins lymphoma
 The present sequence is the variable heavy chain of the B cell specific monoclonal antibody (MAD) hill: hill: is a highly specific anti-B cell lymphoma and anti-lymphocytic leukaemia cell humanised murine MAD. The MAD can be used to diagnose or treat B cell malignancies, e.g. non-Hodgkins lymphoma or chronic
 ----KATLTVDKSTSTAYMBLSSLRSEDTAVYFCAR-----WGQGTTVTVSS
 Variable heavy chain; B cell; monoclonal antibody; MAD; hLL2; B cell lymphoma; lymphocytic leukaemia cell; murine; humanised; diagnosis; treatment; B cell malignancy; non-Hodgkins lymphoma; chronic lymphocytic leukaemia.
 3; Indels 29;
 DB 18; Length 116;
 Ħ
 region 2"
 99..105
/note= "complementarity determining region 3"
 QIQLVQSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWIG---
 31..35 /note= "complementarity determining region
 50..66
/note= "complementarity determining
 Score 363.5; DB 1
Pred. No. 6.7e-27;
9; Mismatches 3
 Location/Qualifiers
 AAW27698 standard; Protein; 116 AA
 Example 3; Fig 5B; 88pp; English.
 Variable heavy chain of MAb hLL2.
 81.0%;
64.7%;
 96US-0013709.
 97WO-US04196
 (first entry)
 on z;
 75; Conservative
 (IMMU-) IMMUNOMEDICS INC.
 Chimeric - Mus sp.
Chimeric - Homo sapiens.
 lymphocytic leukaemia.
 Leung S,
 WPI; 1997-479995/44
 Query Match
Best Local Similarity
 116 AA;
 N-PSDB; AAT88131.
 20-MAR-1996;
 19-MAR-1997;
 14-APR-1998
 WO9734632-A1
 25-SEP-1997.
 Hansen H,
 Sequence
 AAW27698;
 45
 Key
Region
 Region
 Region
 Matches
 RESULT 11
AAW27698
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1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT-
 AAW65774;
 Synthetic
 Sequence
 Peptide
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 The anti-human HMI,24 antibody is the preferred cytotoxic antibody to be used in the treatment of lymphocytic tumours, including T-cell tumours and B-cell tumours better than mycloma. The antibody is preferably monoclonal and has ADCC or CDC type cytotoxicity. It may be chimeric or humanised, and preferably contains a human antibody constant region C gamma is to gamma 1. A preferred antibody is an anti-human HMI.24 antibody on an anti-human HMI.24 antibody or an entibody which binds to an epitope recognising anti-human HMI.24 antibody. The cytotoxic antibody is useful lymphocytic leukaemia, pre-B lymphocytic leukaemia, pre-B lymphoma, so acute or chronic B chronic T lymphocytic leukaemia.
 43
 79
 20 QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYYIHWVRQAPGQGLEWIGYIDPFNGGTSY
 80 NQKFKGKVIMIVDISINIAYMELSSLRSEDTAVYYCARGGNRFAYWGQGILVIVSS 135
 Gaps
 87
 Treatment of lymphocytic tumours using cytotoxic antibody - binding to specific antigen such as HMI.24 and effective against T-cell tumours and B-cell tumours other than myeloma
 44 -----GKATLIVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTTVTVSS
 Cytotoxic antibody; anti-human HM1.24; lymphocytic tumours; pre-B lymphoma; Burkitt's lymphoma; T-cell tumour; B-cell tumour.
 29;
 Length 135;
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI
 Anti-human HM1.24 antibody heavy chain variable region r.
 4; Indels
 DB 13;
 Score 363.5; DB 1. Pred, No. 7.8e-27;
 7; Mismatches
 20..139
/note= "Mature peptide"
 Disclosure; Page 47-48; 82pp; Japanese.
 /note= "Signal peptide"
 Location/Qualifiers
 AAW65773 standard; Protein; 139 AA.
 81.0%;
 98WO-JP00568.
 97JP-0041410.
Yoshimura Y;
 SEIYAKU KK.
 (first entry)
 WPI; 1998-456869/39.
N-PSDB; AAV07581.
 139 AA;
 (CHUS) CHUGAI
 Koishihara Y,
 12-FEB-1998;
 WO9835698-A1
 12-FEB-1997;
 16-NOV-1998
 20-AUG-1998
 Synthetic
 Sequence
 AAW65773;
 Peptide
 Peptide
 RESULT 13
 AAW65773
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Gaps

33;

Indels

Query Match 81.0%; Score 363.5; DB 19; Best Local Similarity 62.5%; Pred. No. 8e-27; Matches 75; Conservative 9; Mismatches 3;

Length 139;

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.,
 The anti-human HMI,24 antibody is the preferred cytotoxic antibody to be used in the treatment of lymphocytic tumours, including T-cell tumours and B-cell tumours B-cell tumours and B-cell tumours B-cell tumours and B-cell
 80 SQKFKGRVTMTADKSTSTAXMELSSLRSEDTAVYYCARGLRRGGYYFDYWQQTTVTVS 139
 79
20 QVQLVQSGAEVKKRGASVKVSCKASGYTFTPYWMQWVRQAPQQGLEWMGSIFPGDGDTRY 79
 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTPYWMQWYRQAPGQGLEWMGSIFPGDGDTRY
 44 ----GKATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 Treatment of lymphocytic tumours using cytotoxic antibody - binding to specific antigen such as HMI.24 and effective against T-cell tumours and B-cell tumours other than myeloma
 Cytotoxic antibody; anti-human HM1.24; lymphocytic tumours; pre-B lymphoma; Burkitt's lymphoma; T-cell tumour; B-cell tumour.
 33;
 Length 139,
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI
 Score 363.5; DB 19; Length
Pred. No. 8e-27;
9; Mismatches 3; Indels
 Anti-human HM1.24 antibody heavy chain variable region s.
 /note= "Mature peptide"
 /note= "Signal peptide"
 Disclosure; Page 48-49; 82pp; Japanese.
 Location/Qualifiers
 AAW65774 standard; Protein; 139 AA
 Query Match
Best Local Similarity 62.5%;
Matches 75; Conservative 5
 97JP-0041410
 98WO-JP00568
 Yoshimura Y;
 (first entry)
 20..139
 SEIYAKU
 WPI; 1998-456869/39.
N-PSDB; AAV07582.
 139 AA;
 (CHUS) CHUGAI
 Koishihara Y,
 16-NOV-1998
 WO9835698-A1
 12~FEB-1998;
 12-FEB-1997;
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human L and H chain C regions, and L and/or H chain V regions containing material originating in mouse anti-HM1.24 antibody. The V containing material originating in mouse anti-HM1.24 antibody. The V containing material originating in mouse anti-HM1.24 antibody. The V complimentarity determining regions of mouse origin and care the man is a reshaped humanised antibody. The C regions are human CK (L-chain) and human C gamma (especially C gamma i) (H-chain). The FR regions of the C contibody REI) and the FR regions of the H chain V region are derived from human subtype HSG1 (e.g. FR1-3 from human antibody HSG1 (e.g. FR1-3 from human antibody HG3 and FR4 from human antibody JH6). The present sequence represents an H chain V region from the present invention. The antibodies are used for the treatment of myeloma, especially by injection, intravenously, intramuscularly or subcutaneously. The antibodies are used for intramuscularly or subcutaneously. The humanised antibody has low antigenicity and is therefore effective therapeutically in humans.
 ñ
 80 SQKFKGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGLRRGGYYFDYWGQGTTVTVSS 139
 80 SQKFKGRVTMTADKSTSTAYMELSSLRSEDTAVYYCARGLRRGGYYFDYWGQGTTVTVSS 139
 43
 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTPYNMQWVRQAPGQGLEWMGSIFPGDGDTRY 79
 44 ----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WQQTTVTVSS 87
 Humanised anti-HM1.24 antibody H chain V region HEF-RVHr-AHM g-gamma-1.
 Gaps
 A humanised anti-HM1.24 antibody has been developed which comprises
 Mouse, human, humanised, anti-HM1.24 antibody; myeloma, FR, CDR, framework region, complimentarity determining region, antigenicity.
 33;
 Query Match 81.0%; Score 363.5; DB 19; Length 139; Best Local Similarity 62.5%; Pred. No. 8e-27; Matches 75; Conservative 9; Mismatches 3; Indels 33;
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI----
 Humanised anti-HM1.24 antibody - for treatment of myeloma
 Tsuchiya M;
44 ----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-
 Ono K,
 Claim 68; Page 127-128; 210pp; Japanese.
 Koishihara Y, Kosaka M, Ohtomo T,
 AAW62205 standard; Protein; 139 AA.
 96JP-0264756.
 97WO-JP03553
 21-SEP-1998 (first entry)
 (CHUS) CHUGAI SEIYAKU KK.
 WPI; 1998-286421/25.
N-PSDB; AAV39357.
 139 AA;
 Mus sp.
Homo sapiens.
 03-OCT-1997;
 04-OCT-1996;
 WO9814580-A1
 Yoshimura Y;
 09-APR-1998.
 Synthetic.
 AAW62205;
 Sequence
 RESULT 15
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Search completed: January 13, 2004, 12:38:24 Job time : 20.2873 secs 86, Appl 200, Appl 200, Appl 15, Appl 159, App 160, App 167, App 167, App 167, Appl 167, Appl 167, Appl 167, Appl 167, Appl 167, Appl 168, Appl 16

Sequence Sequence Sequence

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us-09-990-586-91.rapb

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DEBLEAGH INFORMATION:

APPLICANT: JUAO, JIN.AN
APPLICANT: WONG, HING C.
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
TITLE OF INVENTION: OF USE THEREOF
FILE REFERENCE: 71758/46943-CIP2
CURRENT APPLICATION NUMBER: US/09/990,586
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 09/293,854
PRIOR APPLICATION NUMBER: 09/293,854
SROID NOS: 102
SOFTWARE: Patentin Ver. 2.1
SROID NO 91
 1 OLOLVOSGGEVKKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME
 1 QIQLVQSGGBVKKRQBASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME
 Query Match
Best Local Similarity 100.0%; Pred. No. 9.1e-38;
Matches 87; Conservative 0; Mismatches 0;
US-10-230-880-89

US-09-990-586-88

US-10-230-880-166

US-10-230-880-166

US-10-230-880-168

US-09-990-586-87

US-09-990-586-86

US-09-990-586-86

US-09-990-586-86

US-09-990-586-86

US-09-990-586-86

US-09-990-586-86

US-09-990-586-86

US-10-230-880-167

US-10-230-880-171

US-09-249-011A-24

US-10-230-880-171
 US-09-956-206A-63
 ALIGNMENTS
 61 LSSLRSEDTAVYFCARWGOGTTVTVSS 87
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 Sequence 91, Application US/09990586 Publication No. US20030109680A1 GENERAL INFORMATION:
 RESULT 2
US-09-990-586-92
; Sequence 92, Application US/09990586
 LENGTH: 87
TYPE: PRT
ORGANISM: Homo sapiens
 -09-990-586-91
 US-09-990-586-91
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 January 13, 2004, 12:43:20; Search time 13.9048 Seconds (without alignments) 1260.812 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 US-09-990-586-91 , 449
1 QIQLVQSGGEVKKPGASVRV.....DTAVYFCARWGQGTTVTVSS
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 GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
 US-09-990-586-91
US-09-990-586-92
US-10-230-880-92
US-09-990-586-93
US-09-990-586-94
US-09-990-586-94
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US-09-990-586-95
US-09-990-586-95
US-00-990-586-95
US-00-990-586-95
US-00-990-586-95
 Total number of hits satisfying chosen parameters:
 747907 segs, 201509753 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 Length
 Title:
Perfect score:
 Scoring table:
 OM protein
 Sequence:
 Database
 Run on:
 Result
No.
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9 9

Gaps

Length Indels

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TYPE: PRT
CRGANISM: Homo sapiens
US-09-990-586-93
) TYPE: PRT
) ORGANISM: Homo sapiens
US-10-230-880-92
 RESULT 5
US-09-990-586-93
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 APPLICANT: UTROCRATION

APPLICANT: UTROCRATION

APPLICANT: WONG, JIN-AN

TITLE OF INVENTION: OF USE THEREOF

FILE REPRENCE: 71758/46643-C1P2

CURRENT APPLICATION NUMBER: U5/09/990,586

CURRENT FILING DATE: 2001-11-21

PRIOR APPLICATION NUMBER: 09/293,854

PRIOR APPLICATION DATE: 1999-04-16

NUMBER OF SEQ ID NOS: 102

SOFTWARE: Patentin Ver. 2.1
 1 ÓIÓLVÓSGGEVKKPGÁSVRVSCKÁSGYSFTWVRÓSPGKGLEWIGKÁTLTVDKSTSTÁYME 60
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLIVDKSTSTAYME
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME
 Gaps
 Sequence 91, Application US/10230880

Publication No. US20030190705A1

GENERAL INFORMATION:

APPLICANT: WONG, HING C.

APPLICANT: STINSON, JEFFREY L.

APPLICANT: STINSON, JEFFREY L.

APPLICANT: MOSQUERA, LUIS A.

ITILE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES

FILE REFERENCE: 71758/58066

CURRENT APPLICATION NUMBER: US/10/230,880

CURRENT FILING DATE: 2002-112-23

PRIOR APPLICATION NUMBER: 09/990,586

PRIOR PELING DATE: 2001-11-21

PRIOR APPLICATION NUMBER: 09/293,854

PRIOR PELING DATE: 2001-10-29

PRIOR FILING DATE: 2001-10-29

PRIOR FILING DATE: 2001-10-29

PRIOR FILING DATE: 2001-10-29

SPIOR FILING DATE: 1999-04-16

NUMBER OF SEQ ID NOS: 174

SEQ ID NO 91
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100.0%; Score 449; DB 12; Length 87;
Best Local Similarity 100.0%; Pred. No. 9.1e-38;
Matches 87; Conservative 0; Mismatches 0; Indels
 Query Match 100.0%; Score 449; DB 11; Length 87; Best Local Similarity 100.0%; Pred. No. 9.1e-38; Matches 87; Conservative 0; Mismatches 0; Indels
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
Publication No. US20030109680A1
 TYPE: PRT
CORGANISM: Homo sapiens
US-10-230-880-91
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-92
 LENGIH: 87
 SEQ ID NO 92
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Sequence 93, Application US/09990586

| Bublication No. US2030109680A1
| Publication No. US2030109680A1
| GENERAL INFORMATION:
| APPLICANT: JIAO, JIN-AN
| APPLICANT: WONG, HING
| TILLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
| TILLE OF INVENTION: OF USE THEREOF
| TILLE OF INVENTION: OF USE THEREOF
| TILLE OF INVENTION: OF USE 11-21
| TILLE OF INVENTION: OF USE 11-21
| TILLE OF INVENTION: OF USE 11-21
| PRIOR FILING DATE: 201-11-21
| PRIOR FILING DATE: 1999-04-16
| NUMBER OF SEQ ID NOS: 102
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 93
 ô
 9
 9
 9
 1 OIGLVOSGGEVKKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLIVDKSTSTAYME
 1 ÓIQLVÓSGPEVKKPGASVRVSCKASGÝSPTWYRQSPGKGLEMIGKATLIVDKSTSTAYME
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLIVDKSTSTAYME
 0; Gaps
Sequence 92, Application US/10230880
Publication No. US20030190705A1
GENERAL INFORMATION:
APPLICANT: WONG, HING C.
APPLICANT: WONG, HING C.
APPLICANT: WONGUERA, LUIS A.
TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
FILE REPRENCE: 71758/58066
CURRENT APPLICATION NUMBER: US/10/230,880
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: 09/990,586
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PALENTING OFFE: 2001-10-29
PRIOR FILING DATE: 1999-04-16
 Length 87;
 Query Match 98.2%; Score 441; DB 11; Length 87; Best Local Similarity 98.9%; Pred. No. 5.7e-37; Matches 86; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 100.0%; Pred. No. 9.1e-38;
Matches 87; Conservative 0; Mismatches 0;
 61 LSSLRSEDTAVYFCARWGOGTTVTVSS 87
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 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
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RESULT

RESULT 4 US-10-230-880-92

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TYPE: PRT
CRGANISM: Homo sapiens
US-09-990-586-94
 ; ORGANISM: Homo sapiens US-10-230-880-90
 Вb
 Sequence 90, Application US/09990586
Publication No. US20030109680A1
GENERAL INFORMATION.
APPLICANT: ULAO, JIN-AN
APPLICANT: WONG, HING C.
TITLE OF INVENTION. ANTIBODIES FOR INHIBITING BLOOD COAGULATION ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
TITLE OF INVENTION. OF USE THEREOF
FILE REPERENCE: 17.58/46.943-CIP2
CURRENT APPLICATION NUMBER: US/09/990,586
CURRENT FILING DATE: 20010-11-21
PRIOR APPLICATION NUMBER: 09/293,854
PRIOR FILING DATE: 1999-04-16
SUPPRARE: PATENTING DATE: 1099-04-16
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SUPPRARE: PATENTING DATE: 2.1
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
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 Gaps
Sequence 93, Application US/10230880

Publication No. US20030190705A1

GENERAL INFORMATION:

APPLICANT: WONG, USFFREY L.

APPLICANT: STINSON, JEFFREY L.

TITLE OF INVENTIOR METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES

FILE REFERENCE: 71758/58066

CURRENT APPLICATION NUMBER: 08/990,586

PRIOR APPLICATION NUMBER: 09/990,586

PRIOR FILING DATE: 2001-11-21

PRIOR PLING DATE: 2001-10-29

PRIOR FILING DATE: 2001-10-29
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 Score 441; DB 12;
Pred. No. 5.7e-37;
 0; Mismatches
 61 LSSLRSEDTAVYFCARWGOGTTVTVSS 87
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 98.2%;
98.9%;
 86; Conservative
 TYPE: PRT
CRGANISM: Homo sapiens
US-09-990-586-90
 TYPE: PRT
CRGANISM: Homo sapiens
US-10-230-880-93
 Query Match
Best Local Similarity
Matches 86; Conserv
 SEQ ID NO 90
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APPLICANT: JIAO, JIN-AN
APPLICANT: WONG, HING C.
TITLE OF INVENTION: ANTIBOTIES FOR INHIBITING BLOOD COAGULATION AND METHODS
TITLE OF INVENTION: ANTIBOTIES FOR INHIBITING BLOOD COAGULATION AND METHODS
TITLE OF INVENTION: OF USE THEREOF
TILE REPERENCE: 71758/46543-1072
CURRENT APPLICATION WUMBER: US/09/990,586
CURRENT FILING DATE: 2001-11-21
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 102
SOGTWARRE: PARCHIN Ver. 2.1
SEQ ID NO 94
LENGTH: 87
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Sequence 90, Application US/10230880,
Sequence 90, Application US/10230880,
Publication No. US20030190705A1
GENERAL INFORMATION:
APPLICANT: WONG, HING C.
APPLICANT: STINSON, JEFFREY L.
APPLICANT: STINSON, JEFFREY L.
APPLICANT: STINSON, JEFFREY L.
TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
FILE REFERENCE: 71758/58066
CURRENT APPLICATION NUMBER: 08/190,586
PRIOR PILING DATE: 2001-11-2.2
PRIOR PLING DATE: 2001-11-2.2
PRIOR PLING DATE: 2001-11-2.9
PRIOR PLING DATE: 2001-10-29
PRIOR PLING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PATENTIN UNDER: 09/293,854
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PATENTIN VET: 2.1
 Length 87;
 Length 87;
 Score 439; DB 12;
Pred. No. 9.1e-37;
 Score 438; DB
Pred. No. 1.1e
1; Mismatches
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 61 LSSLRSEDTÁVYFCARWGÓGTTVTVSS 87
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 Sequence 94, Application US/09990586; Publication No. US20030109680A1; GENERAL INFORMATION:
 97.88;
 Query Match
Best Local Similarity 97.7%;
Matches 85; Conservative
 Query Match
Best Local Similarity 97.7
Matches 85; Conservative
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US-09-990-586-95
 RESULT 13
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 Squence 96, Application US/09990586

Squence 96, Application US/09990586

Publication No. US20030109680A1

GENERAL INFORMATION:

APPLICANT: UNCO, JIN-AN

APPLICANT: WONG, HING C.

TITLE OF INVENTION: OF USE THEREOF

TITLE OF INVENTION: ON UMBER: US/09/990, S86

CURRENT FILING DATE: 1999-04-16

PRIOR FILING DATE: 1999-04-16

NUMBER OF SEQ ID NOS: 102

SOFTWARE: PATCHIN UMBER: 02/23, 884

PRIOR FILING DATE: 1099-04-16

SOFTWARE: PATCHIN UMBER: 02/23, 884

FILING DATE: US/09/290, S86

SOFTWARE: PATCHIN UMBER: 02/290, S86

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Sequence 94, Application US/10230880

Publication No. US20030190705A1

GENERAL INFORMATION:
APPLICANT: WONG, HING C.
APPLICANT: STINSON, JEFFREY L.
APPLICANT: STINSON, JEFFREY L.
APPLICANT: STINSON, JEFFREY L.
TITLE OF INVENTION: METHOO OF HUMANIZING IMMUNE SYSTEM MOLECULES
FILE REFERENCE: 17158/5806
CURRENT FILING DATE: 2002-12-23
PRIOR PELICATION NUMBER: 09/990,586
PRIOR PELING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 09/990,586
PRIOR PELING DATE: 2001-10-29
PRIOR PELING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-29
SPIOR FILING DATE: 2001-10-29
 Query Match 96.7%; Score 434;. DB 11; Length 87; Best Local Similarity 97.7%; Pred. No. 2.9e-36; Matches 85; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 97.7%; Pred. No. 1.1e-36;
Matches 85; Conservative 1; Mismatches 1;
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 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 61 LSSLRSEDTAVYFCARWGOGTTVTVSS 87
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-94
 , TYPE: PRT
, ORGANISM: Homo sapiens
US-09-990-586-96
 RESULT 11
US-09-990-586-96
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 APPLICANT: JOIN, JUN-AN
APPLICANT: JOIN, JUN-AN
APPLICANT: JOIN, HING C.
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
TITLE OF INVENTION: ANTIBODIES FOR JUNE
FILE REFREENCE: 71758/46643-C1P2
CURRENT APPLICATION NUMBER: U5/09/990,586
CURRENT PILING DATE: 2001-11-21
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PATCHIN Ver. 2.1
ENGTHARE: PATCHIN Ver. 2.1
 1 QIQLVQSGGBVKKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
 1 OLOLVOSGPELVKPGASVRVSCKASGYSPTWVROSPGKGLEWIGKATLIVDKSTSTAYME 60
 1 QIQLVQSGPEVVKPGASVRVSCKASGYSPTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
 1 OLGLVQSGGEVKKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLIVDKSTSTAYME
 Gaps
 Gaps
Sequence 96, Application US/10230880
Sequence 96, Application US/10230880
Publication No US20030190705A1
GENERAL INFORMATION:
APPLICANT: WONG, HING C.
APPLICANT: STINSON, JEFFREY L.
APPLICANT: STINSON, JEFFREY L.
APPLICANT: STINSON, JEFFREY L.
CURRENT PELICANTION NUMBER: US/10/230,880
CURRENT FILING DATE: 2002-12-23
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 09/990,586
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 1999-4-16
NUMBER OF SEQ ID NOS: 174
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 96
LENGTH: 87
 ö
 Length 87;
 Length 87;
 2; Indels
 Indels
 Query Match

96.0%; Score 431; DB 11;
Best Local Similarity 96.6%; Pred. No. 5.7e-36;
Matches 84; Conservative 1; Mismatches 2;
 Score 434; DB 12;
Pred. No. 2.9e-36;
0; Mismatches 2;
 61 LSSLRSEDTAVYFCARWGOGTTVTVSS 87
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 61 LSSLRSEDTAVYFCARWGOGTTVTVSS 87
 Sequence 95, Application US/09990586 Publication No. US20030109680A1 GENERAL INFORMATION:
 ch
1 Similarity 97.7%;
85; Conservative (
 TYPE: PRT
CORGANISM: Homo sapiens
US-10-230-880-96
 TYPE: PRT
CORGANISM: Homo sapiens
US-09-990.586-95
 Query Match
Best Local Similarity
Matches 85; Conserva
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```
Sequence 89, Application US/09990586

| Sequence 89, Application US/09990586
| Publication No. US2030109680A1
| GENERAL INFORMATION:
| APPLICANT: JIAO, JIN-AN
| APPLICANT: MONG, HING C.
| TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
| TITLE OF INVENTION: OF USE THEREOF
| TILLE OF THE OF THE OF USE THE O
 ö
 ô
 1 QIQLVQSGPELVKPGASVRVSCKASGYSFIWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
 1 OMOLOOSGGELVKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
 0; Gaps
 US-10-230-880-95

US-10-230-880-95

Sequence 95. Application US/10230880

PUDLICATION NO. US20030190705A1

GENERAL INFORMATION:
APPLICANT: WONG, HING C.

APPLICANT: MSTNSON, JEFREY I.
APPLICANT: MOSQUERA, LUIS A.
ITILE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
FILE REFERENCE: 71759/5806

CURRENT FILING DATE: 2002-12-23

PRIOR APPLICATION NUMBER: 09/990,586

PRIOR PILING DATE: 2001-11-21

PRIOR FILING DATE: 2001-11-21

PRIOR FILING DATE: 2001-11-21

PRIOR FILING DATE: 2001-10-29

PRIOR FILING DATE: 1999-04-16

NUMBER: OF SEQ ID NOS: 174

SEQ ID NO 95

LENGTH: 87
 Score 431; DB 12; Length 87;
Pred. No. 5.7e-36;
1; Mismatches 2; Indels
 95.8%; Score 430; DB 11; Length 87; ilarity 95.4%; Pred. No. 7.2e-36; Conservative 2; Mismatches 2; Indels
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 96.0%;
 Query Match
Best Local Similarity 96.6'
Matches 84; Conservative
 TYPE: PRT
CORGANISM: Homo sapiens
US-10-230-880-95
 TYPE: PRT
CORGANISM: Homo sapiens
US-09-990-586-89
 Query Match
Best Local Similarity
Matches 83; Conserva
 RESULT 15
US-09-990-586-89
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Sequence 16, Appl
Sequence 78, Appl
 January 13, 2004, 12:33:50; Search time 7.5227 Seconds (without alignments) 489.353 Million cell updates/sec
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 Sequence 78, 7
Sequence 63, 7
Sequence 27, 7
Sequence 8, At
 Sequence 8,
Sequence 8,
Sequence 8,
 Description
 Sequence
Sequence
Sequence
 Sequence
Sequence
Sequence
 Sequence
Sequence
Sequence
 Sequence
Sequence
Sequence
 Sequence
 Sequence
 1 QIQLVQSGGEVKKPGASVRV.....DTAVYFCARWGQGTTVTVSS
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 US-08-137-117D-102
US-08-436-117-102
US-09-355-925-7
US-09-355-925-8
US-08-561-521-41
PCT-US95-01219-41
 US-08-497-312-16
US-08-525-539A-78
US-08-525-539A-63
 Total number of hits satisfying chosen parameters:
 US-08-497-312-27
US-08-690-102A-8
 328717 segs, 42310858 residues
 SUMMARIES
 Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Issued_Patents_AA:*
 Post-processing: Minimum Match 0% Maximum Match 100%
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 US-09-990-586-91
449
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Match Length DB
 Title:
Perfect score:
 Scoring table:
 Score
 Database :
 Sequence:
 Searched:
 Run on:
 Result
No.
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| で Pre Bull 1 1 日本でまた。 日本: April 2 1 日本 Bull 3 1 日本     | 000<br>0000<br>1000<br>1000<br>1000<br>1000<br>1000<br>1000                                                                                                                     |
| 28 359.5 80.1 116 1 US-08-474-29 359.5 80.1 116 1 US-08-487-31 359.5 80.1 116 1 US-08-487-31 359.5 80.1 116 1 US-08-487-32 359.5 80.1 116 1 US-08-487-359.5 80.1 116 1 US-08-487-359.5 80.1 116 1 US-08-477-35 359.5 80.1 116 1 US-08-477-35 359.5 80.1 116 1 US-08-477-35 359.5 80.1 116 2 US-08-477-39 359.5 80.1 116 2 US-08-477-39 359.5 80.1 116 2 US-08-393-393-395.5 80.1 116 3 US-08-393-41 359.5 80.1 116 3 US-08-393-42 359.5 80.1 116 3 US-08-484-44 359.5 80.1 116 3 US-08-484-45 359.5 80 | TELEX: 389961 1PM040TJ INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICE LENGTH: 87 amino acid TYPE: amino acid STRANDEDNESS: unknown MOLECULE TYPE: protein HYPOTHETICAL: NO |

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Gaps

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86.0%; Score 386; DB 1; Length 87; ilarity 81.6%; Pred. No. 2.6e-33; Conservative 9; Mismatches 7; Indels

Query Match Best Local Similarity Matches 71; Conserv

US-08-497-312-16

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 Sequence 78. Application US/08525339A

Sequence 78. Application US/08525339A

Sater No. 6309636

GENERAL INFORMATION:
APPLICANT: DO COUTO, FERNANDO J.R.
APPLICANT: PEFERSON, JERRY A.
TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
NUMBER OF SEQUENCES:
ADDRESSEE: MORRISON & FORESTER
 1 SVQLVQSGAEVKKPGASVKVSCKASGYTFNWVRQAPGQGLEWMGRVTWTRDTSTSTVYMR 60
OIQLVQSGGEVKKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME 60
 61 NOKFODKATLIVDKSTSTAYMELSSLRSBDTAVYFCARRWRYTMDYWGQGTLVTVSS 117
 1 EVOLVOSGAEVKKPGASVKVSCKASGYSFTGYTMHWVKQSPGMNLEWIGLINPYNGGTVY
 45 -----KATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS 87
 Gaps
 30;
 Length 117;
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWIG
 4; Indels
 CONTEXT: USA
CONTEXT: USA
CONTEXT: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: READABLE FORM:
CURRENT APPLICATION BOLDS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: USA/08/525,539A
CLASSIPICATION: 4-SEP-1995
CLASSIPICATION: TYLER
REGISTRATION: TYLER
REGISTRATION NUMBER: 27633-20001.21
RELEPHONE: (415) 813-5600
TELEPHONE: (415) 494-0792
TELEX: (415) 494-0792
TELEX: (415) 494-0792
TELEX: TOGALAI
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: Amino acids
 Score 370; DB 4;
Pred. No. 1.7e-31;
4; Mismatches 4;
 LSSLRSEDTAVYFCARWGOGTTVTVSS 87
 LSSLRSEDTAVYYCARWGQGTLVTVSS 87
 SEE: MORRISON & FOERSTER: 755 Page Mill Road Palo Alto
 82.4%;
 Query Match
Best Local Similarity 67.5:
---hes 79; Conservative
 single
 linear
 STRANDEDNESS:
 USA
 ;
TOPOLOGY:
US-08-525-539A-78
 US-08-525-539A-63
 COUNTRY:
 STREET:
 CITY:
STATE:
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DO COUTO, FERNANDO J.R. CERIANI, ROBERTO L.

Sequence 63, Application US/08525539A Patent No. 6309636 GENERAL INFORMATION: APPLICANT: DC COUTO, FERNANDO J.R. APPLICANT: CERIANI, ROBERTO L.

```
TITLE OF INVENTION: Method for obtaining modified
TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine
TITLE OF INVENTION: antibody variable domains, compositions containing them.
WUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR
STREET: 215 Y 15, ATABEY PLAYA
CITY: HAVANA
 'n
 44
 20 EVQLVQSGAEVKKPGASVKVSCKASGYSFTGYTMHMVKQSPGMNLEWIGLINPYNGGTVY 79
 RECOMBINANT PEPTIDES DERIVED FROM THE MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND METHODS OF HUMANIZING ANTIBODY PEPTIDES
 80 NQKFQDKATLIVDKSTSTAYMELSSLRSEDTAVYFCARRWRYTMDYWGQGILVTVSS 136
 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 30;
 DB 4; Length 136;
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWIG-
 4; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
 COMPUTER: Floppy disk compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/525,539A FILING DATE: 14-5EP-1995 CLASSIFICATION: 424 ATTORNEY/ACEVER.
 Score 370; DB 4
Pred. No. 2e-31;
 4; Mismatches
 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKEY NUMBER: 27633-20001.21
TELECOMMUNICATION INFORMATION:
TELEFHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TITLE OF INVENTION: RECOMBLIANT PE.
TITLE OF INVENTION: MC3 ANTI-BA46,
TITLE OF INVENTION: MC3 ANTI-BA46,
TITLE OF INVENTION: METHODS OF HUM.
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORESTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
CCUNTRY: USA
 Sequence 27, Application US/08497312
Patent No. 5712120
GENERAL INFORMATION:
 TELBERAX: (412,
TELERAX: (612,
TELEX: 706141
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
"VPR: amino acid
"VPR: amino acid
 63:
 82.4%;
 Query Match
Best Local Similarity 67.5
Matches 79; Conservative
 STATE:
COUNTRY: CUBA
 US-08-525-539A-63
 US-08-497-312-27
 RESULT 4
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```
Sequence 8, Application US/09127902
Sequence 81 2027
Septent NO. 6187287
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, HAM
TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
 1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYMLHWVRQAPGQGLEWIGYINPRNDYTEY 60
 61 NQNFKDKATITADESTNTAYMELSSLRSEDTAFYFCARRDITTFYWGQGTTVTVSS 116
 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-----WGQGTTVTVSS
 29;
 Score 363.5; DB 1; Length 116; Pred. No. 7.8e-31;
 Length 116;
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWIG
 1 OIOLVOSGGEVKKPGASVRVSCKASGYSFT----WVROSPGKGLEWIG
 Query Match
Best Local Similarity 64.7%; Pred. No. 7.8e-31;
Matches 75; Conservative 9; Mismatches 3; Indels
 Indels
 STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
CONDUTER: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BR PC compatible
COMPUTER: BR PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/127,902
FILING DATE:
FILING DATE:
 PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/690,102
FILING DATE: 01-UUL-1996
APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-ANG-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISSTRATION NUMBER: 28,665
REPERBENCE/DOCKET NUMBER: 18733/463/IMIN
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 9; Mismatches
 81.0%;
ilarity 64.7%;
Conservative
 116 amino acids
amino acid
 116 amino acids
amino acid
 (202) 672-5399
 TELEX: 904136
INFORMATION FOR SEQ ID NO:
 SEQUENCE CHARACTERISTICS
 SEQUENCE CHARACTERISTICS
 , MOLECULE TYPE: protein US-09-127-902-8
 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
 Query Match
Best Local Similarity
Matches 75; Conserv
 US-08-690-102A-8
 TOPOLOGY:
 ò
 8
 GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
NUMBER OF SEQUENCES: 2.1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Poley & Lardner
 ų,
 9
 1 OIOLVOSGGEVKKPGASVRVSCKASGYSFTWVRQSPGKGLEWIGKATLTVDKSTSTAYME
 Gaps
 Query Match 81.2%; Score 364.5; DB 1; Length 86; Best Local Similarity 79.3%; Pred. No. 4.4e-31; Matches 69; Conservative 10; Mismatches 7; Indels 1
 CUNTRY WASHINGTON, D.C.
CUNTRY: WASHINGTON, D.C.
ZIP: 2007-5109
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/690,102A
FILING DATE: U-JUL-1996
CLASSIFICATION NUMBER: US/08/690,102A
FILING DATE: 12-AUG-1994
ATTONREY/AGENT INFORMATION:
NAME: SAXE, BETTHARD
REGISTRATION NUMBER: 28,665
REGISTRATION NUMBER: 28,665
REGISTRATION NUMBER: 1893463/IMIN
TELEPHONE: (202)672-5300
 ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
 61 LSSLRSEDTAVYFCARWGQGTTVTVSS 87
 60 LSSLRSEDTAVYCARWGEGTLVTVSS 86
APPLICATION NUMBER: US/08/497,312
FILING DATE: 30-UNN-1995
APPLICATION DATA:
APPLICATION NUMBER: CU 80/94
FILING DATE: 30-UNN-1994
ATTORNEY/AGENT INFORMATION:
NAME: BOND, LAURENCE B.
REGISTRATION NUMBER: 30,549
REFERENCE/DOCKET NUMBER: 2629US
TELECHONE: 801/532-1922
TELECHONE: 801/531-1922
 Sequence 8, Application US/08690102A Patent No. 5789554
 TELEX: 388961 1PM04UT
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
 : 86 amino acids
amino acid
 TELEX: 904136
INFORMATION FOR SEQ ID NO:
 unknown
 TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
 STRANDEDNESS:
 RESULT 5
US-08-690-102A-8
 US-08-497-312-27
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20 QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYXIHMVRQAPGQGLEWIGYIDPFNGGTSY 79
 1 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTSYWLHWVRQAPGQGLEWIGYINPRNDYTEY 60
 61 NQNFKDKATITADESTNTAYMELSSLRSEDTAFYFCARRDITTFYMGQGTTVTVSS 116
 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS 87
 45 -----KATLIVDKSTSTAYMELSSLRSEDTAVYFCAR------WGOGTTVTVSS 87
 81.0%; Score 363.5; DB 1; Length 135; larity 65.5%; Pred. No. 9.2e-31; Conservative 7; Mismatches 4; Indels 29
-- WVRQSPGKGLEWIG
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWI
 US-08-137-117D-102
; Sequence 102, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEGUENCES: 158
; CORRESPONDENCE ADRESS:
 COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: 1000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 24-DEC-1993
RICH APPLICATION DATA:
APPLICATION NUMBER: W PCT/JP92/00544
FILING DATE: 24-APR-1992
RICH APPLICATION NUMBER: US 3-95476
FILING DATE: 19-FEB-1992
PRICH APPLICATION NUMBER: 25,258
FILING DATE: 25-APR-1991
ATPLICATION NUMBER: 25,258
REFRENCE/DOCKET NUMBER: 25,258
 E: Foley & Lardner
3000 K Street, N.W., Suite 500
 TELEX: 904136
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
 135 amino acids
amino acid
 MOLECULE TYPE: protein
 Query Match
Best Local Similarity
Matches 76; Conserva
 CITY: Washington
STATE: D.C.
COUNTRY: USA
 ADDRESSEE:
STREET: 300
 US-08-137-117D-102
 TOPOLOGY:
 LENGIH:
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 쉱
 TITLE OF INVENTION: IMMUNOCONJUGATES AND HUMANIZED
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
NUMBER OF SEQUENCES: 21
COMPUTER READABLE FORM:
MEDIUM TYPE: Floopy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM COMPUTER:
 1 OVOLVOSGAEVKKPGSSVKVSCKASGYTFTSYWLHWVRQAPGGGLEWIGYINPRNDYTEY 60
 GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: LEUNG, Shui-on
APPLICANT: LEUNG, Shui-on
APPLICANT: QU, Zhengaxing
TITLE OF INVENTION: GIVYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
TILE REFERENCE: 018733/0879
CURRENT APPLICATION NUMBER: US/09/155,107
CURRENT FILING DATE: 1998-11-17
EARLIER APPLICATION NUMBER: WO PCT/US97/04196
EARLIER APPLICATION NUMBER: US 60/013,709
EARLIER PILING DATE: 1996-03-20
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Ver. 2.0
 61 NQNFKDKATITADESTNTAYMELSSLRSEDTAFYFCARRDITTFYWGQGTTVTVSS 116
 61 NQNFKDKATITADESTNTAYMELSSLRSEDTAFYFCARRDITTFYWGQGTTVTVSS 116
 Gaps
 45 -----KATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS 87
 ---WGQGTTVTVSS 87
 29;
 Query Match

81.0%; Score 363.5; DB 3; Length 116;
Best Local Similarity 64.7%; Pred. No. 7.8e-31;
Matches 75; Conservative 9; Mismatches 3; Indels 29.
 Query Match

81.0%; Score 363.5; DB 5; Length 116;
Best Local Similarity 64.7%; Pred. No. 7.8e-31;
Matches 75; Conservative 9; Mismatches 3; Indels 29
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWIG
 Sequence 8, Application PC/TUS9509641 GENERAL INFORMATION:
 Sequence 8, Application US/09155107
Patent No. 6254868
) MOLECULE TYPE: protein
PCT-US95-09641-8
 LENGTH: 116
TYPE: PRT
ORGANISM: Homo sapiens
 US-09-155-107-8
 SEC ID NO 8
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 8
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Sequence 7, Application US/09355925 Patent No. 6503510
 08-09-355-925-8
; Sequence 8, Application US/09355925
; Patent No. 6503510
; GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: Artificial Sequence
 TYPE: PRT
ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 62.5³
Matches 75; Conservative
 ò
 43
80 NQKFKGKVTMTVDTSTNTAYMELSSLRSEDTAVYYCARGGNRFAYWGQGTLVTVSS 135
 20 ÓVÓLVÓSGAEVKKPGASVKVSCKASGYSFTSYYIHMVRÓAPGGGLEWIGYIDPFNGGTSY
 80 NQXFKGKVIMIVDISINIAYMELSSLRSEDTAVYYCARGGNRFAYWGQGTLVIVSS 135
 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS 87
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWI-----
 Query Match 81.0%; Score 363.5; DB 2; Length 135; Best Local Similarity 65.5%; Pred. No. 9.2e-31; Matches 76; Conservative 7; Mismatches 4; Indels 29
 Sequence 102, Application US/08436717

Patent No. 5817790

GENERAL INFORMATION:

APPLICANT: SATO, Koh

APPLICANT: BENDIG, Mary

APPLICANT: BENDIG, Mary

APPLICANT: SALDANSA, Jose

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

TITLE OF INVENTION: INSTRIBUTION: RESHAPED HUMAN ANTIBODY

TITLE OF INVENTION: INSTRIBUTION: ORRESOURCES:

MUMBER OF SEQUENCES: 158

CORRESONDENCE ADDRESS:
 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/436,717
 FILMS DATE:
FILMS APPLICATION DATA:
APPLICATION NUMBER:
TILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 19-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER: HELOIG C.
REGISTRATION NUMBER: 55.258
RESTSRENCE/DOCKET NUMBER: 55.258
 SEE: Foley & Lardner: 3000 K Street, N.W., Suite 500 Washington
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 REPERENCE/DOCKET NUMBER: 53.
TELECOMOUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
 TELEX: 904136
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
 ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 135 amino acids
amino acid
 , MOLECULE TYPE: protein US-08-436-717-102
 ADDRESSEE:
 RESULT 10
US-08-436-717-102
 COUNTRY:
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80 SQKFKGRYTWTADKSTSTAYMELSSLRSEDTAVYYCARGIRRGGYYFDYWGQGTTVTVSS 139
 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTPYWMQWVRQAPGGGLEWMGSIFPGDGDTRY 79
 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 Gaps
 FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: Amino acid
CTHER INFORMATION: sequence of H chain V region version r of
CTHER INFORMATION: humanized anti-HM1.24 antibody
US-09-355-925-7
 FEATURE:
CHBR INFORMATION: Description of Artificial Sequence: Amino acid
CHBR INFORMATION: sequence H chain V region version s of
CTHRE INFORMATION: anti-HM1.24 antibody
US-09-355-925-8
 81.0%; Score 363.5; DB 4; Length 139;
62.5%; Pred. No. 9.5e-31;
tive 9; Mismatches 3; Indels 33;
 33;
 1 OIQLVQSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI----
GENERAL INFORMATION:
APPLICANT: KOISHIHARA, YASUO
APPLICANT: KOISHIHARA, YASUO
TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
FILE REFERENCE: 053466/0255
CURRENT APPLICATION NUMBER: US/09/355,925
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT/JP98/00568
PRIOR APPLICATION NUMBER: JP 9-41410
PRIOR PILING DATE: 1997-02-12
PRIOR PLING DATE: 1997-02-12
NUMBER OF SEQ ID NOS: 8
SOFWMARE: Patentin Ver: 2.1
SEQ ID NO
 APPLICANT: KOISHIHARA, YASUO
APPLICANT: YOSHIMURA, YASUO
TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS
FILE REPERENCE: 053466/025
CURRENT APPLICATION NUMBER: US/09/355,925
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT/JP98/00568
PRIOR APPLICATION NUMBER: P9 9-41410
PRIOR APPLICATION NUMBER: JP 9-41410
PRIOR FILING DATE: 1997-02-12
PRIOR FILING DATE: 1997-02-12
NUMBER OF SEQ ID NOS: 8
SOFFWARE: Patentin Ver: 2.1
SEQ ID NO 9
 Length 139;
 Query Match
81.0%; Score 363.5; DB 4; Length 1
Best Local Similarity 62.5%; Pred. No. 9.5e-31;
Matches 75; Conservative 9; Mismatches 3; Indels
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 E: Floppy disk
IBM PC compatible
 INFORMATION FOR SEQ ID NO: 41: SEQUENCE CHARACTERISTICS:
 116 amino acids
 STREET: One Market Pl
CITY: San Francisco
STATE: California
COUNTRY: USA
 TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-01219-41
 single
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 amino acid
 STRANDEDNESS:
 94105
 US-08-458-516-10
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 1 QVQLVQSGABVKKPGASVKVSCKASGYSFTSYYIHWVRQAPGQGLEWVGYIDPFNGGTSY 60
 87 MGOGTTVTVSS 87
20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTPYWMQWVRQAPGQGLEWMGSIFPGDGDTRY 79
 61 NOKFKGKVTMTVDTSTNTAYMELSSLRSEDTAVYYCARGGNRFAYWGQGTLVTVSS 116
 44 -----GKATLIVDKSTSTAYMELSSLRSEDTAVYPCAR------WGQGTTVTVSS 87
 80.7%; Score 362.5; DB 2; Length 116; 64.7%; Pred. No. 9.9e-31; tive 8; Mismatches 4; Indels 29
 Sequence 41, Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendid, Mary M.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT----WVRQSPGKGLEWI
 ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California
 ZIE: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR-
 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGBNT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 PCT-US95-01219-41; Sequence 41, Application PC/TUS9501219; GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
 Bendig, Mary M.
Leger, Olivier J.
 Query Match
Best Local Similarity 64.7.
Pertage 75; Conservative
 aingle
 MOLECULE TYPE: protein
 linear
 STRANDEDNESS:
 US-08-561-521-41
 COUNTRY:
 APPLICANT:
APPLICANT:
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1 QVQLVQSGAEVKKPGASVKVSCKASGYSFTSYYIHWVRQAPGQGLEWVGYIDPFNGGTSY 60
 61 NOKFKGKVTMTVDTSTNTAYMELSSLRSEDTAVYYCARGGNRFAYWGQGTLVTVSS 116
 44 -----GKATLTVDKSTSTAYMELSSLRSEDTAVYFCAR------WGQGTTVTVSS
 29;
 DB 5; Length 116;
 Sequence 10, Application US/08458516

Sequence 10, Application US/08458516

GENERAL INFORMATION:
APPLICANT: Co. Man. Sung
APPLICANT: Tso, Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
CUNTRY: USA
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Commsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
 4; Indels
 1 QIQLVQSGGEVKKPGASVRVSCKASGYSFT-----WVRQSPGKGLEWI
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
FILING DATE: 25-JAN-1995
 Query Match
80.7%; Score 362.5; DB 5;
Best Local Similarity 64.7%; Pred. No. 9.9e-31;
Matches 75; Conservative 8; Mismatches 4;
 APPLICATION TO THE STANDARD TO
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
CLASSIFICATION + 24
PRIOR APPLICATION OF A.
FILING DATE: US 08/059,159
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 11823-37-3
TELECOMMUNICATION NUMBER: 10:
FRETERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION NUPCRMATION:
TELEFRAX: 415-326-240
TOPOLOGY: Innear
MOLECULE TYPE: protein
FRAGGENT TYPE: N-terminal fragment
US-08-458-516-10

OUGLY MATCH

80.2%; SCOUR 360; DB 1; Length 119;
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Search completed: January 13, 2004, 12:46:33 Job time : 8.52227 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
 Copyright
```

OM protein - protein search, using sw model

January 13, 2004, 12:22:35 ; Search time 7.75633 Seconds (without alignments) 1326.664 Million cell updates/sec Run on:

US-09-990-586-97 553 1 RTVAAPSVFIFPPPBDEQLKS.......EVTHQGLSSPVTKSFNRGEC 107 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues

Searched:

283308

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |                |             |             |       |       |                    |       |             |               |       |                |             |                |               |             |       |             |              |       | •     |               |       |       |             |             |             |             |        |        |                 |
|-----------|----------------|-------------|-------------|-------|-------|--------------------|-------|-------------|---------------|-------|----------------|-------------|----------------|---------------|-------------|-------|-------------|--------------|-------|-------|---------------|-------|-------|-------------|-------------|-------------|-------------|--------|--------|-----------------|
|           | Description    | cappa chain | cappa chain | cappa | cappa | Ig kappa chain C r | cappa | cappa chain | cappa chain C | cappa | cappa chain pr | cappa chain | cappa chain V- | kappa chain C | cappa chain | cappa | cappa chain | oclonal anti | cappa | sappa | kappa chain - | cappa | cappa | kappa chain | kappa chain | kappa chain | cappa chain | e Pvt- | kappa  | g kappa chain - |
| SUMMARIES |                | 024,4       | 12          | 243   | 69    |                    |       |             |               |       |                |             | PT0219         |               |             |       |             |              |       |       |               |       |       |             |             |             |             | 782    | JL0029 | 161             |
|           | E E            | 2 JE        |             |       |       | 7                  |       |             |               |       |                |             |                |               |             |       |             |              |       |       |               |       |       |             |             |             |             |        |        |                 |
|           | Length DB      | 1           | ᆏ           | н     | 'n    | 106                | н     | Н           | 66            | 66    | 4              | 0           | 178            | 0             | -           | Н     | -           | Н            | щ     | Ч     | ч             | N     | ~     | 3           | m           | 3           | 0           | N      | N      | ~               |
| 6         | Query<br>Match | 00          | 0           | 00    | 6     | 99.1               | ۲.    | 4.          | 'n            | ۲,    |                | è.          | è.             | 4.            | 4.          | 4.    | 4.          | ω,           | ω,    | ش     | 'n            | რ     |       | 63.7        | س           | ω.          | 'n.         | ω.     | ď.     | ď               |
|           | Score          | 553         | 553         | 553   | 550   | 548                | 537   | 520         | 513           | 507   | 372            | 367         | 366            | 359           | 358         | 358   | 358         | 352          | 352   | 352   | 352           | 352   | 352   | 352         | 352         | 352         | 350         | 350    | 348    | 345             |
|           | Result<br>No.  | -           | 7           | е     | 4     | S                  | 9     | 7           | 80            | Q,    | 10             | 11          | 12             | 13            | 14          | 15    | 16          | 17           | 18    | 19    | 50            | 21    | 22    | 23          | 24          | 25          | 56          | 27     | 28     | 5               |

0

Gaps

.; 0

Length 215;

Ouery Match
Best Local Similarity 100.0%; Pred. No. 2.6e-47;
Matches 107; Conservative 0; Mismatches 0; Indels

109 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 168

g ò

1 RIVAAPSVEIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD

|                  | Ig kappa-B4 chain<br>Ig kappa-2 chain C |                | Ig kappa-1 chain C<br>Ig kappa-B9 chain | lambda-like | kap   | L1 chai | Lambda | Ig light chain pre | light c | kappa-B5 chai | Ig kappa chain (WM |
|------------------|-----------------------------------------|----------------|-----------------------------------------|-------------|-------|---------|--------|--------------------|---------|---------------|--------------------|
| S68212<br>A56169 | G20907<br>K4RBBS                        | A20969<br>K4RB | F53275<br>K9RB                          | A49633      | KSRBV | A46518  | B26167 | A21177             | K3FG    | KSRB          | S29593             |
| 77 77            | 7 7                                     | 7              | ۲ ۲                                     | 1 (7)       | Н     | 01      | 7      | N                  | ٦       | -             | 73                 |
| 214              | 106                                     | 229            | 104                                     | 238         | 104   | 118     | 103    | 213                | 108     | 103           | 197                |
| 58.0<br>56.4     | 55.8                                    | 50.2<br>46.6   | 46.3                                    | 44.3        | 43.6  | 42.9    | 41.8   | 41.8               | 40.7    | 40.4          | 40.1               |
| 321              | 308.5                                   | 277.5          | 256                                     | 245         | 241   | 237     | 231    | 231                | 225     | 223.5         | 222                |
| 30               | 332                                     |                | 36                                      | 8 8         | 39    | 40      | 41     | 42                 | 43      | 44            | 45                 |

# ALIGNMENTS

| RESULT 1 JE0244 Ig kappa chain NIG2 precursor - human C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000 C; Accession: JE024 R; Alim, M.A.; Halara, V.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; Submitted to JIPID, November 1998 A; Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy A; Reference number: JE0243 A; Accession: JE0244 A; Accession: JE0244 A; Accession: JE0244 A; Accession: JE0244 A; A; Moblecule type: protein A; Residues: 1-215 < ALIN A; Residues: 1-215 < ALIN F; 16-90 /Domain: immunoqlobulin homology < INM> | Query Match Best Local Similarity 100.0%; Score 553; DB 2; Length 215; Best Local Similarity 100.0%; Pred. No. 2.6e-47; Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 RIVAAPSVFIFPPSDEQLKSGTASVVCLINNFYPREAKVQWKVDNALQSGNSQESVTEQD 60 Db 109 RIVAAPSVFIFPPSDEQLKSGTASVVCLINNFYPRBAKVQWKVDNALQSGNSQESVTEQD 168 | QY 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107 | Ig kappa chain NIG26 precursor - human CiSpecies: Homo sapiens (man) CiSpecies: Homo cispecies: Homo cispecies: Homo cispecies: Homo cispecies: Mularia, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, TRAIIM, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, TRAIIM, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, TA; Reference number: JE0241 A; Reference number: JE0241 A; Accession: JE0242 A; Accession: JE0242 A; Molecule type: protein C; Superiamily: immunoglobulin V region; immunoglobulin homology F;16-91/Domain: immunoglobulin homology < IMM> |
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Gaps

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109 RTVAAPSVFIFPPSDEQLKSGTASVVGLLNNFYPREAKVOWKVDNALQSGNSQESVTEQD 168
 Agy Agye and the following following the following follo
 Ig kappa chain C region - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Date: 19-Mar-1997 #sequence_revision 18-Jul_1997 #text_change 21-Jan-2000
 1 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL
 9 FIFPPSDEQLKSGTASVVCLLANNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL
 2 TVAAPSVFIFPPSDEQLKSGTASVVCLLINNFYPREAKVQWKVDNALQSGNSQESVTEQDS
 1 TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS
 1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 106
 Length 215;
 A,Molecule type: mRNA
A,Residues: 1-99 <EHR>
A,Cross-references: EMBL:X65287
C,Superfamily: immunoglobulin C region; immunoglobulin homology
C,Keywords: immunoglobulin
F;19-88/Domain: immunoglobulin homology <IMM>
 Length 99;
 DB 2; Length 99;
 Ig kappa chain C region (allotype Inv(1,2)) - human (fragment)
 Indels
 0; Indels
 SKDSTYSLSSTLTLSKADYEKHKVYAGEVTHQGLSSPVTKSFNRGE
 62 KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK 100
 69 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 SSTLTLSKADYEKHKLYACEVTHQGLSSPVTKSFNRGEC 99
 o'
 91.7%; Score 507; DB 2; I 100.0%; Pred. No. 3.5e-43; iive 0; Mismatches 0;
Score 520; DB 2;
Pred. No. 4.7e-44;
0; Mismatches 2;
 Score 513; DB 2;
Pred. No. 9e-44;
1; Mismatches
 94.0%;
 92.8%;
Local Similarity 99.0%;
les 98; Conservative 1
 Conservative
 Similarity 98.1
14; Conservative
 Local Similarity
hes 99; Conserv
 104;
 Query Match
Best Local S:
Matches 104
 Query Match
Best Local S:
Matches 98
 Query Match
Best Local S:
Matches 99
 엄
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 à
 8
 A;Gener; GDB:1GKC
A;Cross-references: GDB:120088; OMIM:147200
A;Cross-references: GDB:120088; OMIM:147200
A;Cross-references: GDB:120088; OMIM:147200
A;Cross-references: GDB:120088; OMIM:147200
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin homology <IMM>
F;19-88/Domain: immunoglobulin homology <IMM>
F;26-86/Disulfide bonds: #status experimental
F;106/Disulfide bonds: interchain (to heavy chain) #status experimental
 RESULT 6
JED0241

IG Mappa chain Am37 precursor - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 0.5-lec-1998 #sequence_revision 05-bec-1998 #text_change 21-Jan-2000
C;Accession: JED041
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T Ribalim, M.B.; Structure 1998
A;Description: Structure relationship of Kappatype light chains with AL amyloidosis: Mul
 A23746

[A23746]

[A23746]

[A2746]

[A
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 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 169
 9
 61
 9
 TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS
 TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS
 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
 Gaps
 Gaps
 .
 ö
 SKDSTYSLSSTTLTSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 216
 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 KDSTYSLSSTLTLSKADYERHKVYACEVTHQGLSSPVTKSFNRGEC 107
 97.1%; Score 537; DB 2; Length 216; 97.2%; Pred. No. 9.9e-46;
 A;Molecule_type: profein
A;Residues: 1-215 <LED>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: hereroterramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>
 A;Molecule type: protein
A;Residues: 1-216 <ALT:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-92/Domain: immunoglobulin homology <IMM>
 3; Indels
 ó
 Score 548; DB 1;
Pred. No. 3.4e-47;
 99.1%; Scot. 100.0%; Pred. No. ...
 Best Local Similarity 97.2%; Pred. No. 9.9e
Matches 104; Conservative 0; Mismatches
 Matches 106; Conservative
 Query Match
Best Local Similarity
 A; Contents: annotation C; Genetics:
 A;Status: preliminary
 A; Accession: JE0241
 62
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Gaps

0

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Gaps

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Search co
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 Ig kappa chain V region (Mabl3-1) - mouse (fragment)
N;Alternate names: immunoglobulin light chain
N;Alternate names: immunoglobulin light chain
C;Species: Mus musculus (house mouse)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: S68241; S68214
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T. submitted to the EMBL Data Library, March 1994
A;Description: Specific peroxidase activity by formation of an antibody L-chain-porphyri
 A, Molecule type: mRNA
A, Residues: 1-218 <-TAK.
A, Residues: 1-218 <-TAK.
A, Cross-references: ENBL: D29670; NID: 9473962; PIDN: BAA06141.1; PID: 9473963
R, Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
ERSB. Lett. 373-276, 1995
A, Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A, Reference number: 868211; MUID: 96085223; PMID: 7498516
 ö
 ö
 111 RADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD 170
 1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 3 AAPTVSIFPPSMEQLTSGGATVVCFVNNFYPRDISVKWKIDGSEQRDGVLDSVTDQDSKD 62
AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD 63
 1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 RESULT 14
S42772
IG kappa chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S42772
 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-217 <SCH>
A;Cross-references: EMBLX75536; NID:g414143; FIDN:CAA53226.1; PID:g414144
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-93/Domain: immunoglobulin homology <IMM>
 Gaps
 6
 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 107
 Query Match 64.7%; Score 358; DB 2; Length 217; Best Local Similarity 61.7%; Pred. No. 4.8e-28; Matches 66; Conservative 15; Mismatches 26; Indels
 Query Match
Best Local Similarity 61.7%; Score 358; DB 2; Length 218;
Best Local Similarity 61.7%; Pred. No. 4.9e-28;
Matches 66; Conservative 15; Mismatches 26; Indels
 A;Cross-references: EMBL:D29670
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
 63 STYSMSSTLSLTKVEYERHNLYTCEVVHKTSSSPVVKSFNRNEC 106
 64 STYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 107
 R;Schellekens, G.A.
submitted to the BMBL Data Library, November 1993
A;Reference number: $42771
A;Accession: $42772
 Status: nucleic acid sequence not shown
 Molecule type: mRNA
Residues: 'NI',3-212 <TAW>
 A; Accession: S68214
 A, Accession: S68241
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61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 completed: January 13, 2004, 12:44:41
ne : 7.75633 secs
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us-09-990-586-97.rsp

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ALIGNMENTS
GC_RABIT
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BPC_SUMU
BPC_RAT
GCI_MOUSE
GCI_MOUSE
MUC_MOUSE
GCA_RAT
GCA_MOUSE
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P01839 orycclagus
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P20763 gallus gall
P11272 rana catesb
P01841 orycclagus
P01841 orycclagus
P01842 homo sapien
P01847 orycclagus
P2076 rattus nory
P15814 homo sapien
P2076 cattus nory
P15816 eus scrofa
P01845 mus musculu
 homo sapien
rattus norv
sus scrofa
mus musculu
cavia porce
mus spretus
mus musculu
mus musculu
mus musculu
homo sapien
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musculu
musculu
 P01834 homo sapien
P01835 rattus norv
P01836 rattus norv
 mus musculu
 January 13, 2004, 12:19:34 ; Search time 4.67249 Seconds (without alignments) 1076.912 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 US-09-990-586-97
553
1 RIVAAPSVFIFPPSDEQLKS.......BVTHQGLSSPVTKSFNRGEC 107
 Description
 P06336
P01863
P01865
P01859
P01861
P01867
P01867
P01867
 127863
 GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 127863 seqs, 47026705 residues
 SUMMARIES
 KACA_RAT
KACA_RADE
KACE MOUSE
KAC4_RABIT
KAC9_RABIT
KAC6_RABIT
LAC_CHICK
KAC6_RABIT
LAC_CHICK
LAC_RADIT
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CACA MOUSE
GCAM MOUSE
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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 Title:
Perfect score:
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14
 Database :
 Sequence:
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 Result
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P01870 oryctolagus P06337 mesocricetu P20768 suncus muri P01855 rattus norv P01869 mus musculu P01873 mus musculu P01873 mus musculu P204760 rattus norv P22436 mus musculu P2436 mus musculu P2436 mus musculu P03987 mus musculu
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| RACHUMAN STANDARD; PRT; 106 AA.  PO1314:  DY 21-JUL-1986 (Rel. OI, Created)  13-JUL-1986 (Rel. OI, Last sequence update)  DY 21-JUL-1986 (Rel. OI, Last sequence update)  DY 1017-102 (Mandalia)  DY MARCHART (Mandalia)  DY SEQUENCE (MARCHART)  RACHART (MANDALIA)  RACHART |
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us-09-990-586-97.rsp

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11778 MW;
 MGD; MGI:96495; Igk-C.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
 EMBL; V00807; CAA24189.1; -.
 cell 15:1067-1075(1978).
 102
86
106
 PIR, B90262; KIMS.
PDB, 1ATF, 01-FBB-97.
PDB, 1ESK, 02-07T-00.
PDB, 1RSK, 03-JUN-95.
PDB, 1RSB, 08-APR-98.
PDB, 1KCS, 11-MAY-02.
PDB, 1KCS, 11-MAY-02.
PDB, 1KCY, 11-MAY-02.
PDB, 1KCY, 11-MAY-02.
PDB, 1CV, 11-MAY-02.
PDB, 25CB, 09-JUL-99.
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106 1
 SEQUENCE FROM N.A.
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 kappa chain
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 62
 APTVSIFPPSMEQLTSGGATVVCFVNNFYPRDISVKWKIDGSEQRDGVLDSVTDQDSKD
 4 AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 Gape
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
 SEQUENCE (MOPC 21).

MEDLINE-37305310, PubMed=4638343;

Svasti J., Milstein C.;

"The complete amino acid sequence of a mouse kappa light chain.";
 ;0
 MEDLINE=73008889; PubMed=5073237; Svasti J., Milstein C.; wilstein C.; Milstein C.; Wilstein C.; Biothe disulphide bridges of a mouse immunoglobulin G1 protein."; Biochem. J. 126:837-850(1972).
 Sheppard H.W., Gutman G.A.; "Albalic forms of rat kappa chain genes: evidence for strong selection at the lavel of nucleotide sequence."; Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain. HIR; A02118; KIRFA.
HSSP; P01842; 2MCG.
 106 106 ' INTERCHAIN (WITH A HEAVY CHAIN) 106 AA, 11732 MW, B7E120D9700DDD66 CRC64;
 / Match 64.9%; Score 359; DB 1; Length 106; Local Similarity 63.5%; Pred. No. 3.3e-29; Loss 66; Conservative 16; Mismatches 22; Indels
 STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 R HSSP; POLSES; ALKEA.
R HSSP; POLSES; 2007110; Ig-like.
R InterPro; IPR003597; Ig-d.
R InterPro; IPR003506; Ig-MHC.
R Ffam; PF00047; Ig; 1.
RPASTE; SMO407; IG; 1.
PROSITE; PS5035; IG LIKE; 1.
Immunoglobulin domain; Immunoglobulin C region.
NON_TER.
1 1
 21-JTL-1986 (Rel. 01, Created)
21-JTL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Mus musculus (Mouse).
 (Rel. 42, Last annotation update)
 106 AA
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 Kappa chain C region, A allele.
Rattus norvegicus (Rat).
 106 AA
 PRT;
 MEDLINE=82082587; PubMed=6273908;
 Biochem. J. 128:427-444(1972)
 DISULFIDE BONDS (MOPC 21).
 STANDARD;
 STANDARD;
 102
86
106
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 NCBI_TaxID=10116;
 KAC MOUSE
P01837;
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 Query Match
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 SEQUENCE FROM N.A.
MEDLINE=81191915; PubMed=6282318;
Max E.E., Maizel J.V. Jr., Leder P.;
"The nucleotide sequence of a 5.5-kilobase DNA segment containing the mouse kappa immunoglobulin J and C region genes.";
J. Biol. Chem. 256:5116-5120(1981).
 MEDLINE-88329081; PubMed-3138116; de Waele R., Fjers W.; de Waele P., Feys W.; van de Voorde A., Molemans F., Fiers W.; "Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed against the tumour marker human placental alkaline
 SEQUENCE FROM N.A.
MEDINE-B119849; MEDAME=6785724;
Altenburger W., Neumaier P.S., Steinmetz M., Zachau H.G.;
"DNA sequence of the constant gene region of the mouse immunoglobulin
 SEQUENCE FROM N.A.
MEDLINE=82059477; PubMed=6170937;
Hamlyn P.H., Gait M.J., Milstein C.;
"Complete sequence of an immunoglobulin mRNA using specific priming and the dideoxynucloctide method of RNA sequencing.";
Nucleic Acids Res. 9:4485-4494(1981).
SEQUENCE FROM N.A., AND REVISIONS TO 53-59.
SEQUENCE FROM N.A., AND REVISIONS TO 53-59.
Hamlyn P.H., Brownlee G.G., Cheng C.-C., Gait M.J., Milstein C.; Hamlyn P.H., Brownlee G.G., Cheng C.-C., Gait M.J., Milstein C.; "Complere sequence of constant and 3' noncoding regions of an immunoglobulin mRNA using the dideoxymucleotide method of RNA
 INTERCHAIN (WITH A HEAVY CHAIN) 4851FF5EF49BAEB5 CRC64;
 Sur. J. Biochem. 176:287-295(1988).
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 Nucleic Acids Res. 9:971-981(1981)
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26 85
104 104 IN
104 AA; 11079 MW;
 interPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
 EMBL; K01363; AAA31355.1; -. PIR; A02124; K5RBV.
 48; Conservative
 100
 Similarity
 HSSP; P01842; 2MCG
 NCBI_TaxID=9031;
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 4 APIVLIFPPAADQVAIGIVIVCVANKYFP-DVIVIWEVDGTIQITGIENSKTPQNSADC 62
 5 APTVLLFPPSADQLTTZTVTIVCVANKFRPDDITVTWKVDDEIQQSGIENSTTPQSPEDC 64
 APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS 64
 5 APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS 64
 MEDLINE=76176480; PubMed=817288; Rodkey S., Hood L.;
Farnsworth V, Goodfaliesh R., Rodkey S., Hood L.;
Immunoglobulin allotypes of rabbit kappa chains: polymorphism of a control mechanism regulating closely linked duplicated genes?";
Proc. Natl. Acad. Sol. U.S.A. 73:1233-1296 (1976).
-!- MISCELLANBOUS: THIS CHAIN WAS OBTAINED FROM POOLED IMMUNOGLOBULIN OF HOMOZYGOUS B9 RABBITS.
 3; Gaps
 21-JUL-1986 (Rel. 01, Created)
15-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 01, Last sequence update)
16-SEP-2003 (Rel. 42, Last annotation update)
17 kappa-B9 chain C region.
19 kappa-B9 cuniculus (Rabbit).
19 kappa-B9 cuniculus (Rabbit).
19 kappa-B9 cuniculus (Rabbit).
19 kappa-B9 cuniculus (Rabbit).
10 kappa-Bappa-B9 coniculus (Rabbit).
10 kappa-Bapp
 Bukaryotā; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 DB 1; Length 104;
 104 104 INTERCAAIN (WITH A HEAVY CHAIN)
104 AA; 11347 MW; 427B1668B0EC8D98 CRC64;
 / Match 10 11 Length 10 12 Length 10 Local Similarity 46.6%; Pred. No. 5.5e-18; Los 18; Conservative 18; Mismatches 34; Indels
 -1- SIMILARITY: Contains 1 immunoglobulin-like domain. PIR; A02120; K9RB.
HSSP; P01842; TSR.
HSSP; P01842; TSR.
HSSP; P01842; TSR.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
Ffam; PF00047; Igf. 1.
SMART; SM0407; Igf. 1.
SMART; SM0407; IG_MEC; FALSE NEG.
Immunoglobulin domain; Immunoglobulin C region.
NON TER 6 100
 63 TYNLSSTLTLTSTQYNSHKEYTCKVT-QGTTS-VVQSFNRGDC 103
 TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-Appa chain B5 variant C region.
Oryctolagus cuniculus (Rabbit).
 104 AA
 104 AA
 STANDARD;
 STANDARD;
 NCBI_TaxID=9986
 RABIT
 RABIT
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 64
 AND OTHER
 regions.";
Nucleic Acids Res 11:7205-7214(1983).
Nucleic Acids Regions From Witch The Sequence Was Region. The CONTAINS A TERMINATOR OFF THE DIFFERENCES BETWEEN THIS AND OTHER SEQUENCED BS C REGIONS ARE UNCLEAR. THE CDNA CLONE WAS MADE USING MENA FROM TRYPANOSOME-INFECTED BS-HOMOZYGOUS RABBITS.
 5 APSVFIFPPSDEQLKSGTASVVCLLMNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS
 DECOUNCE STANDARD; PRT; 103 AA.
P20763;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
17-SEP-2003 (Rel. 42, Last annotation update)
18-SEP-2003 (Rel. 42, Last annotation update)
19-SEP-2003 (Rel. 42, Last annotation update)
 SEQUENCE FROM N.A.
MEDLINE=87218480; PubMed=3107981;
Parvari R., Ziv E., Lentner F., Tel-Or S., Burstein Y., Schechter I.;
"Analyses of chicken immunoglobulin light chain cDNA clones indicate
a few germline V lambda genes and allotypes of the C lambda locus.";
EMBO J. 6:97-102(1987).
 Gaps
[1]
SEQUENCE FROM N.A. (CLONE PKBS-F2).
MEDLINE=84041515; PubMed=6314281;
BERNStein K.E., Skurla R.M. Jr., Mage R.G.;
"The sequences of rabbit kappa light chains of b4 and b5 allotypes differ more in their constant regions than in their 3' untranslated
 .;
;
 INTERCHAIN (WITH A HEAVY CHAIN)
7771850205381751 CRC64;
 43.6%; Score 241; DB 1; Length 104; 46.6%; Pred. No. 2e-17; tive 18; Mismatches 35; Indels
 65 TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 63 TYNLSSTITIKEDEYNSHDEYTCOVA-QGSGSPVVQSFSRKNC 104
 PERMI, PF00047, 1g, 1.
SMART; SM00407, 1gc, 1.
PROSITE; PS502981; 1.
PROSITE; PS50290; 1G MHC; FALSE NEG.
Immunoglobulin domain; Immunoglobulin C region.
 IG-LIKE
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 Appella E.;
"Amino acid sequences of two mouse immunoglobulin lambda chains.";
Proc. Natl. Acad. Sci. U. S.A. 68:590-554 (1971).
-!- MISCELLANEOUS: THE MOPC 315 CELL LINE PRODUCES 2 LIGHT CHAINS, 1
-!- MISCELLANEOUS: THE MOPC 315 CELL LINE PRODUCES 2 LIGHT CHAINS, 1
-!- MISCELLANEOUS: THE NPS ALANDAL LAMBDA-1 CHAIN THAT IS MISSING
A LANGE PART OF THE V REGION. THE C REGION SEQUENCE (SHOWN HERE)
APPEARS COMPLETELY NORMAL.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 SEQUENCE FROM N.A. (S43).
MEDLINE=82220143; PubMed=6283385;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1g lambda-1 chain C region.
Mus musculus (Mouse).
Musmamalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TAXID=10090;
 murine immunoglobulin lambda light chains.";
 SEQUENCE FROM N.A. (MOPC 315).
MEDLINE=81148806; PubMed=6259534;
Bothwell A.L.M., Packind M., Schwartz R.C., Sonenshein G.E.,
Gefter M.L., Baltimore D.;
"Dual expression of lambda genes in the MOPC-315 plasmacytoma.";
Nature 290:65-67(1981).
 Immunoglobulin domai\overline{\mathbf{n}}_i; Immunoglobulin C region; 3D-structure. NON TER
 TYNLSSTLTLQKSNYNSHNEYTCQVA-QGAGS-VVQSFSRKNC 103
 TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 MEDLINE=83014953; PubMed=6812053;
Selaing E., Miller J., Wilson R., Storb U.;
"Evolution of mouse immunoglobulin lambda genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685(1982).
 105 AA
 SEQUENCE (MYELOMA PROTEIN MOPC 104E). MEDLINE=71107854; PubMed=5276767;
 IG-LIKE
 EMBL, J00587; AABS9672.1;

FMR, A39322; L1MS.

PDB, LJMH; Go-FBB-02.

INTERPRO; IPR007110; Ig-1ike.

INTERPRO; IPR0031597; Ig-61.

INTERPRO; IPR003597; Ig-61.

FRAM; PR0047; ig; I.

PROSITE; PS06385; IG LIKE; I.

PROSITE; PS06385; IG LIKE; I.
 EMBL; J00582; AAA51636.1; -.
 STANDARD;
 "Somatic variants of muz
Nature 298:380-382(1982)
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86
 SEQUENCE FROM N.A.
 Baltimore D.;
 RESULT 12
LAC1 MOUSE
ID LAC1 MOUSE
AC P01843;
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<u>ب</u>
 4 SSPSVTLPPPSSEELETHKATLVCTITDFYPGVVTVDWKVDG---TPVTQGMETTQPSKQ 60
 The
 4 AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD
 Gaps
 ø
 SEQUENCE (BENCE-JONES PROTEIN KERN).
MEDILINE-71150346; PubMed-5549586;
Ponsting1 H., Hess M., Allschmann N.;
Structural rule of antibodies. Primary structure of a monoclonal immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones-immunoglobulin-L-chain of the lambda acid sequence and its genetic interpretation.";
 of a human myeloma
 "Comparative studies on the structure of the light chains of human immunoglobulins. IV. Assignment of a subsubgroup."; J. Biochem. 93:421-429(1983).
 Milstein C., Clegg J.B., Jarvis J.M.; "Immunoglobulin lambda-chains. The complete amino acid sequence of
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
 MEDINE=70166723; PubMed=4909564;
Titani K., Wikler M., Shinoda T., Putnam F.W.;
"The amino acid sequence of a lambda type Bence-Jones protein.
"The amino acid sequence and the location of the disulfide
 7;
 Query Match 38.1%; Score 210.5; DB 1; Length 105; Best Local Similarity 42.5%; Pred. No. 2.2e-14; Matches 45; Conservative 20; Mismatches 34; Indels 7;
 MEDLINE-83186114; PubMed=6404900;
Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
Shimizu A.;
 64 ST--YSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 CHAIN).
INTERCHAIN (WITH HEAVY CHAII)
ET -> TE (IN REF. 4).
MISSING (IN REF. 4).
HS -> SH (IN REF. 4).
S -> SS (IN REF. 4).
S -> OIN REF. 4).
E -> O (IN REF. 4).
H -> SP (IN REF. 4).
H -> SP (IN REF. 4).
H -> OIN REF. 4).
H -> OIN REF. 4).
 SEQUENCE (BENCE-JONES PROTEIN X), AND DISULFIDE BONDS
MEDLINE=69088380; PubMed=4883841;
 Hoppe-Seyler's Z. Physiol. Chem. 352:247-266(1971)
 PARTIAL SEQUENCE (MYELOMA PROTEIN NEWM).
MEDLINE=74109253; Pubmed=4814727;
Chen B.L., Poljak R.J.;
"Amino acid sequence of the (lambda) light chain of mininoglobulin (lgG New).";
 LAC_HUMAN STANDARD; PRT; 105 AA. P01842; P80421; P01842; P80422; 21-UTL-1986 (Rel. 01, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) IGHambda chain C regions.
 SECUENCE (BENCE-JONES PROTEIN NIG-64).
 bridges.";
J. Biol. Chem. 245:2171-2176(1970)
 SEQUENCE (BENCE-JONES PROTEIN SH)
 104 IN 20 ET 56 Q Q AS 85 BS 85 S S 96 E I 1575 MW;
 Bence-Jones protein.";
Biochem. J. 110:631-652(1968)
 Homo sapiens (Human)
 104
19
56
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96
 NCBI_TaxID=9606;
 DISULFID
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us-09-990-586-97.rsp

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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 6 PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS--QESVTEQDSKD 63
 6 PSVILFPPRSEELKDNKATLVCLISDFYPRTVKVNWKAD-----GNSVTQGVDTTQP8KQ 60
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
 11; Gaps
 SEQUENCE FROM N.A.
MEDLINE=87305594; PubMed=3114047;
Steen M.L., Hellman L., Pettersson U.;
"The immunoglobulin lambda locus in rat consists of two C lambda genes and a single V lambda gene.";
Gene 55:75-84(1987).
 Biochem. J. 197:177-183 (1981).
-!- MISCELLANEOUS: THIS LAMBDA CHAIN EXPRESSES THE C7 ALLOTYPIC SPECIFICITY.
 36.8%; Score 203.5; DB 1; Length 105; 44.3%; Pred. No. 1.1e-13; ive 15; Mismatches 33; Indels 11
 64 ST--YSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 61 SNNKYAASSFLHLTANQWKSYQSVTCQVTHEG--HTVEKSLAPAEC 104
 104 INTERCHAIN (WITH HEAVY CHAIN)
11484 MW; B427513272E8663D CRC64;
 -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
HSSP; P01842; 7FAB.
 InterPro; Frb:
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
Pfam; Pr00047; Igcl. 1.
SMART; SM00407; IGcl. 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; FALSE_NEG.
Immunoglobulin domain; Immunoglobulin C region.
NON_TER
 Pfam; PPO0047; 1911.
SMART, SMO0047; 1911.
PROSITE; PSS0835; 1G_LIKE; 1.
PROSITE; PS02290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region.
NON_TER
 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
115-FEB-2003 (Rel. 42, Last annotation update)
11g lambda-1 chain C region.
Rattus norvegicus (Rat)
 104 AA
 EMBL; M22520; AAA41419.1; ALT_INIT
HSSP; P01842; 7FAB.
 .mmunoglobulin lambda-chains.";
 nterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
 Local Similarity 44.3% hes 47; Conservative
 STANDARD;
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104 1
105 AA;
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OBtcd0 homo sapien
OBnek0 homo sapien
 January 13, 2004, 12:20:44 ; Search time 19.1572 Seconds (without alignments) 1441.318 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 1 RIVAAPSVFIFPPSDEQLKS......EVTHQGLSSPVTKSFNRGEC 107
 Description
 830525
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 830525 segs, 258052604 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 QQNEK1
QQTCD0
QQNWSQ
QQNWSQ
QQNWFQ
QQNWFQ
QQNWFQ
QQNWFQ
QQNWIZ
QQ
 ___i_rus:*
p_vertebrate:*
p_unclassified:*
 Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
 sparchea:*
sparchea:*
spbacteria:*
spfungl:*
sphuman:*
spinvertebrate:*
spmammal:*
spporganele:*
 sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 US-09-990-586-97
 rodent:*
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Match Length DB
 sp_plant:*
 SPTREMBL 23:*
 Title:
Perfect score:
 Score
 Database :
 Seguence:
 Searched:
 Run on:
 Result
No.
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| QBnejl homo sapien Q9ddw4 mus musculu Q8n5f4 homo sapien Q8wuk4 homo sapien Q8wuk4 homo sapien Q8wuk4 homo sapien Q9wuk1 mus musculu Q96i69 homo sapien Q96i61 mus musculu Q99i11 mus musculu Q99i11 mus musculu Q99i11 mus musculu Q99i11 mus musculu Q98i11 homo sapien Q8nfi7 homo sapien Q8nfi7 homo sapien Q81c77 homo sapien Q91205 mus musculu Q91206 mus musculu Q81c77 homo sapien Q81c77 homo sapien Q81c76 mus musculu Q81206 mus musculu M801206 mus musculu Q81206 mus musculu M801206 musculu                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | mus<br>mus<br>quus<br>ging                                                      |
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| Q8NBJ1<br>Q9D8W4<br>Q8NSF4<br>Q8NSF4<br>Q8NSF4<br>Q8NTG6<br>Q8WTG3<br>Q9WTG3<br>Q9GT69<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9DG1<br>Q9D | 1 099LC4<br>1 09R1A4<br>1 098R3V9<br>095M34<br>2 090544<br>3 090529<br>3 090529 |
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| 20202020<br>111020202020<br>11020202020<br>110202020<br>110202020<br>1102020202                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 139.55<br>139.55<br>139.55<br>127.51                                            |
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# ALIGNMENTS

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128 RIVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD_187
 1 RIVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 0; Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Query Match
100.0%; Score 553; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.7e-49;
Matches 107; Conservative 0; Mismatches 0; Indels (
 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 Strausberg R.,
Strausberg R.,
Strausberg R.,
Submitted (UTN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BCO30813, AAH30813.1;
EMBL, BCO30813, AAH30813.1;
InterPro; IPR003595; Ig cl.
InterPro; IPR003596; Ig v.
Pfam, PF0047; ig, 2.
SMART; SM04407; IG21; 1.
SWART; SM0406; IGv; 1.
RROSITE; PS50835; IG LIKE; 2.
R PROSITE; PS02290; IG MHC; 1.
 Hypothetical protein.
SEQUENCE 234 AA; 25530 MW; 6316E8DEF8D132F8 CRC64;
 01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
11-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
 234 AA
PRT;
PRELIMINARY;
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 rissum=Lung,
 Q8NEK1
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us-09-990-586-97.rspt

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EMBL; BC019474; AAH19474.1;
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 2.
SMART; SM00406; IGv; 1.
 Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI TaxID=10090;
 TISSUE=Colon;
 Query Match
 RESULT 9
Q91W12
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 QBVCP0
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 128 RADAAPTVSIFFPPSSEQLISGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD 187
 9
 1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
 Gaps
 0; Gaps
 Ultrong (Tremblrel, 19, Created)
01-DEC-2001 (Tremblrel, 19, Last sequence update)
01-DEC-2001 (Tremblrel, 23, Last annotation update)
Hypothetical 25-9 kDa protein.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Musmmalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinse, Mus.
 ö
 SKDSTYSLSSTLTLSKADYEXHKVYACEVTHOGLSSPVTKSFNRGEC 107
 Match 63.7%; Score 352; DB 11; Length 234; Local Similarity 60.7%; Pred. No. 1.3e-28; les 65; Conservative 15; Mismatches 27; Indels (
 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 188 SKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
 Length 234;
 Query Match 63.7%; Score 352; DB 11; Length 2. Best Local Similarity 60.7%; Pred. No. 1.3e-28; Matches 65; Conservative 15; Mismatches 27; Indels
 Straubberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015292, AAH15292.1;
InterPro; BR003006; 1g_MHC.
InterPro; IPR003066; 1g_V.
InterPro; IPR001865; Ribosomal_S2.
Ffam; PF00047; 1g; 2.
SMART; SR00406; IGv. 1.
PROSITE; PS000290; IG MHC; 1.
 Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
 EMBL; BC05540; AAF8840.1; -... GENEL, CENTRAL BENEL, BC05540; AAF8840.1; -... InterPro; IPR00306; Ig_MHC.
InterPro; IPR0030596; Ig_V.
SMAR; SM00406; IgV; 1.
PROSITE; PS00290; IG MHC; 1.
EROSITE; PS00290; IG MHC; 1.
EROCHENC 234 AA; 25702 MW; 148377F9C1CDOAEE CRC64;
 Hypothetical protein.
SEQUENCE 234 AA, 25929 MW, BODOBOEGEB7812D2 CRC64;
 QBR062;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25.9 kDa protein.
Mus musculus (Mouse).
 PRT;
 PRELIMINARY;
 PRELIMINARY;
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 rissum=Colon;
 61
 Query Match
 Q8R062
 RESULT 7
QBR062
ID QBR0
AC QBR0
DT 01-J
DT 01-M
DE HYPO
OS MUS:
 RESULT 6
(291 WP8)
(10 0) WP8
(10 0) WP8
(11 0) WP8
(12 0) WP8
(13 0) WP8
(14 0) WP8
(15 0) WP8
(16 0) WP8
(17 0) WP8
(18 0) WP8
(18 0) WP8
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128 RADAAPTVSIFPPSSEQLISGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD 187
 9
 1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
 Gaps
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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 Query Match
63.7%; Score 352; DB 11; Length 234;
Best Local Similarity 60.7%; Pred. No. 1.3e-28;
Matches 65; Conservative 15; Mismatches 27; Indels
 61 SKDSTYSLSSTITLSKADYBKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 61 SKDSTYSLSSTLTLSKADYBKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 188 SKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
 Strausberg R.;
Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC027418; AAHJ7181.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00396; Ig_W.
Ffan: PF0047; Ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS00290; IG_MHC; 1.
PROSITE; PS00290; IG_MHC; 1.
PROSITE; PS00290; IG_MHC; 1.
PROSITE; PS00290; IG_MHC; 1.
SPROSITE; PS00290; IG_MHC; 1.
SPROSITE; PS00290; IG_MHC; 1.
 ch
1 Similarity 60.7%; Score 352; DB 11; Length 23
1 Similarity 60.7%; Pred. No. 1.3e-28;
65; Conservative 15; Mismatches 27; Indels
 Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
 SMARY, SMO0466, IGV; 1.
PROSITE; PS00290; IG MHC; 1.
Hypothetical protein. 25702 MW; 102551C58AC2FA9F CRC64;
 Q8VCP0
Q8VCP0.
Q8VCP0.
Q8VCP0.
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25.7 kDa protein.
Mus musculus (Mouse)
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completed: January 13, 2004, 12:43:08
me : 20.1572 secs
 SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
 Query Match
Best Local Similarity 59.8*
Matches 64; Conservative
 Hypothetical protein
 Homo sapiens (Human)
 Pfam; PF00047; ig;
SMART; SM00407; TG
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 Query Match
Best Local S:
Matches 43,
 NON TER
SEQUENCE
 Search co
 RESULT 15
SO TENED DE REPRESENTA DE PETETO DE
 임
 Db
 à
 133 RADAAPTVSIPPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD 192
 9
 9
 Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.; "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a
 1 RIVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
 1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
Gapa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
 01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 13, Last annotation update)
Kappa light chain of Mab7 (Fragment).
Kappa light chain of Mab7 (Fragment).
Buks musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 193 SKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 239
 Query Match 63.7%; Score 352; DB 11; Length 239; Best Local Similarity 60.7%; Pred. No. 1.4e-28; Matches 65; Conservative 15; Mismatches 27; Indels
 Strausberg R.;
Submitted (UNN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (UNN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC031498, AAH31498.1;
InterPro; IPR001298; ABH-short.
InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003596; IG.
InterPro; IPR003596; IG.
SMART; SM00407; IG. 2.
SMART; SM00407; IG. 2.
SMART; SM00406; IG.; 1.
PROSITE; PS000290; IG. MHC; 1.
15; Mismatches 27; Indels
 26366 MW; D7BE84398AA341F0 CRC64;
 Last sequence update)
Last annotation update)
 Created)
 PRT;
 01-CCT-2002 (TrEMBLrel. 22, 01-CCT-2002 (TrEMBLrel. 22, 101-MAR-2003 (TrEMBLrel. 23, 14) prothetical protein.

Mus musculus (Mouse).
65; Conservative
 PRELIMINARY;
 PRELIMINARY;
 SEQUENCE FROM N.A.
TISSUE=Breast tumor;
 l protein
239 AA;
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 NCBI_TaxID=10090;
 Hypothetical SEQUENCE 23
 QSKOFB
 RESULT 14
 OSPRIAS

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 4 AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA-LQSGNSQESVTEQDSK 62
 5 AADSVTLFPPSSEBLQANKATLVCLISDFYPGAVTVAWKADSSPVKAG--VETTTPSKQS
 1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
 Gaps
 Gaps
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 / Match 38.2%; Score 211.5; DB 4; Length 106; Local Similarity 41.0%; Pred. No. 2e-14; les 43; Conservative 26; Mismatches 31; Indels 5
 TISSUE-Lymph node;
Ducetrerhoeft A., Lauber J., Mewee H.W., Weil B., Wiemann S.;
Submitted (MAR.2002) to the EMBL/GenBank/DDBJ databasee.
EMBL; AL713800; CAD28551.1;
InterPro; IPR007110; 1g-11ke.
InterPro; IPR007997; Ig-11ke.
InterPro; IPR003006; Ig-MHC.
 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 Length 214;
single chain antibody (scFV).";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

R HSSP; PO1679; ZFBJ.

R InterPro; IPR007110; Ig-11ke.

R InterPro; IPR003006; Ig_MHC.

R InterPro; IPR00356; Ig_V.

R SMART; SM0047; ig; 2.

R PROSITE; PS50089; IG_MHC; 1.

R PROSITE; PS50089; IG_MHC; 1.

R PROSITE; PS10290; IG_MHC; 1.

R NOW TER 1 1 1

T NOW TER 214 AA; 23922 MW; S2BAZ05FDE995E2A CRC64;
 SERVENTA SET OF SERVICE SET OF 63 DSTYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 107
 106 AA; 11265 MW; 145272BBE65F4565 CRC64;
 QBTCJ5 PRELIMINARY; PRT; 106 AA. 08TCJ5; 00.001-JUN-2002 (TrEMBLrel. 21, Created) 01.JUN-2002 (TrEMBLrel. 21, Last sequence update) 01.JUN-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical protein (Fragment).
 62.7%; Score 347; DB 11;
59.8%; Pred. No. 3.9e-28;
ive 15; Mismatches 28;
```

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RESULT 1
AAW40578
 Human kappa CL dom
Human kappa light
Human Kappa-CL dom
Human Kappa protei
Human kappa CL dom
Human kappa light
Sequence of human
Human kappa light
Sequence of human
 January 13, 2004, 12:18:44; Search time 24.9511 Seconds (without alignments) 680.681 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 1 RIVAAPSVFIFPPSDEQLKS......EVIHQGLSSPVTKSFNRGEC 107
 | SIDS1/gcgdata/geneseq/geneseqp.embl/AA1980.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp.embl/AA1981.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp.embl/AA1982.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp.embl/AA1983.DAT:*
| SIDS1/gcgdata/geneseqgeneseqp.embl/AA1985.DAT:*
| SIDS1/gcgdata/geneseqgeneseqp.embl/AA1985.DAT:*
| SIDS1/gcgdata/geneseqgeneseqp.embl/AA1985.DAT:*
| SIDS1/gcgdata/geneseqgeneseqp.embl/AA1987.DAT:*
| SIDS1/gcgdata/geneseqgeneseqp.embl/AA1989.DAT:*
| SIDS1/gcgdata/geneseqgeneseqp.embl/AA1989.DAT:*
| SIDS1/gcgdata/geneseqgeneseqp.embl/AA1989.DAT:*
| SIDS1/gcgdata/geneseqgeneseqp.embl/AA1989.DAT:*
 DAT: *
 Description
 DAT
 /SIDS1/gogdata/geneseg/genesegp-emb1/AA2001.DAT:
/SIDS1/gogdata/geneseg/genesegp-emb1/AA2002.DAT:
/SIDS1/gogdata/geneseg/genesegp-emb1/AA2003.DAT:
 1107863
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
 -emb1,
 /SIDS1/gcgdata/geneseq/geneseqp-embl/SIDS1/gcgdata/geneseq/geneseqp-embl/SIDS1/gcgdata/geneseq/geneseqp-embl/SIDS1/gcgdata/geneseq/geneseqp-embl/SIDS1/gcgdata/geneseq/geneseqp-embl
 /SIDS1/gcgdata/geneseq/geneseqp-embl
/SIDS1/gcgdata/geneseq/geneseqp-embl
 /SIDS1/gcgdata/geneseq/geneseqp-embl
 /SIDS1/gcgdata/geneseq/geneseqp-embl
 /SIDS1/gcgdata/geneseq/geneseqp-emb]
 /SIDS1/gcgdata/geneseq/geneseqp
 /SIDS1/gcgdata/geneseq/geneseqp
 Total number of hits satisfying chosen parameters:
 1107863 seqs, 158726573 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 AAW40578
AAY50152
AAY08745-
 AAW92425
AAB27000
ABG31883
ABB98755
AAP93559
 BLOSUM62
Gapop 10.0 , Gapext 0.5
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 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 US-09-990-586-97
553
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 Query
Match Length
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 Title:
Perfect score:
 Scoring table:
 Score
 Database :
 Sequence:
 Searched:
 Run on:
 Result
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| P-selectin ligand Humanised anti-CDI Antibody fusion pr Humanised high pot Humanised high pot Humanised high pot Humanised high pot |                                         | Human RSV antibody | Human RSV antibody |
|-------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 120<br>130<br>130<br>130<br>130<br>130<br>130<br>130<br>130<br>130<br>13                                                            | 556555555555555555555555555555555555555 | ABP66569 ABP66571 ABP66573 ABP66577 ABP66577 ABP66581 ABP66583 ABP66587 ABP66589                                                                                                                                                                                          | 00000000                                                                                                                                                                                      |
| 000000000000000000000000000000000000000                                                                                             | 88888888888888888888888888888888888888  | **************************************                                                                                                                                                                                                                                    | 88888888888888888888888888888888888888                                                                                                                                                        |
| O H H H H H H                                                                                                                       |                                         | 213<br>213<br>213<br>213<br>213<br>213<br>213<br>213                                                                                                                                                                                                                      |                                                                                                                                                                                               |
| 0000000                                                                                                                             |                                         | 0.0000000000000000000000000000000000000                                                                                                                                                                                                                                   | 000000000                                                                                                                                                                                     |
| ហលលលលលល                                                                                                                             | ո տ տ տ տ տ տ տ տ                       |                                                                                                                                                                                                                                                                           |                                                                                                                                                                                               |
| O H 121 10 44 10 10 1                                                                                                               | 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                     | で ほ み ね ね ね ね ね<br>ひ 8 9 0 1 2 3 4 5                                                                                                                                                          |
|                                                                                                                                     |                                         |                                                                                                                                                                                                                                                                           |                                                                                                                                                                                               |

#### ALIGNMENTS

Immunoglobulin G; IgG molecule; human; Fc region; LFA-1 receptor; disorder; salvage receptor binding epitope; cell adherence interaction; lymphocyte; T cell inflammatory response. Human kappa CL domain protein fragment. AAW40578 standard; protein; 107 AA (;;) 95US-0422101 95US-0422101 21-JUL-1998 (first entry) Presta LG, Snedecor BR; (GETH ) GENENTECH INC. 4PI; 1998-250490/22. 14-APR-1995; 14-APR-1995; Homo sapiens US5739277-A. 14-APR-1998. AAW40578; 

Polypeptide(s) that are not Fc fragments and have an increased half-life - are useful for the treatment of LFA-1 mediated disorders

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focal ischaemic stroke by administering novel anti-COI8 antibody which has cerebroprotective properties. The invention particularly describes a method of treating focal ischaemic stroke caused by the obstruction of a main cerebral artery which comprises administering an anti-CDI8 antibody to increase the blood flow or reduce the infarct size, where: (1) the antibody binds to an extracellular domain of CDI8 and inhibits or reduces antibody binds CDI8 with an affinity of less than 4 nm, or (3) the antibody dissociates CDIB/CDI8 complex. This sequence represents the human Kappa-CL domain which is used to illustrate the method of the
 1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQMKVDNALQSGNSQESVTEQD 60
 This invention describes a method for improving the clinical outcome in
 1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLINNFYPREAKVQWKVDNALQSGNSQESVTEQD
 Length 107;
 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 Indels
 Query Match
100.0%; Score 553; DB 20;
Best Local Similarity 100.0%; Pred. No. 6.4e-49;
Matches 107; Conservative 0; Mismatches 0;
 Disclosure; Fig 4A-B; 25pp; English
 AAW92425 standard; peptide; 107
 Human Kappa protein CL domain.
 23-APR-1999 (first entry)
 107 AA;
 Homo sapiens
 US5869046-A.
 invention
 AAW92425;
 Sequence
 RESULT
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Gaps

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Antibody; salvage receptor binding epitope; Fab; F(ab')2; immunoglobulin; CH region; CL region; Kidney; Fc region; CH1 domain; CH2 domain; IgG; kappa protein; renal clearance rate; circulatory half-life. This invention describes a method for preparing a variant Fab or F(ab')2 polypeptide having increased half-life in vivo, where the polypeptide contains an Ig or Ig-like domain comprising a CH1 and/or CL region, is cleared from the kidneys and does not contain an IgG Fc region. The method involves altering the polypeptide within the CH1 or CL region to incorporate a salvage receptor binding epitope taken from two loops of a CH2 domain of an IgG Fc region. The polypeptides have a reduced renal Production of antibody fragments with reduced renal clearance - by introducing salvage receptor binding epitope into CH1 or CL region Disclosure; Column 55-58; 38pp; English. 95US-0422092. 95US-0422092. Snedecor BR; (GETH ) GENENTECH INC. WPI; 1999-152694/13 14-APR-1995; 14-APR-1995; 39-FEB-1999 Presta LG, 

The present sequence was used in a method for improving the in vivo half-life of polypeptides. The polypeptides comprise an Ig constant domain, and a salvage receptor binding expitope within the Ig or Ig-like domain. The salvage receptor binding taken from two loops of the CH2 domain. The salvage receptor epitope is taken from two loops of the CH2 domain of an Fc region of an Ig molecule. The modified polypeptides are useful for preventing or treating in IPA-1-mediated disorders, e.g. Crohu's disease, psoriasis, meningitis, allergic conditions (e.g. eczema), antigen-antibody complex mediated isseases. B-cell lymphomas. They are also useful for wound repair, reducing inflammatory responses and inducing tolerance to immunostimulants. They may also be used in diagnostic assays. The nucleic aidids and modified polypeptides are useful for the passive immunisation of patients, as well as for affinity purification of an antigen from recombinant cell culture or natural sources.

Disclosure; Fig 2; 38pp; English.

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 Salvage receptor binding epitope; immunomodulator; LFA-1 agonist;
mutagenesis; anti-CD18 Fab H52; immunoglobulin; Ig; Crohn's disease;
psoriasis; meningitis; allergy; eczema; B-cell lymphoma; wound repair;
 1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
 1 RIVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVOWKVDNALOSGNSOESVTEOD
 New nucleic acid encoding new modified polypeptides with increased circulatory half-life useful for preventing/treating LFA-1-mediated disorders, e.g. reducing inflammatory responses or inducing tolerance
 Gaps
clearance rate and an increased circulatory half-life. This sequence represents a human kappa protein CL domain used in the method of the
 .
0
 Length 107;
 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 61 SKDSTYSELSSTLTLSKADYBKHKVYACEVTHQGLSSPVTKSFNRGEC
 Indels
 100.0%; Score 553; DB 20;
100.0%; Pred. No. 6.4e-49;
ive 0; Mismatches 0;
 AAB27000 standard; Frotein; 107 AA
 95US-0422112.
 95US-0422112.
 (first entry)
 Local Similarity 100.
 Presta LG, Snedecor BR;
 Human kappa CL domain.
 inflammation; vaccine.
 (GETH) GENENTECH INC.
 to immunostimulants
 WPI; 2000-610925/58
 Similarity
 107 AA;
 14-APR-1995;
 Homo sapiens
 14-APR-1995;
 25-JAN-2001
 JS6121022-A.
 invention.
 AAB27000;
 Sequence
 Query Match
 Best Loca
Matches
 RESULT 5
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Human, P-selectin ligand, glycoprotein; fusion protein; infection;
 AAM52145 standard; Protein; 193
 WO200174905-A1
 04-NOV-1999
 05-FEB-2002
 11-OCT-2001
 Synthetic.
 AAY29770;
 Young RJ;
 Sequence
 61
 Query Match
 AAM52145;
 Best Loca
Matches
 RESULT 10
 AAM52145
 AAY2977
 RESULT
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 It is employed in the prepn. of CD4 fusions. The insert site is given in the Features Table. CD4 fusion proteins can have antiviral and finanuomodilatory activity are esp. useful for treating HIV infections, regardless of genetic variation within the virus. They and antibodies raised against them can also be used diagnostically for assaying adhesons and their Ilgands.

(Updated on 25-WAR-2003 to correct PR field.)
 9
 96
 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
 CD4, variants
fused to other
 ;
0
 tch al Similarity 100.0%; Score 553; DB 10; Length 143; al Similarity 100.0%; Pred. No. 9.2e-49; 107; Conservative 0; Mismatches 0; Indels 0.
 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 107
 97 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 143
 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 New nucleic acid sequences encoding adheson, esp. partic. with trans-membrane domain inactivated or peptide, useful esp. for treating HIV infections
 'note="light variable and joining"
 Sequence of human kappa light chain fragment.
 8..38
'note="light constant'
 Example; Figure Fig 5; 78pp; English
 Location/Qualifiers
 'note="insert site"
 HIV; antiviral; therapy; diagnosis.
 AAP93559 standard; protein; 143 AA
 87US-0104329.
88US-0250785.
 88WO-US03414
 (updated)
(first entry)
 label=
 Gregory TJ;
 GETH) GENENTECH INC.
 WPI; 1989~114397/15.
p-PSDB; AAP93559.
 Query Match
Best Local Similarity
Matches 107; Conserv
 143 AA;
 02-OCT-1987;
 28-SEP-1988;
 Ното варіеля
 03-OCT-1988;
 WO8902922-A.
 06-APR-1989.
 25-MAR-2003
28-JAN-1991
 Capon DJ,
 37
 61
 Sequence
 AAP93559;
 Key
Region
 Region
 Region
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 The invention relates to a compound which comprises a target cell-specific portion, comprising an humanised monoclonal antibody, having specificity for polymorphic epithelial mucin (PEM) or its antigen having transment and a cytotoxic portion having endonucleolytic activity, exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.
 09
 polymorphic epithelial mucin, PEM1;
1; human; cytostatic; cancer; apoptosis.
 87 RIVAAPSVEIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVIEQD
 1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
 comprising humanised to treat cancer has target cell-specific portion polymorphic epithelial mucin, and cytotoxic portion having endonucleolytic activity -
 Gaps
 P-selectin ligand and kappa chain constant region fusion protein.
 ;
0
 Length 193;
 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 Indels
 Match 100.0%; Score 553; DB 22; Local Similarity 100.0%; Pred. No. 1.3e-48; es 107; Conservative 0; Mismatches 0;
 Claim 20; Figure 3; 176pp; English.
 AAY29770 standard; Protein; 201 AA.
 Humanised monoclonal antibody; cytotoxic; endonuclease; DNase
 26-MAR-2001; 2001WO-GB01324
 03-APR-2000; 2000GB-0008049.
02-OCT-2000; 2000US-237159P.
 Humanised HMFG1 light chain.
 (first entry)
(first entry)
 (ANTI-) ANTISOMA RES LTD.
 WPI; 2001-662969/76.
 193 AA;
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us-09-990-586-97.rag

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4PI; 2001-582150/65.
 213 AA;
 40200164751-A2
 0-DEC-2001
 sapiens
 07-SEP-2001.
 Young JF,
 AAE10510;
 Sequence
 AAE10512
 RESULT 13
 4AE10510
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 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
106 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165
 9
 1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
 Prodn. of recombinant antibody (Ab), Ab fragment or Ab/enzyme fusion protein - by cytoplasmic expression in thio:redoxin:reductase deficient E. coli
 Gaps
 Production of recombinant antibodies (Ab), Ab fragments or Ab fragment/enzyme fusion proteins can be used for tumour therapy, especially when the fusion protein comprises a tumour-specific Ab fragment and an enzyme capable of converting a non-toxic product to a toxic drug. The fusion proteins are constructed in expression vectors and expressed in thioredoxinreductase deficient E.ooli, allowing expression products to be isolated in soluble functional form without renaturation. The Ab fragment is an FAb fragment or an antigen binding region. In the fusion protein, the Ab component is humanised and the enzyme component is a human cytoplasmic enzyme. This fusion protein comprises the antibody constant and variable
 ..
 Antibody; fusion protein; recombinant antibody; tumour therapy;
 Query Match 100.0%; Score 553; DB 17; Length 213; Best Local Similarity 100.0%; Pred. No. 1.5e-48; Matches 107; Conservative 0; Mismatches 0; Indels 0
 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 107
 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 213
 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC
 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
 light chain regions. (Updated on 25-MAR-2003 to correct PR field.)
 AAW04301 standard; Protein; 213 AA
 Example 1; Figure 5a; 12pp; German
 95DE-1013676,
 (updated)
(first entry)
 Antibody fusion protein.
 (BEHW) BEHRINGWERKE AG
 WPI; 1996-457328/46
 213 AA;
 N-PSDB; AAT38397.
 11-APR-1995;
 25-MAR-2003
14-FEB-1997
 13-MAR-1996;
 16-OCT-1996.
 EP737747-A2
 Bosslet K,
 Synthetic.
 AAW04301;
 61
 Sequence
 167
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 Db
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107 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
 High potency recombinant antibody, useful for preventing and treating diseases induced or caused by viruses, especially respiratory syncytial virus and parainfluenza virus, has high kinetic association rate
 The invention relates to a high potency antibody including its immunologically active portions, fragments and segments other than vitaxin. The antibody has increased potency, high rate constant for antibody-antigen complex formation and high affinity for any desired antigen. The high potency antibody is also useful for nullifying or ameliorating the effects of addictive drugs, such as cocaine. The high potency has specificity for antigenic determinants found on microbes such as viruses, bacteria or fungi, antigens found on ancore cells and toxic substances or product of toxic substances. The high potency antibody is useful for preventing or treating a disease caused by a virus such as respiratory syncytial virus (RSV) and parainfluenza virus (PIV). The present sequence is humanised high potency antibody full length light chain variable region.
 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
 Gaps
 Human, light chain; respiratory syncytial virus infection; virucide; parainfluenza virus; therapy; high potency antibody; drug; cocaine; cancer cell; toxic substance.
 Humanised high potency antibody clone 25 full length light chain.
 ö
 Length 213;
 167 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
 61 SKDSTYSLSSTLTLSKADYBKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 Indels
 Wu H,
 Query Match 100.0%; Score 553; DB 22; Best Local Similarity 100.0%; Pred. No. 1.5e-48; Matches 107; Conservative 0; Mismatches 0;
 Huse WD,
 Claim 23; Page 75-76; 98pp; English.
AAE10510 standard; Protein; 213 AA.
 AAE10512 standard; Protein; 213 AA
 Johnson LS,
 01-MAR-2001; 2001WO-US06815.
 01-MAR-2000; 2000US-0186252
 (first entry)
 (MEDI-) MEDIMMUNE INC.
 Koenig S,
 RESULT 14
AAE10512
ID AAE10
XX
AC AAE10
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Sequence 42, A Sequence 44, A Sequence 46, A Sequence 48, A Sequence 50, A Sequence 52, A Sequence 52, A

Sequence Sequence Sequence

Sequence Sequence

Sequence

Sequence Sequence Sequence

Sequence

Sequence Sequence Seguence Sequence

Sequence

Sequence Sequence Sequence Sequence

Sequence

Sequence

Title: Perfect score:

Sequence:

OM protein

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Run

Scoring table:

Searched:

Database :

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US-09-996-288-213
US-09-996-288-223
US-09-996-288-223
US-09-996-288-233
US-09-996-288-243
 NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1729C1
TELECOMMUNICATION INFORMATION:
 ALIGNMENTS
 PRIOR APPLICATION DATA:
APPLICATION UNMBER: 09/251652
FILING DATE: 17-FEB-2000
APPLICATION NUMBER: 08/788800
FILING DATE: 22-JAN-1997
APPLICATION NUMBER: 60/093038
FILING DATE: 23-JAN-1996
ATTORNEY/AGENT INFORMATION:
 US-09-811-384-5
 Sequence 5, Appli
 January 13, 2004, 12:43:20 ; Search time 17.1013 Seconds (without alignments) 1260.812 Million cell updates/sec
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Sequence 38, 7
Sequence 40, 7
 US-09-990-586-97
553
1 RIVAAPSVPIFPPSDEQLKS.......EVTHQGLSSPVIKSFNRGEC 107
 Description
 Sequence
Sequence
Sequence
Sequence
Sequence
 Sequence
Sequence
 Sequence
 Sequence
 Sequence
 Sequence
 Published Applications AA:*

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| cgn2_6/ptodata/2/pubpaa/USO5_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
 US-09-990-586-97
US-09-990-586-99
US-10-1159-066-99
US-10-310-113-168
US-10-310-113-168
US-10-310-113-168
US-10-230-880-99
US-10-230-880-99
US-10-36-679
US-10-36-679
US-10-320-231A-77
US-10-320-231A-77
US-10-320-231A-77
US-10-3796-848A-48
 Total number of hits satisfying chosen parameters:
 747907 segs, 201509753 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - protein search, using sw model
 Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
 BLOSUM62
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Score

Result Š. 

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 1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
 APPLICANT: WONG, THING C.
APPLICANT: WONG, JEFFREY L.
APPLICANT: WONG, JEFFREY L.
APPLICANT: WOSQUERA, LUIS A.
TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
FILE REFREENCE: 71758/58066
CURRENT APPLICATION NUMBER: U5/10/230,880
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: 09/990,586
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 90/293,854
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PALENTIN VET. 2.1
SEQ ID NO 99
 APPLICANT: WONG, THING C.
APPLICANT: WONG, UEFREY L.
APPLICANT: WONG, UEFREY L.
APPLICANT: MOSQUERA, LUIS A.
TILE OF INVENTION WHENEY US/10/230,880
CURRENT APPLICATION NUMBER: US/10/230,880
CURRENT PLLING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: 09/990,586
PRIOR APPLICATION NUMBER: 09/990,586
PRIOR PLILING DATE: 2001-11-21
PRIOR PLILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 174
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SEQ ID NOS: 174
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 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
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100.0%; Score 553; DB 12;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0;
 Query March
100.0%; Score 553; DB 12;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0;
 RESULT 8
US-10-230-880-99
is Sequence 99, Application US/10230880
is Publication No. US2030190705A1
igeneral INFORMATION:
 TYPE: PRT
ORGANISM: Homo sapiens
 ; ORGANISM: Homo sapiens
US-10-230-880-97
 TYPE: PRT
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 1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 Sequence 168, Application US/10310113

Fublication No. US20030176664A1

GENERAL INFORMATION:

APPLICANT: ADIAO, JUN-AN

APPLICANT: WONG, HING C.

APPLICANT: WONG, HING C.

APPLICANT: WONG, HING C.

TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING

TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING

TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING

TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING

TITLE OF INVENTION: UNBER: US/10/310,113

CURRENT FILING DATE: 2001-11-21

PRIOR PELING DATE: 2001-11-21

PRIOR FILING DATE: 2001-11-21

PRIOR FILING DATE: 2001-10-29

PRIOR FILING DATE: 1999-04-16

NUMBER OF SEQ ID NOS: 169

SOFTWARE: PATENTIN VENE: 2.1

SEQ ID NOS: 169

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Matches 107; Conservative
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US-10-310-113-168
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US-10-310-113-166
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Gaps

1 RTVAAPSVPIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD Length 107;

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 106 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVOWKVDNALQSGNSQESVTEQD 165
106 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165
 APPLICANT: Young, James F.
APPLICANT: Young, James F.
APPLICANT: Johnson, Leslie S.
APPLICANT: Huse, William D.
APPLICANT: Wu, Herren
APPLICANT: Wut, Herren
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
TITLE OF INVENTION: Froducing Them
FILE REFERENCE: 469201-526
CURRENT FILING DATE: 2001-10-80
PRIOR PLILING DATE: 2001-10-80
PRIOR PLILING DATE: 2000-03-01
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin Ver. 2.1
 1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
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) OTHER INFORMATION: Description of Artificial Sequence: Light chain of COTHER INFORMATION: high potency antibody.

US-09-796-848A-38
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 ö
 Query Match 100.0%; Score 553; DB 14; Length 212; Best Local Similarity 100.0%; Pred. No. 1.5e-52; Matches 107; Conservative 0; Mismatches 0; Indels 0
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 166 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 212
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 Sequence 5, Application US/10011125
; Deblication No. US20020142389A1
; GENERAL INFORMATION:
APPLICANT: Chen, Christina Yu-Ching
APPLICANT: Chen, Christina Yu-Ching
FILE REFERENCE: P180AR1
CURRENT APPLICATION UNMBER: US/10/011,125
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
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; NUMBER OF SEQ ID NOS: 10
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: LENGTH: 212
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 TYPE: PRT ORGANISM: Artificial Sequence
 ORGANISM: Artificial Sequence
 RESULT 14
US-09-796-848A-38
 SEQ ID NO 38
LENGTH: 213
 61
 TYPE: PRT
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 107 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
 GENERAL INFORMATION:
APPLICANT: Young, James F.
APPLICANT: Young, James F.
APPLICANT: Young, James F.
APPLICANT: Wu, Herren
BPLICANT: Wu, Herren
APPLICANT: Watchins, Jefter
TITLE OF INVENTION: Producing Them
FILE REFERENCE: 469201-526
CURRENT FILING DATE: 2001-10-30
PRIOR FILING DATE: 2000-03-01
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
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) OTHER INFORMATION: Description of Artificial Sequence: Light chain of CTHER INFORMATION: high potency antibody.

US-09-796-848A-40
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Job time : 18:1013 secs
 Sequence 40, Application US/09796848A Patent No. US20020098189A1
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Matches 107; Conservative 0; Mismatches 0; Indels
 Sequence 8, Application US/08422101
Patent No. 5739277
GENERAL INFORMATION:
APPLICANT: Brad Snedecor
APPLICANT: Brad Snedecor
TITLE OF INVENTION: Altered Polypeptides with Increased
TITLE OF INVENTION: Half-Life
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
 ZIDENTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/422,101

APPLICATION NUMBER: US/08/422,101

APPLICATION NUMBER: BFILD STR. APPLICATION DATA: APPLICATION NUMBER: ATTORNEY AGENT INFORMATION: NAME: Lee, Wendy M. REGISTRATION NUMBER: LEE, WENDY M. REGIST
 US-09-109-207C-15
US-09-109-207C-17
 US-08-466-151-9
US-09-109-207C-13
 ALIGNMENTS
 ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
 REFERENCE/DOCKET NUMBER: 932
TELECOMONIOLONION:
TELEPRONE: 415/225-1994
TELEFAX: 415/952-9881
TELEFAX: 415/952-9881
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
 LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-422-101-8
 US-08-422-101-8
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 5.1.6
Compugen Ltd.
 US-08-788-800-11
US-09-041-889-11
US-08-437-642B-24
US-08-437-642B-39
US-08-437-642B-40
US-08-837-058-11
 -07-934-373C-40
 Total number of hits satisfying chosen parameters:
 328717 segs, 42310858 residues
 SUMMARIES
 GenCore version
Copyright (c) 1993 - 2004
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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 January 13, 2004, 12:33:50
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
 US-09-990-586-97
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Match Length
 Title:
Perfect score:
 Scoring table:
 Score
 Seguence:
 Searched:
 Database
 Result
No.
 Run on:
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Gaps

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TOPOLOGY:
 US-08-422-112-8
 RESULT 7
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 셤
 ਨੇ
 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
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Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels (
 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Leonard Presta
APPLICANT: Brad Snedecor
TITLE OF INVENTION: Altered Polypeptides with Increased
TITLE OF INVENTION: Half-Life
 COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 OPERATING SIGERIES
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/422,093
FILING DATE: 14-APR-1995
CLASSIFFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Lee, Wendy M.
 ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
 ATTORNEY AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION UNDMER: 40,378
REGISTRATION UNDMER: P0997
REFERENCE/DOCKET NUMBER: P0997
TELECOMMUNICATION INFORMATION:
TELEFAX: 415/252-1994
TELEFX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 mmino acids
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Patent No. 6096871
 REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 9:
TELECOMONICATION INFORMATION
TELEPHONE: 415/25-1994
TELEFAX: 415/952-9881
 TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
 : 107 amino acids
Amino Acid
 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech
 TYPE: amino acid
TOPOLOGY: linear
 TOPOLOGY: Linear
CLASSIFICATION:
 USA
 94080
 COUNTRY:
 US-08-422-093-8
 US-08-788-800-5
 엄
 엄
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1 RTVAAPSVFIFPPSDBQLKSGTASVVCLLNNFYPRBAKVQWKVDNALQSGNSQBSVTEQD 60
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 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
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 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 107
 Length 107;
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 Sequence 8, Application US/08422112
Patent No. 6121022
GENERAL INFORMATION:
APPLICANT: Leonard Fresta
APPLICANT: Leonard Fresta
APPLICANT: Altard Snedecor
TITLE OF INVENTION: Altered Polypeptides with Increased
TITLE OF INVENTION: Half-Life
NUMBER OF ISEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
 Indels
 Query Match

100.0%; Score 553; DB 3;

Best Local Similarity 100.0%; Pred. No. 4.9e-57;

Matches 107; Conservative 0; Mismatches 0;
100.0%; Score 553; DB 3;
100.0%; Pred. No. 4.9e-57;
iive 0; Mismatches 0;
 US-09-301-593-20
; Sequence 20, Application US/09301593A
 REFERENCE/DOCKET NUMBER: 9:
TELECOMMUNICATION INFORMATION
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
Query Match
Best Local Similarity 100.
Matches 107; Conservative
 amino ació
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COUNTRY:
 à
 107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
 108 RIVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSSVTEQD 167
 0; Gaps
 100.0%; Score 553; DB 1; Length 214; 100.0%; Pred. No. 1.2e-56; Ative 0; Mismatches 0; Indels C
 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 167 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 168 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
 Sequence 12, Application US/08458516
Patent NO. 5777085
GENERAL INFORMATIONS
GENERAL INFORMATIONS
APPLICANT: Tao, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIB/IIIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSPEN: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458.516
 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REPERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
 ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 24, Application US/07934373C Patent No. 5821337 GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
 LENGTH: 214 amino acids
TYPE: amino acid
STRANDEDNESS: single
 Query Match
Best Local Similarity 100.0
Matches 107; Conservative
 415-326-2422
 , MOLECULE TYPE: protein US-08-458-516-12
 CITY: San Francisco
STATE: California
 linear
 FILING DATE:
 TELEPHONE:
 RESULT 11
US-07-934-373C-24
 TELEFAX:
 COUNTRY:
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108 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 167
 1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
 Gaps
 ö
 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
 168 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 214
 Query Match
100.0%; Score 553; DB 2; Length 21.
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 107; Conservative 0; Mismatches 0; Indels
 ZING STATES AND STATES
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PER PC compatible
COMPUTER: PC-DOS/MS-DOS
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
 Sequence 39, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
 P0709P2
 REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: POT
TELECOMMUNICATION INFORMATION:
 ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
 STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
 214 amino acids
Amino Acid
 1 DNA Way
 ; TOPOLOGY: Linear
US-07-934-373C-24
 TELEPHONE:
 JS-07-934-373C-39
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Qy 61 SKOSTYSLSSTLTLSKADVEKHYVACCUTRQGLSSPVTKSPRGEC 107

Db 168 SKOSTYSLSSTLTLSKADVEKHYVACCUTRQGLSSPVTKSPRGEC 214

RESULT 15
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Search completed: January 13, 2004, 12:46:33 Job time : 9.25153 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

January 13, 2004, 12:22:35 ; Search time 24.0664 Seconds (without alignments) 1326.664 Million cell updates/sec Run on:

US-09-990-586-98 1778 1 EFASTKGPSVFPLAPSSKST.....MHEALHNHYTQKSLSLSPGK 332 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308

283308 seqs, 96168682 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:\*
1: \$\overline{p}\div 1:\*
2: \$\overline{p}\div 2:\*
3: \$\overline{p}\div 4:\*
4: \$\overline{p}\div 4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|        |        | de    |        |                 | SOLUTION |               |
|--------|--------|-------|--------|-----------------|----------|---------------|
| Result | Č      | Query |        |                 |          |               |
|        | Score  | March | Length | 8 :             | ID       | Description   |
| Н      | 176    | ė,    | m      | Н               | GHHU     | gamma-1 chain |
| ~      | 1630.5 | ä     | ~      | ~               | A23511   | датта-3       |
| ო      | 628.   | ä     | ₽~     | N               | A60764   | gamma-3 chain |
| 4      | 1604   | ö     | N      | Н               | G2HU     | gamma-2 chain |
| ß      | ö      | o,    | 2      | -               | G4HU     | gamma-4 chain |
| 9      | 263.   | 71.1  | 374    | ~               | 869339   | eavy chain V  |
| 7      | 56     | ä     | a      | N               | 147159   | gamma 2a      |
| 89     | 26     | ö     | വ      | 4               | S31866   | gamma-1 chai  |
| σ      | 25     | ö     | N      | ~               | I47160   | gamma         |
| 10     | 25     | ö     | m      | ~               | PT0207   | gamma chain   |
| 11     | 23     | e,    | C      | a               | I47158   | O             |
| 12     | ö      | φ.    | N      | Н               | GHRB     | gamma chain C |
| 13     | 22     | o,    | N      | ď               | 147161   | gamma 3       |
| 14     | 212.   | ω.    | N      | <del></del> 1   | G2GP     | gamma-2 chain |
| 15     | 199.   | ۲.    | ~      | 0               | 831459   | gamma-        |
| 16     | ö      | œ.    | 5      | ~               | S22080   | heavy chain   |
| 17     | 161    | 'n.   | 0      | N               | C30554   | heavy         |
| 18     | 2      | 4.    | 4      | 7               | PC4436   | oclonal anti  |
| 19     | 5      | 4     | N      | ~               | PS0017   | gamma-1 chai  |
| 20     | 115    | 4.    | œ      | <del>, -1</del> | G3HUWI   | gатта-3 ≿     |
| 21     |        | 4.    | m      | ~               | PS0018   | gamma-2b      |
| 22     | 14     | 4.    | (A     | н               | G1MS     | gamma-1 chain |
| 23     | ₩.     | 4.    | N      | н               | G3MSC    | датта-3       |
| 24     | ~      | 'n    | σ      | н               | G1MSM    | gamma-1 chain |
| 25     | 13     | ۳.    | σ      | H               | G3MSM    | gamma-3 chain |
| 26     | 12     | θ.    | n      | Н               | G2MSA    | gamma-2a cha  |
| 27     | N      | ۳.    | φ      | 7               | S37483   | gamma-2a cha  |
| 28     | 1123.5 | ۳,    | m      | H               | G2MSAB   | gamma-2a cha  |
| 29     | 12     | ω.    | σv.    | ы               | GZMSAM   | gamma-2a cha  |
|        |        |       |        |                 |          |               |

| Ig gamma-2c chain<br>Ig gamma-2a chain<br>Ig gamma-2a chain | Ig gamma-2 chain C<br>Ig gamma-2b chain<br>Ig gamma-2b chain | Ig gamma 4 chain c<br>Ig gamma-2b chain<br>Ig gamma heavy cha | Ig epsilon chain C<br>Ig heavy chain VHI<br>Ig heavy chain V-I | Ig gamma-1 chain C<br>Ig heavy chain pre<br>Ig gamma-1 heavy c<br>Ig heavy chain (DO |
|-------------------------------------------------------------|--------------------------------------------------------------|---------------------------------------------------------------|----------------------------------------------------------------|--------------------------------------------------------------------------------------|
| S00847<br>PS0019<br>S40295                                  | S06611<br>G2MSBM<br>S01321                                   | 147162<br>G2MS11<br>146732                                    | S38864<br>S69340<br>A36040                                     | S14236<br>S04845<br>A49444<br>S69131                                                 |
| 010101                                                      | 212                                                          | 01 H 0                                                        | 0.U U                                                          | 0000                                                                                 |
| 329<br>446                                                  | 327<br>405<br>475                                            | 277<br>474<br>180                                             | 548<br>249<br>218                                              | 152<br>249<br>240<br>241                                                             |
| 625.5<br>62.5<br>62.5                                       | 61.4<br>60.9<br>60.0                                         | 60.0<br>89.0<br>89.8                                          | 37.7<br>32.5<br>32.3                                           | 32.1<br>30.0<br>29.0                                                                 |
| 1118.5                                                      | 1092.5<br>1082<br>1067                                       | 1066<br>1064.5<br>707                                         | 670.5<br>577.5<br>574.5                                        | 571<br>554<br>534<br>532                                                             |
| 30                                                          | 9 9 9<br>9 4 9                                               | 9 8 8<br>9 8                                                  | 9 4 4<br>0 0 1                                                 | 4 4 4 4<br>0 6 4 0                                                                   |

### ALIGNMENTS

| <br>RESULT 1<br>GHHU<br>Ig gamma-1 chain C region - human                                                                                                                                                                                    |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <br>C;Species: Homo sapiens (man)<br>C;Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text_change 16-Jul-1999<br>C;Accession: A93431; S36861; E33887; E90563; A90564; E91568; A91723; A02146<br>R;Ellison, J.W.; Berson, B.J.; Hood, L.E. |
| <br>Nucleic Acids Res. 10, 4071-4079, 1982 A;Title: The nucleotide sequence of a human immunoglobulin C-gammal gene. A;Reference number: A93433; MUID:82274238; PMID:6287432                                                                 |
| <br>A;Accession: A94443<br>A;Molecule type: DNA<br>A;Residues: 1-330 <ell></ell>                                                                                                                                                             |
| Aiross-references: EMBLIA13/0<br>AiNote: this sequence has the Gim(17) allotypic marker, 97-Lys, and the Gim(1) markers,<br>AiNote: Lys-330 is removed after translation                                                                     |
| R;Harris, L.J.<br>submitted to the EMBL Data Library, October 1992<br>A;Reference number: 833904                                                                                                                                             |
| <br>A; Accession: S36861 A; Molecule type: Unan                                                                                                                                                                                              |
| <br>Ajresidues: 2-530 cmAto<br>Ajross-references: BMBL:217370<br>Dirababachi n. 1164a G. Chata M. Nikaido T. Nakai S. Honio T.                                                                                                               |
| <br>41 11 11 11 11 11 11 11 11 11 11 11 11 1                                                                                                                                                                                                 |
| <br>A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a A;Reference number: S33887; MUID:83001943; PMID:6811139                                                                                          |
| <br>A;Accession: S33887 A;Molecule type: DNA                                                                                                                                                                                                 |
|                                                                                                                                                                                                                                              |
| <br>; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Ede                                                                                                                                                                                          |
| <br>A; Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequer A; Reference number: A90563; MUID:71064024; PMID:5489771                                                                                       |
| A; Concents: myeloma procein su<br>A; Accession: B90563                                                                                                                                                                                      |
| <br>A,Molecule Lype: process<br>A,Residues: 1-96,'R', 98-135 <cun> A,Note: this secures the Clm(3) marker 07-2rd</cun>                                                                                                                       |
|                                                                                                                                                                                                                                              |
| <br>DICCHEMISTIFY 9, 31/1-3181, 13/0 A)Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid seque                                                                                                                |
| A;Neterence number: Ayosow; Mold:/loow.or.                                                                                                                                                                                                   |
| A;Molecule type: protein<br>A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,<br>A;Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met                                                |
| ngl,<br>vler'<br>Die                                                                                                                                                                                                                         |

```
A;Gene: GDB:1GHG2
A;Gene: GDB:119338; OMIN:147110
A;Gene: GDB:119338; OMIN:147110
A;Gene: GDB:19338; OMIN:147110
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into 1 C;Superfamily: immunoglobulin cregion; Immunoglobulin homology cimis
C;Superfamily: immunoglobulin homology cimis
F;313-200.50 Domain: immunoglobulin homology cimis
F;329-306,Domain: immunoglobulin homology cimis
F;314-200,246-304,Disulfide bonds: #status experimental
F;71-83,140-200,246-304,Disulfide bonds: #status experimental
F;7102,103,106,109/Disulfide bonds: interchain (to havy chain) #status experimental
F;106,109/Disulfide bonds: interchain (to havy chain) #status experimental
F;106,109/Disulfide bonds: interchain (to havy chain) #status experimental
 and 264-268
60-Ala and in the amidat
 117 PSVFLEPPKRDTLMISRTPEVICVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFN 176
 Gramma-4 chain C region - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Dacession: 0.2-Apr-1983 #Sequence revision 02-Apr-1982 #text_change 16-Jul-1999 C;Accession: A90933, #So249; A02150 R;Ellison, J: Buxbaum, J:/ Hood, L. DNA 1, 11-18, 1981 A;11cles: Nucleotide sequence of a human immunoglobulin C-gamma4 gene. A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
 61 GLYSLSSVVIVPSSNFGIQIYICNVDHKPSNIKVDKIVERKCCVE---CPPCPAPP-VAG
 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
 243 LTKNOVSLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
 ASTKGPSVPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
 STFRVVSVLTVVHODWLNGKEYKCKVSNKGLPAPIEKTISKTKGOPREPQVYTLPPSREE
 Rivilstein, C.; Frangione, B.

A) Fitle: Disulphide bridges of the heavy chain of human immunoglobulin G2.

A) Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.

A) Reference number: A90233, MUID:72033500; PMID:4940472

A) Contents: annotation; myeloma protein Sa, disulfide bonds

A) Frangione, B.; Milstein, C.; Pink, J.R.I.

Nature 221, 145-148, 1969

A) Title: Structural studies of immunoglobulin G.

A) Reference number: A93157; MID:69064124; PMID:5782707

C) Genetics:
 Gaps
 4.
 A; Contents: annotation; Zie, revisions to residues 25, 59, 60, A; Note: the revised sequence differs from that shown in having ned
 13; Indels
 90.2%; Score 1604; DB 1;
91.2%; Pred. No. 3.9e-105;
live 12; Mismatches 13;
 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 326
A,Molecule type: protein
A,Residues: 228-275 <400F>
R,Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
 Query Match
Best Local Similarity 91.23
Matches 301; Conservative
 303
 297
 63
 123
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 Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin
A;Reference number: A93132; MUID:80114419; PMID:118920
 100
 61 GLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPLGDTTHTCPRCPEPKSC 120
 195
 LMISRIPEUTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLH 240
 QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 300
 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 315
 301 GFYPSDIAVEWESSGQPENNYNTTPPVIDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHE 360
 121 DIPPPCPRCPEPKSCDIPPPCPRCPEPKSCDIPPPCPRCPAPELLGGBSVFLFPPKPKT 180
 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 255
 62
 9
 -- EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT
 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
 Gaps
 47;
 Length 377;
 ; Score 1628.5; DB 2; Length
; Pred. No. 9e-107;
10; Mismatches 11; Indels
 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV-----
 ALHNHYTOKSLSLSPGK 332
 361 ALHNRFTOKSLSLSPGK 377
 Query Match
Best Local Similarity 82.0%;
Matches 309; Conservative 1
 A,Contents: Zie
A,Accession: A93132
 316
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 122
 117 PSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQFN 176
 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEOYN 182
 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKS 300
 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 120
 9
 152 SHEDPEVKENWYVDGVEVENAKTKPREEQYNSTYRVVSVLTVLHODWLNGKEYKCKVSNK 211
 ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 271
 121 ALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESSGO 180
 9
 Gramma chain C region - chimpanzee
Gramma chain C region - chimpanzee
Gramma chain C region - chimpanzee)
Gramma chain roglodytes (chimpanzee)
Gramma chain roglodytes (chimpanzee)
Gramma chaich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A; Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A; Reference number: PT0207; MUID:91287716; PMID:2062315
 61 GLYSLSSMVTVPASSLSSKSYTCNVMHPATTIKVDKRVGTKTKPPCP1CPACESP----G
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 1 APKTAPLVYPLAPCGRDISGPNVALGCLASSYFPEPVTVTWNSGALTSGVHTFPSVLQPS
 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
 3 ASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
 Gaps
 1 SNTKVDKKVEPKSCDTTHTCPPCAAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
 92 SNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
 Gaps
 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 325
 181 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 234
 .
9
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0
 Length 234;
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A;Residues: 1-234 <ERR>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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F;48-117/Domain: immunoglobulin homology <IMM>
 Indels
 2; Indels
 54;
 Score 1254; DB 2;
Pred. No. 8.5e-81;
 297 SWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328
 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
 70.5%; Sco...
98.7%; Pred. No. e...
1; Mismatches
 Mismatches
 42;
 Conservative
 231; Conservative
 Local Similarity
 A; Accession: PT0207
 230;
 Query Match
Best Local S
Matches 231
 301
 63
 123
 183
 177
 243
 61
 212
 272
 Matches
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 Igg gamma-1 chain C region - synthetic (5)Secies: s
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 Gispecies: Sus scrofa domestica (domestic pig)
Gispecies: Sus scrofa domestica (domestic pig)
Gispecies: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
Giscession: 147160
Rikacskovics, I:; Sun, J:; Butler, J.E.
J: Immunol: 153, 3565-3573, 1994
A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A/Reference number: 147158; MUID:95015845; PMID:7930579
A/Accession: 147160

177 STYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPHAEE 236
 153
 213
 EDPEVKFNWYVDGVEVHNAKTKPREEQINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL 136
 137 PAPIEKTISKAKCQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 196
 PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 273
 17 TVAQADVESKSCDKTHTCPPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSH 76
 274 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
 255
 LIKNOVSLICLVKGFYPSDIAVEMESNGQ--PENNYKTIPPVLDSDGSFFLYSKLIVDKS
 94 TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSH
 154 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
 A;Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C;Genetics:
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 Length 255;
 Length 328;
 immunoglobulin C region; immunoglobulin homology
in: immunoglobulin homology <IMM>
 6; Indels
 DB 4;
 70.7%; Score 1257; DB 2; 69.3%; Pred. No. 8e-81;
 cch 70.9%; Score 1260; DB 4; al Similarity 97.5%; Pred. No. 3.6e-81; 233; Conservative 0; Mismatches 6
 301 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
 297 SWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328
 Query Match
Best Local Similarity
 133-202/Domain:
 A;Gene: IgG2b
C;Superfamily:
F;133-202/Domai
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Matches 233
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C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgW, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin C region; immunoglobulin homology cIM2> F;21-81/bomain: immunoglobulin homology cIM2> F;21-310/bomain: immunoglobulin homology cIM3> F;28-79/bisulfide bonds: #status experimental F;28-79/bisulfide bonds: #status experimental F;178/Binding site: carbohydrate (Asn) (covalent) | #status experimental F;248-308/Disulfide bonds: #status experimental F;248-308/Disulfide bonds: #status experimental
 62
 116
 180
 176
 240
 236
 296
 GLYSLSSVVTVPASTSGAQTFICNVAHPASSTKVDKRVEPGCPDPCKHC-RCPPPELPGG 260
 201
 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 122
 PSVFLFPPKPKDTLMISRTPBVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
 62
 9
 Gramma-1 chain - sheep (fragment)
Gramma-1 chain - sheep (fragment)
Gramma-1 chain - sheep)
Gramma-1 charless aries, Ovis ammon aries (domestic sheep)
Gram-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
Gramma-1 S.; Nau, F.
Submitted to the EMBL Data Library, December 1992
A.Reference number: 831459
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 61 GLYSLISMVIVPSSQKAT---CNVAHPASSTKVDKTVEPIRTPZPBPCTCPKCPPPBNL
 117 GGPSVFIFPPKPKDTLMISLTPRVTCVVVDVSQDEPEVQFTWFVDNKPVGNAETKPRVEQ
 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLTVD
 DELSKSKYGVTCLINFFPADIHVEWASNRVPVSEKEYKNTPPIEDADGSYFLYSKLTVD
 ARTTAPSVFPLAASCVDTSGSMMTLGCLVKGYFPEPVTVKWNSGALTSGVHTFPAVLQ-S
 177 YNTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIBKTISKTKGAPRMPDVYTLPPSR
 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLQSS
 Gaps
 Gaps
 9;
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 Length
 homology
 Indels
 Indels
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 DB 1;
 ;Superfamily: immunoglobulin C region; immunoglobulin
;Keywords: immunoglobulin
;277-346/Domain: immunoglobulin homology <IMM>
 62;
 68.2%; Score 1212.5; DB 70.3%; Pred. No. 1.1e-77; ive 28; Mismatches 62
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Best Local Similarity 67.5%; Pred. No. 1.3e
Matches 224; Conservative 38; Mismatches
 Cross-references: EMBL:X69797
 Best Local Similarity 70.3
Matches 234; Conservative
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A,Residues: 1-472 <PAT>
 63
 181
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 LTKNOVSLICLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKS 300
 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 122
 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
 9
 g gamma-2 chain C region - guinea pig
Species: Cavia porcellua (guinea pig)
Date: 07-May-1981 #sequence revision 07-May-1981 #text change 16-Jul-1999
Accession: A94553; A90352; A903894; A90385; A02<u>1</u>51
 APKTAPSUYPLAPCGRDTSGPNVALGCLASSYFPEPVTMTWNSGALTSGVHTFPSVLQPS
 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
 A; Contents: annotation; disulfide bonds
A;Note: Cys-16 is involved in a heavy-light chain bond
A;Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
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heterodontu
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 mus musculu
 gallus gall
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 MEDLINE=71064024; PubMed=5489771; Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D., Waxdal M.J., Edelman G.M.; Waxdal M.J., Edelman G.M.; The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."; Biochemistry 9:3161-3170(1970).
 SEQUENCE FROM N.A.
MEDLINE-2274238; PubMed-6287432;
Ellison J.W., Berson B.J., Hood L.E.;
"The nucleotide sequence of a human immunoglobulin C gammal gene.";
Nucleic Acids Res. 10:4071-4079(1982).
 Amino
 SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
MEDLINE-83289131; PubMed-6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 "The covalent structure of a human gamma G-immunoglobulin, 8. Amiacid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
Biochemistry 9:3171-3181(1970).
 SEQUENCE (MYELOMA PROTEIN NIE).
MEDLLIES-77070569, PubMed-826475;
Ponstingl H., Hilschmann N.,
"The rule of antibody structure. The primary structure of a
monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The
chymotryptic peptides of the H-chain, alignment of the tryptic
peptides and discussion of the complete structure.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
 P20758
P20758
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P23086
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P01875
 P01880
P97797
 • SEQUENCE OF 136-329 (EU).
MEDIANE-71064025; PubMed=5530842;
Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
Edelman G.M.;
 MEDDINE=71064027; PubMed=4923144;
Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. X.
 Last sequence update)
Last annotation update)
 330 AA
 ALIGNMENTS
 ALCI_GORGO
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ALC_MOUSE
MVC_CHICK
ALC_RABIT
MVCM_ICTPU
DTC_HUMAN
SHSI_MOUSE
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 21-UUJ-1986 (Rel. 01, Created)
21-UUJ-1986 (Rel. 01, Last seqn
15-SEP-2003 (Rel. 42, Last anno
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IGHG1.
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ID GC1_H
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heterodontu
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- 2004 Compugen Ltd.
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 127863 seqs, 47026705 residues
 SUMMARIES
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GC3M MOUSE
GCAA MOUSE
GCAB MOUSE
GCAM MOUSE
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MOUSE
HUMAN
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MUC_MOUSE
MUCM_RABIT
MUC_SUNMU
 MUCM MOUSE
 MUCB_HUMAN
HVCS_HETFR
HVCM_HETFR
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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GC_RABIT
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GC1_RAT
GCB_RAT
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 RAT
 HUMAN
 AUC MESAU
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 GenCore (c) 1993
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 US-09-990-586-98
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Match Length
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 Score
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(WITH HEAVY CHAIN)
(WITH HEAVY CHAIN)
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 99.4%; Score 1767; DB 1; 100.0%; Pred. No. 6.5e-126; ive 0; Mismatches 0;
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 Query Match
Best Local Similarity 100.
Matches 330, Conservative
 3330
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 MEDLINE=77070267; PubMed=1002129; Detekr L., Schwarz J., Redichel W., Hilschmann N.; Erker L., Schwarz J., Redichel W., Hilschmann N.; Erker C. antibody structure. The primary structure of a monoclonal 1gG1 immunoglobulin (myeloma protein Nie), I: Purification and Characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges."; Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 MISCELLANBOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 198, 267&272.
 Immunoglobulin domai\overline{\mathbf{n}}_i Immunoglobulin C region, Glycoprotein, 3D-structure.
 GO; GO:0005624; C:membrane fraction; NAS.
GO; GO:0005823; F:antigen binding activity; TAS.
GO; GO:000595; P:immine response; NAS.
InterPro; IPR007110; IG-11ke.
InterPro; IPR003597; Ig-c1.
InterPro; IPR003597; Ig-c1.
Ffam; PF00047; Ig; 3.
SWART; SW0647; IG; 3.
PROSITE; PS00290; IG-MHC; 2.
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MEDLINE=81208100; PubMed=7236608;
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CH2.
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Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970),
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1D5B; 04-FEB-00.
1D6V; 04-OCT-00.
 A93433; GHHU
 DISULFIDE BONDS
 Deisenhofer J.;
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Eur. J. Biochem. 228:886-893(1995)
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 TISSUE=Fetal liver,
MEDLINE=8423592; PubMed=6129676;
Krawinkel U., Rabbitts T.H.;
"Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
 SEQUENCE OF 1-121 (DOT).
MEDLINE=9525528; PubMed=7737190;
Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
"Characterization of the two unique human anti-flavin monoclonal immunoglobulins.";
 [5]
SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
MEDLINE=80001357; PubMed=113060;
CONDIG S., Parx D.M., Hofmann T.;
"The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.";
Can. J. Blochem. 57:758-767(1979).
 Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
 Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T., "Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.";
Cell 29:671-679(1982)
 Ellison J.W., Hood L.E., "Linkage and sequence homology of two human immunoglobulin gamma
 SEQUENCE OF 238-275 (ZIE).
MEDILIBE-80114419, PubMed=118920;
HOfmann I., Parr D.M.;
"A note of the amino acid sequence of residues 381-391 of human
 MEDLINE=81007873; PubMed=6774012;
Wang A.-C., Tung E., Fudenberg H.H.;
The primary structure of a human IgG2 heavy chain: genetic,
evolutionary, and functional implications.";
J. Immunol. 125:1048-1054(1980).
 heavy chain constant region genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982)
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
19 gamma-2 chain C region.
 330
 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
 326 AA
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 301 QGGNVFSCSVMHEALHNHYTQKSLSLSPGK
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MEDLINE=82197621; PubMed=6804948;
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Mol. Immunol. 16:923-925(1979)
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 Homo sapiens (Human)
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P01859;
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303
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 2
 122
 GLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVE---CPPCPAPP-VAG 116
 123 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
 62
 9
 63 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
 3 ASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
 Gaps
Milstein C., Frangione B.; "Disulphide bridges of the heavy chain of human immunoglobulin G2."; "Blochem. "J. 121:217-225(1971).
 AT OR NEAR THE COMPLEMENT-BINDING SITE. REMOVED POST-TRANSLATIONALLY (PROBABLE) S -> A (IN MYELOMA PROTEINS TIL & ZIE).
 . 7
 CHAIN).
CHAIN).
CHAIN).
 INTERCHAIN (WITH A LIGHT CHAIN)
 Length 326;
 Indels
 (WITH A HEAVY (W
 /FTId=VAR 003889.
C -> S (IN REF. 3).
8310878C6878CF9C CRC64;
 PIR; A9906, G2HU.
HSSP; PO1857; IFC1.
HSSP; PO1857; IFC1.
GENEW; HGNC:5526; IGHG2.
MIM; 147110; -.
GO; GO:0005624; C:membrane fraction; NAS.
GO; GO:0005823; F:antigen binding activity; TAS.
GO; GO:0006955; P:immun response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig-c1.
InterPro; IPR00366; Ig-mHC.
Pfam; PF000477; IG; 3.
SMART; SM00407; IGG1; 2.
 90.2%; Score 1604; DB 1;
91.2%; Pred. No. 1.2e-113;
sive 12; Mismatches 13;
 region
 MEDLINE-69064124; PubMed-5782707;
Frangione B., Milstein C., Pink J.R.L.;
"Structural studies of immunoglobulin G.";
Nature 221:145-148(1969).
 SMART; SM00407; 1g; 3.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 2.
Immunoglobulin domain; Immunoglobulin C 1
 INTERCHAIN
INTERCHAIN
INTERCHAIN
 U
 INTERCHAIN
 HINGE.
CH2.
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109
141
247
327 AA;
 Similarity
 SEQUENCE OF 1-128.
 NCBI_TaxID=9986;
 F-I haplotype.
DISULFID
DISULFID
DISULFID
SEQUENCE
 GC RABIT
PO1870;
 н
 243
 63
 123
 183
 298
 Query Match
Best Local
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 242
 236
 LIKNOVSLICLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSDGSFFLYSKLIVDKSRW 302
 STYRVVSVLTVLHQDWLNGKBYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
 STPRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREE
 SEQUENCE OF 1-30 AND 81-326.
MEDLINE=70207560; PubMed=4192699;
Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
"Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of a gama 4 chain.";
Biochem. J. 117:33-47(1970).
 gene.
 C region; 3D-structure.
 INTERCHAIN (WITH A HEAVY CHAIN)
 CHAIN)
 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
 SEQUENCE FROM N.A.
MEDLINE=83157104; PubMed=6299662;
Ellison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4
DNA 1:11-18(1981).
 CH1.
HINGE.
CH2.
CH3.
INTERCHAIN (WITH A LIGHT CH
 MIM; 147130; ---
GO; GO:0005624; C:membrane fraction; NAS.
GO; GO:0005823; F:antigen binding activity; TAS.
GO; GO:0006955; P:immune response; NAS.
INTERPO; IPR00310; Ig-1ike.
INTERPO; IPR003597; Ig c1.
INTERPO; IPR003697; Ig c1.
INTERPO; IPR003697; Ig m.
INTERPO; IPR00306; Ig mHC.
Pfam; PF00047; Ig; 3.
PROSITE; PS00896; IG LIKE; 3.
PROSITE; PS00896; IG LIKE; 3.
PROSITE; PS00896; IG MHC; 2.
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1G gamma-4 chain C region.
 Ą.
 OOGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 326
 327
 Immunoglobulin domain, Immunoglobulin.
NON TER 1 1 1 2 CH1.
 EMBL; K01316; AAB59394.1; ALT_INIT.
 PIR, A90933, G4HU.
PDB, 1ADQ, 16-SEP-98.
Genew, HGNC:5528, IGHG4.
 STANDARD;
 98
110
220
327
14
83
 NCBI_TaxiD=9606;
 GC4 HUMAN
P01861;
 177
 237
 243
 303
 DOMAIN
DISULFID
DISULFID
DISULFID
 183
 297
 NOMAIN
 DOMAIN
 RESULT 3
GC4_HUMAN
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ij
 117
 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 122
 PSVFLFFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
 118 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN 177
 178 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE 237
 9
 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
 61 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESK---YGPPCPSCPAPEFLGG
 LIKNOVSLICLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSDGSFFLYSKLIVDKSRW
 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
 STYRUVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
 SEQUENCE FROM N.A.
MEDLINE-84030930; PubMed-6313520;
Bernstein K.E., Alexander C.B., Mage R.G.;
"Nucleotide sequence of a rabbit 1gG heavy chain from the recombinant
 MEDIJINE=76135469; PubMed=1243651;
Pratt D.M., Mole L.E.;
"Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype.";
Biochem. J. 151:337-349(1975).
 Gaps
 ASQUENCE OF 88-266 FROM N.A.
MEDLINE-83299917; PubMed-6193512;
Martens C.L., Moore K.W., Stelnmetz M., Hood L., Knight K.L.;
"Heavy chain genes of rabbit 1gg: isolation of a cDNA encoding gamma heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
 21-JUL-1986 (Rel. 01, Created)
15-JUL-1986 (Rel. 01, Last sequence update)
15-SED-2003 (Rel. 42, Last annotation update)
16 gamma chain C region.
19 gamma chain C region.
20 yccoclagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 SEQUENCE OF 132-161.
MEDLINE=70110015; PubMed=5461106;
Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
"Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin G.";
 3;
 89.5%; Score 1590.5; DB 1; Length 327; 90.9%; Pred. No. 1.2e-112; ive 12; Mismatches 15; Indels 3;
 INTERCHAIN (WITH A HEAVY CHAIN)
 3EDBD811EF208E7A CRC64;
 Ą.
 303 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
 QEGNVFSCSVMHEALHNHYTQKSLSLGK 327
 323
109
201
305
3540 MW;
 mmunogenetics 18:387-397(1983)
 Matches 300; Conservative
 STANDARD;
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246 NQVSLICLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSDGSFFLYSKLTVDKSRWQQG
 (Rel. 01, Last sequence update) (Rel. 38, Last annotation update)
 329 AA
 Trischmann T.M.; Submitted (APR-1975) to the PIR data bank
 NVFSCSVMHEALHNHYTQKSLSLSPGK 332
 MEDLINE=71058474; PubMed=4922544;
 Biochemistry 13:4796-4803(1974).
 Biochemistry 13:4804-4811(1974)
 01, Created)
 STANDARD;
 Pfam; PF00047; ig; 2.
 [2]
SEQUENCE OF 4-68.
 NCBI_TaxID=10141;
 SEQUENCE OF 1-3.
 DISULFIDE BONDS.
 21-JUL-1986 (
21-JUL-1986 (
15-JUL-1999 (
 antibodies.
 GC2 CAVPO
P01862;
 306
 297
 RESULT 5
GC2_CAVPO
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 185
 125
 116
 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIBKTISKAKGQPREPQVYTLPPSRDELTK 245
 65
 63
 64 SLSSVVSVTSSS---QPVTCNVAHPATNTKVDKTVAPSTCSK----PTCPPPELLGGPSV
 SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV
 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY
 KAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNSGTLTNGVRTFPSVRQSSGLY
 7; Gaps
 D12 ALLOTYPIC MARKER, REF.3 HAS THE D11 AND E15
 69.2%; Score 1230.5; DB 1; Length 323; 70.0%; Pred. No. 1.5e-85;
 57; Indels
 vPV (IN REF. 2).

E (IN REF. 3 AND 4).

(IN REF. 5).
 Pfam; Processing State of the S
 IG-LIKE 1.
IG-LIKE 2.
IG-LIKE 3.
T -> M (1N D11 MARKER).
T -> A (1N B15 MARKER).
N -> E (1N REF. 2).
 -> S (IN REF. 5).
69E8AA118D579A8B CRC64;
 34; Mismatches
 VPV
 EMBL) MACTON GHEB.
HSSP, PO1857; IFCI.
INTERPRO; IPR007110; IG-like.
INTERPRO; IPR003597; IG_CI.
INTERPRO; IPR003006; IG_MHC.
J. 116:249-259(1970),
 35404 MW;
 EMBL; M16426; AAA31289.1; -.
 Conservative
 Query Match
Best Local Similarity
Matches 229; Conserv
 323 AA;
 1114
1104
1104
1144
1144
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1103
Biochem.
 9
 99
 126
 186
 177
 SEQUENCE
 DOMAIN
DOMAIN
VARIANT
 CONFLICT
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296
 Oliveira B., Lamm M.E.;
"Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
"Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
Biochemistry 10:26-31(1971).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
13 INRRED GUINEA PIGS.
PIR; A94553; GZGP.
HSSP, PO1842; 7FAB.
InterPro; IPRO07310; Ig-like.
InterPro; IPRO03507; Ig-di.
InterPro; IPRO03507; Ig-di.
RSVSLICMINGFYPSDISVEWEKNGKAEDNYKTTPAVLDSDGSYFLYNKLSVPTSEWQRG
 SEQUENCE OF 69-133 AND 312-329.

MEDIATE=7105846; PubMed=5538616;

"Turner K.J., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
and hinge region cyanogen bromide fragments.";
Biochemistry 10:9-17(1971).
 MEDLINE=71058471; PubMed=5538606;
Birshtein B.K., Hussain Q.Z., Cebra J.J.;
Structure of heavy chain from strain 13 guinea pig
immunoglobulin-G(2). 3. Amino acid sequence of the region around the
half-cystine joining heavy and light chains.";
 SEQUENCE OF 134-226.
MEDLINE=75036072; PubMed=4429665;
Tracey D.B., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig IgG2
 SEQUENCE OF 227-311.
MEDLINE-75036673; PubMed=4609467;
Trischmann T.M., Cebra J.J.;
"Primary structure of the CH3 homology region from guinea pig IgG2 antibodies.";
 Euteleostomi;
 Ig gamma-2 chain C region.
Cavia porcellus (Guinea pig).
Bukaryota, Merazoa; Chordata; Craniata; Vertebrata; Buteleostc
Mammalia; Butheria; Rodentia; Hystricognathi; Caviidae; Cavia
 PROSITE; PSS0835; IG'LIKE; 3.
PROSITE; PS00290; IG'MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
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GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH--TCPPCPAPELL 120
 116
 180
 GGPSVFIFPPKPKDTLMISLTPRVTCVVVDVSQDEPBVQFTWFVDNKPVGNAETKPRVEQ 176
 240
 236
 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLTVD 298
 62
 9
 ARTTAPSVFPLAASCVDTSGSMMTLGCLVKGYFPEPVTVKWNSGALTSGVHTFPAVLQ-S
 GLYSLISMVTVPSSQKAT----CNVAHPASSTKVDKTVEPIRTPZPBPCTCPKCPPPENL
 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
 Gaps
 SEQUENCE (DISEASE PROTEIN WIS).
MEDLINE=81021548; PubMed=6774747;
Frangione B., Rosenwasser B., Prelli F., Franklin B.C.;
Primary structure of human gamma 3 immunoglobulin deletion mutant:
gamma 3 heavy-chain disease protein Wis.";
Biochemistry 19:4304-4308(1980).
 Homo sapiens (Human),
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
 REVISIONS TO 12-97 (PROTEIN WIS).
MEDLINE=77118561; PubMed=402363;
Michaelsen T.E., Frangione B., Franklin E.C.;
Michaelsen T.E., Frangione B., Franklin E.C.;
Wrimary structure of the 'hinge' region of human 1gG3. Probable quadruplication of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
 .
.
 ; Score 1212.5; DB 1; Length 329;
; Pred. No. 3.5e-84;
28; Mismatches 62; Indels 9;
 MEDLINE-77021516; PubMed-823945;
Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
"The amino acid sequence of 'heavy chain disease' protein ZUC
Structure of the Pc fragment of immunoglobulin G3.";
 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
1g gamma-3 chain C region (Heavy chain disease protein) (HDC)
IGHG3.
 CHAIN).
CHAIN).
CHAIN).
 INTERCHAIN (WITH A LIGHT CHAIN)
 36074 MW; 5D231B7164D1FBA9 CRC64;
 INTERCHAIN (WITH A HEAVY
INTERCHAIN (WITH A HEAVY
INTERCHAIN (WITH A HEAVY
 REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC)
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 N-LINKED (GLCNAC.
 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 331
 KSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG 329
 290 AA
 68.2%;
 Best Local Similarity 70.33
Matches 234; Conservative
 STANDARD;
 329 AA;
 GC3 HUMAN
P01860;
NON TER
DISÜLFID
DISÜLFID
 DISULFID
DISULFID
DISULFID
 DISULFID
CARBOHYD
DISULFID
 63
 61
 121
 117
 177
 241
 237
 299
 297
 181
 SEQUENCE
 Query Match
 GC3_HUMAN

JC5_GC3_H

AC POISE

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DT 21-JU

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 -!- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
 AND ALL OF THE CHI REGION.
MISCELLANBOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
CAPACA.3 HEAVY CHAINS.
MISCELLANBOUS: DISEASE PROTEIN OWN WAY REPRESENT AN ALLELIC FORM
MISCELLANBOUS: DISEASE PROTEIN OWN WAY REPRESENT AN ALLELIC FORM
OR ANOTHER CAMMA CHAIN SUBCLASS.
MISCELLANBOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
TIMES AS LONG AS IN OTHER CAMMA CHAINS AND CONTAINS THREE
IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
 -i- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
-i- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
 SEQUENCE FROM N.A. (DISEASE PROTEIN OWM).

MEDLINE-S24247835; PubMed=6808505.

Alexander A., Steinmetz M., Barritault D., Frangione B.,

Franklin E.C., Hood L., Buxbaum J.N.;

Franklin E.C., Hood L., Buxbaum J.N.;

Gamma Heavy chalt disease in man: cDNA sequence supports partial

gene deletion model.";

Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).

-!- STBUNIT: DIMER LINKED B N1 2. DISULEIDE BONDS; IT HAS AN EXTRA

INTERCRAIN DISULEIDE BOND AT POSITION 7 IN ADDITION TO THE 11

NORMALLY PRESENT IN THE HINGE REGION.
 DIMER)
DIMER)
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 N-LINKED (GLCNAC. . .).
REMOVED POST-TRANSLATIONALLY
 N-LINKED (GLCNAC...).
INTERCHAIN (WITH HEAVY OINTERCHAIN (WITH HEAVY OINTERCHA
 PYRROLIDONE CARBOXYLIC N-LINKED (GLCNAC. . .).
Biochem. Biophys. Res. Commun. 71:907-914(1976)
 EMBL; J00231; AAA52805.1; ALT_SEQ.
HSSP; P01857; 1FC1.
 183
289
43
73
 SEGMENT (12-28)
 184
 DOMAIN
DOMAIN
DOMAIN
REPEAT
REPEAT
MOD RES
 DISULFID
DISULFID
DISULFID
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CARBOHYD
MOD RES
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 122
 113
 179
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 233
 240 RDELIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 299
 D
O
 62
 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
 1 AETTAPSVYPLAPGTALKSNSMVTLGCLVKGYPPEPVTVTWNSGALSSGVHTFPAVLQ-S
 63 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
 60 GLYTLTSSVTVPSSTWPSQTVTCNVAHPASSTKVDKKIVPRNCG--GDCKPC---ICTG
 123 ---PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
 114 SEVSSVFIFPPKFKDVLTITLTPKVTCVVVDISQDDFEVHFSWFVDDVEVHTAQTRPPEE
 180 QYNSTYRUVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
 GEB RAT STANDARD; PRT; 333 AA.

AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DF 19-SEP-2003 (Rel. 42, Last annotation update)
DF 19-SEP-2003 (Rel. 42, Last annotation update)
OS Rattus norvegicus (Rat).
OS Rattus norvegicus (Rat).
OC Bukaryota, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Marinae; Rattus.
 Gaps
 ch 64.8%; Score 1152; DB 1; Length 326; Il Similarity 63.1%; Pred. No. 1.2e-79; 210; Conservative 53; Mismatches 60; Indels 10;
 (POTENTIAL)
 INTERCHAIN (WITH A HEAVY CHAIN) INTERCHAIN (WITH A HEAVY CHAIN)
 N-LINKED (GLCNAC. . .) (PO 013BAB45EF49B9DA CRC64;
 300 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
 MEDLINE-89232738; PubMed=3149946;
 109
111
200
304
176
35946 MW;
 109
111
140
246
3
176
136 AA;
 SEQUENCE FROM N.A.
 DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
SEQUENCE
 Query Match
 Local
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 118
 220
 160
 119 KWYVDGVQVHNAKTKPREQQFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKT 178
 221 ISKAKGOPREPOVYTLPPSRDELTKNOVSLITCLVKGFYPSDIAVEWESNGOPENNYKTTP 280
 238
 ### PROBLEM | Part | Pa
 EPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHBDPEVQF
 101 BPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
 161 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
 179 ISKTKGQPREPQVYILDPSKEEMTKNQVSLICLVKGFYPSDIAVEWESSGQPENNYNTTP
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus. NCBI TaxID=10116;
 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHBALHNHYTQKSLSLSPGK 332
 ;
 Query Match 65.0%; Score 1156; DB 1; Length 290; Best Local Similarity 90.5%; Pred. No. 5.3e-80; Matches 210; Conservative 13; Mismatches 9; Indels (
 TId=VAR 003896.
E69CBC95705B2F46 CRC64;
 QV -> EB (IN ZUC).

P - L (IN QM).

P - L (IN QM).

FTIG=VAR 003891.

FTIG=VAR 003891.

FTIG=VAR 003892.

T -> A (IN QM).

FTIG=VAR 003892.

T -> A (IN QM).

S -> N (IN QM).
 MISSING (IN ZUC)
/FTId=VAR_003895
 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-1 chain C region.
Rattus norvegicus (Rat).
 LT.
SEQUENCE FROM N.A.
MEDLINE-89232738; PubMed=3149946;
 290 AA; 32331 MW;
 STANDARD;
 279
 127
 134
 139
 182
 227
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 182
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 SEQUENCE
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GCC AAT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                  Bvolution of immunoglobulin subclasses. Primary structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [mmunoglobulin domain; Immunoglobulin C region; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN)
CHAIN)
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N -> D (IN REF. 3).
N -> D (IN REF. 3).
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276 N -> D (IN REF. 3).
278 N -> D (IN REF. 3).
35704 MW, A338812F3D1F2C93 CRC64;
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/FTId=CAR_000055.
                                                                                                                                      DISULFIDE BONDS (MOPC 21).

SUBDILINE=7300889; PubMed=5073237;

Svasti J. Milstein C.;

"The disulphide bridges of a mouse immunoglobulin (Biochem. J. 126.837-850(1972).

-!- SUBCELLULAR LOCATION: Secreted.

-!- ALTENMATUP PRODUCTS:

Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.2%; Score 1142; DB 1;
62.0%; Pred. No. 6.9e-79;
ive 56; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                           Name=Secreted;
IsoId=P01868-1; Sequence=Displayed;
Note=May be the major isoform;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Membrane-bound;
IsoId=P01869-1; Sequence=External;
                                                               murine myeloma gamma1 chain.";
J. Biol. Chem. 253:6068-6075(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alternative splicing, 3D-structure, NON TER 1 1 1 CH1, DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, V00793; CAA24173.1; EMBL, V00793; CAA24173.1; EMBL, V00793; CAA24173.1; EMBL, V00795; CAA24175.1; EMBL, V00795; CAA24176.1; EMBL, PRO03506; Ig_MHC. PAM, PRO0407; IGC.1; EMBL, PRO0407; IG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART, SM00407, IGC1; 2.
PROSITE, PS50835, IG_LIKE; 3.
PROSITE, PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; V00793; CAA24172.1; -.
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Best Local Similarity 62.0
Matches 206; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244
324
276
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324 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                               177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237 PPSRDELIKNOVSLICLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSDGSFFLYSKLT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPPTEQLTEQTVSLTCLTSGFLPNDIGVEWTSNGHIEKNYKNTEPVMDSDGSFFMYSKLN 297
                                                                                                                                                                                                                                                                             62
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                                                                                                                                                                                                                                                                        3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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Rogers J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MODC 31C).
MEDIATR=80202559; PubMed=6769752;
Obata M., Yamawaki. Fubmed=6769752;
Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Imminoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE=80045036; PubMed=115593; Honjo T., Cataoka T., Kawakami T., Takahashi N., Mano Y.; Takahashi N., Mano Y.; Takahashi N., Mano Y.; Cloning and complete nucleotide sequence of mouse immunoglobulin gamma 1 chain gene."; Cell 18:559-568(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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•
                                                                                                                                                                      DB 1; Length 333;
     INTERCHAIN (WITH A HEAVY CHAIN) INTERCHAIN (WITH A HEAVY CHAIN)
                                                                                                                                                                                                                    68; Indels
                                                                                                                36497 MW; 55F8B64D48D460A6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 gamma-1 chain C region secreted form.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324 AA
                                                                                                                                                             64.5%; Score 1146.5; 64.0%; Pred. No. 3.3e; ive 44; Mismatches
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MEDLINE=78242288; Pubmed=98524;
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
  112
115
147
253
333 AA;
                                                                                                                                                                                    al Similarity
215; Conserv
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P01868;
                                                   DISULFID
DISULFID
SEQUENCE
DISULFID
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                                                                                                                                                             Query Match
                                                                                                                                                                                             Local
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GCI MOUSE

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1 TITAPSVYPLVPGCSDISGSSVTLGCLVKGYFPEPVTVKWNYGALSSGVRTVSSVLQ-SG 59
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GCIM_MOUSE
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                                                                                                             240
                                                   180
-LYTLSSSVIVPSSPRPSETVICNVAHPASSTKVDKKIVPRDCG----CKPCICTVPEV- 114
                                                                --ssvFIFPPREXDVLTITLTPRVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQ 172
                                                                                                                           300
                                                                                                                                                                                     YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
                                              GGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                   DELIKNOVSLICLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSDGSFFLYSKLIVDKS
                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=85027161; PubMed=6092053; Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.M., Blattner F.R.; "Structural analysis of the murine IgG3 constant region gene."; EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HISP, POINTS, CARROLL HISP, POINTS, CARROLL HILDERPO, IPRO07110; Ig-like.
InterPro; IPR003110; Ig-like.
InterPro; IPR00310597; Ig-d.
InterPro; IPR003006; Ig-MHC.
Pfam; PF00047; Ig; 3.
SWART; SW00407; IG-LIKE; 3.
PROSITE; PS00250; IG-MHC, 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.
DOMAIN I 97 CH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 64.2%; Score 1141; DB 1; Length 329; Best Local Similarity 64.0%; Pred. No. 8.3e-79; Matches 212; Conservative 47; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36228 MW; F45827174182BAD6 CRC64;
                                                                                                                                                                                                                             301 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
                                                                                                                                                                                                                                                293 NWEAGNTFICSVLHEGLHNHHTEKSLSHSPGK 324
                                                                                                                                                                                                                                                                                                                                                                01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ig gamma-3 chain C region, secreted form.
                                                                                                                                                                                                                                                                                                                                       329 AA.
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CH2.
CH3.
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PIR; B02156; G3MSC.
                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                  GC3 MOUSE
P22436;
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                                                                                                                                                                                                                                        239 QMSKKKVSLTCLVTNFFSEALSVBWERNGELEQDYKOTPPILLDSDGTYFLYSKLTVDTDS 298
64 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP--PCPAPELLG
                       NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                                                                      GPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metarza; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINES 80045036; PubMed=115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
Takahashi N., Mano Y.;
Gloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
Cell 18:559-568(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O., "mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-44 FROM N.A.
MEDILIPE-82221990; PubMed=6283537;
MEDILIPE-82221990; PubMed=6283537;
Vamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 323-366 FROM N.A. MSDLINE-SEXESTISSES PUDMEd=6799207;
MSDLINE-SEXISSES; PuDMEd=6799207;
Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl Eisenberg D., Wall R.;
Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains.";
Cell 26:19-27(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
Name=Membrane-bound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain.";
Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 gamma-1 chain C region, membrane-bound form.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                   299 WLQGEIFTCSVVHEALHNHHTQKNLSRSPGK 329
                                                                                                                                                                                                                                                                                             WQQGNVFSCSVMHEALHNHYTQXSLSLSPGK 332
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Note=May be the major isoform;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 323-393 FROM N.A. MEDLINE=82197626; PubMed=6804950;
                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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P01869;
21-JUL-1986 (
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4; Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 -LYTLSSSVTVPSSPRPSETVTCNVAHPASSTKVDKKIVPRDCG----CKPCICTVPEV- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP--CPAPELL 120
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DR PDB; 126.9; 24.00.0.

DR PDB; 126.9; 13.00.0.

DR PDB; 11.00.0.

DR PDB; 12.00.0.

DR PDB; 1
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61.9%; Pred. No. 2.1e-78;
iive 56; Mismatches 60; Indels 10;
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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4CC88343B7A1CE27 CRC64;
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HINGE.
CH2.
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                                                                                                                                                                                                                                EMBL, V00793; CAA24172.1; -. EMBL, V00793; CAA24173.1; -. EMBL, V00793; CAA24174.1; -. PIK, B02159; GIMSM.
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205; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       Wall R.; "The structure of the mouse immunoglobulin in gamma 3 membrane gene
                                                                                                                      23-0cT-1986 (Rel. 02, Created)
1-ATG-1991 (Rel. 19, Last sequence update)
15-UTL-1999 (Rel. 18, Last annotation update)
16-UTL-1999 (Rel. 38, Last annotation dorm.)
19 gamma-3 chain C region, membrane-bound form.
19 gamma-3 chain C region, membrane-bound form.
Eukaryotai, Melazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=85027161; PubMed=6092053;
Mels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blatther F.R.;
"Structural analysis of the murine IgG3 constant region gene.";
EMBO J. 3:2041-2046(1984).
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                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 328-398 FROM N.A.
MEDLINE-84041483; PubMed-6314258;
Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Transmembrane; Alternative splicing.

NON TER 1 1 1 1 1 1 DOMAIN 1 97 CH1.
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342 E -> Q (IN REF. 2).
388 P -> F (IN REF. 2).
43929 MW; CF7F264B50A41B95 CRC64;
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CH3.
POTENTIAL.
CYTOPLASMIC (POTENTIAL)
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63.8%; Pred. No. 7.2e-78;
293 NWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG 323
                                                                                          398 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      segment.";
Nucleic Acids Res. 11:6775-6785(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig cl.
InterPro; IPR003006; Ig_MHC.
Pfam; PP00047; Ig; 3.
SMART; SM00407; Igc. 12.
PROSITE; PS00835; IG_LIKE; 3.
PROSITE; PS00895; IG_MHC; 1.
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Best Local Similarity 63.8°
Matches 210; Conservative
                                                                                            STANDARD;
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3466
3363
3333
3888
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988
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                                                                                         GC3M MOUSE
P03987;
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CONFLICT
SEQUENCE
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21-UTJ-1986 (Rel. 01, Created)
21-UTJ-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Mus musculus (Mouse).
Mus musculus (Mouse).
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IG-LIKE 2
IG-LIKE 3
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PDB; 1E4X; 12-JUL-01.
PDB; 1MNU; 06-MAY-99.
INLEXPRO; 1PR007110; IG-1ike.
INTEXPRO; 1PR003597; IG_C1.
INTEXPRO; 1PR003006; IG_MHC.
Pfam; PF00047; IG; 2.
SMART; SM00407; IGC1; 2.
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P01864;
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MOD RES
SEQUENCE
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121
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                     60 FYSLSSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPR-IPKPSTPPGSSCPPGNILG
                                                                                                                                                                                                      239 OMSKKKVSLTTCLVTNPFSEAISVEWERNGELEODYKNTPPILDSDGTYFLYSKLTVDTDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=81223894; PubMed=6787604; Ollo R., Auffray C., Morchamps C., Rougeon F.; Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes suggests that exons can be exchanged between genes in a multigenic family.";
LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP--PCPAPELLG
                                                                                                                        119 GPSVPIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQPREAQY
                                                                                                                                                                            182 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                       GPSVFLFFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDILINE=81198976; PubMed=6262729;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
"The complete nuclectide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.";
Nucleic Acids Res. 9:1365-1381(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-81076554; PubMed=6777755;
Sikorav J.-L., Auffray C., Rougeon F.;
Strocture of the constraint and 3° untranslated regions of the murine Balb/c gamma 2a heavy chain messenger RNA.";
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BOLISDLINE-4415517; PubMed-4811970;
BOLISDLOS A., FOUGER-8N M., ROCCA-Serra J.;

"Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function.";

Eur. J. Biochem. 43:423-435(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
N.C.E. TaxID=10090;
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-!- SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig gamma-2A chain C region, A allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Balb/c gamma 2a heavy chain messenger RNA.";
Nucleic Acids Res. 8:3143-3155(1980).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 YNSTLRVVSALPIQHQDMMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS00290; IG MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; 3D-structure; Repeat.
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 120 PDLLGGFSVFIFFPKIKDVLMISLSPMVTCVVVDVSEDDFDVQISWFVNNVEVHTAQTQT 179
                                                  237 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
                                                                                                                       240 PPPAESEMTKKEFSLTCMITGFLPAEIAVDWTSNGRTEQNYKNYATVLDSDGSYFMYSKLR
                                  177 REBOYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-8222190; PubMed=6283537;
MEDLINE-8222190; PubMed=6283537;
Mucalevaria Kataoka Y., Nakai S., Miyata T., Honjo T.,
"Nucalevaria sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.",
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
-I. ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Note=Probably the major isoform;
-!- SIMILARITY; Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                        300 VQKSTWERGSLFACSVVHEVLHNHLTTKTISRSLGK 335
                                                                                                                                                                      297 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
                                                                                                                                                                                                                                                                                                                          21.JUL-1986 (Rel. 01, Created)
01.AUC-1991 (Rel. 19, Last sequence update)
15.58P-2003 (Rel. 42, Last annotation update)
19 gamma-2A chain C region, membrane-bound form.
                                                                                                                                                                                                                                                                                          399 AA
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INTERCHAIN
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IG-LIKE 2.
IG-LIKE 3.
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                                                                                                                                                                                                                                                                                            STANDARD;
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325
15
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107
110
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                                                                                                                                                                                                                                                                                          GCAM MOUSE
P01865;
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R PIR; A02155; GRMSAB.

R PDB; 1BOG; 23-MAR-99.

R PDB; 1HHF; 26-MAN-01.

R PDB; 1HHF; 12-JAN-01.

R PDB; 1HHF; 12-JAN-01.

R INTERPO; IPRO07110; Ig-1ike.

R INTERPO; IPRO03006; Ig_MHC.

R INTERPO; IPRO03006; Ig_MHC.

R RAMARY; SM0047; ig; 3.

R RAMARY; SM0047; ig; 3.

R PROSITE; PS50835; IG_LIKE; 3.

R PROSITE; PS50835; IG_LIKE; 3.

R PROSITE; PS00290; IG_MHC; 1.

W Immunoglobulin domain; Immunoglobulin C region; Alternative splicing;
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-!- MISCELLANBOORS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
FROM BALB/C MICE, AT 15% OF THE POSITIONS.
-!- SIMILARITY: Contains 3 immunoglobulin-like domains.
 Sukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBL_TaxID=10090;
                                                                                 STRAIN=CS7BL/6;
MEDLINE=82037861; PubMed=6170065;
Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
Schreier P.H., Bothwell A.L.M. the nucleic acid sequences of the IgG2aa and IgG2ab alleles of the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
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                                                                                                                                                                                                                     WEDLINE-82037777; PubMed-6794027;
WEDLINE-82037777; PubMed-6794027;
DOGILA M.J., Lauwereys M., Strosberg A.D.;
"Multiple amino acid substitutions between murine gamma 2a lchain For regions of Igla and Iglb allotypic forms.";
Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
-i- SUBCELLUIAR LOCATION: Secreted (Potential).
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335 AA; 36596 MW; FA3382792CBB13C6 CRC64;
                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=2;
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Note=Probably the major isoform,
Name=Membrane-bound;
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IG-LIKE 2.
IG-LIKE 3.
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Best Local Similarity 61.3
Matches 206; Conservative
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179 YNSTLRVVSALPIQHQDMMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPE 238
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                                                                                                                                                                                                                                                                                 61 -LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNLL 118
                                                                                                                                                                                                                                                                                                                            121 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 180
                                                                                                                                                                                                                                                                                                                                                181 YNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPQVYTLPPSR 240
                                                                                                                                                                                            3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62
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                                                                                                                                                               4; Gaps
112 INTERCHAIN (WITH A HEAVY CHAIN).
204
308
363 POTENTIAL.
399 CYTOPLASHIC (POTENTIAL).
180 N-LINKED (GLCNAC. ..) (POTENTIAL)
44020 MW, 4C38138BFAED3FF0 CRC64;
                                                                                                                            Query Match 63.0%; Score 1121; DB 1; Length 399; Best Local Similarity 63.4%; Pred. No. 3.4e-77; Matches 210; Conservative 44; Mismatches 73; Indels
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399 AA;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Strausberg R.B.

Submitted (FEB.2002) to the EMBL/GenBank/DDBJ databases.

REMBL, BC024289; AAH3289.1; -.

RINEEPERO; IPR007110; Ig-11ke.

RINEEPERO; IPR003596; Ig-V.

RINEEPERO; IPR003596; Ig-V.

R PROSITE; PS50835; IG-LIKE; 4.

R PROSITE; PS50835; IG-LIKE; 4.

R PROSITE; PS50290; IG-MHC; 2.

M Hypothetical protein.

W Hypothetical protein.

W SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;
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01-UUN-2002 (TERMELrel. 21, C)
01-UUN-2002 (TERMELrel. 21, Li
01-MAR-2003 (TERMELrel. 23, Li
Hypothetical protein.
Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                            1 EFASTKGPSVFPLAPSSKST......MHEALHNHYTQKSLSLSPGK 332
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                    GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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445 GFYPSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVWHF 504
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Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
"The nuclectide sequence of a long CDNA clone isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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InterPro; IPR0031997; Ig-c1.
InterPro; IPR0031997; Ig-mHC.
Pfam; PF00047; ig; 3.
PROSITE; PS00319; IG-IKE; 3.
PROSITE; PS003290; IG-IKE; 2.
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01-0cT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
PLJ00385 protein (Fragment).
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90.9%; Score 1615.5; DB 4
Best Local Similarity 81.6%; Pred. No. 1.9e-138;
Matches 306; Conservative 11; Mismatches 11;
                                                                                   316 ALHNHYTOKSLSLSPGK 332
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                                                                                                                                                                                                                                                LIKNOVSLICLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLIVDKSRW 302
                                                                                                                                                                                                                                                                                382 LIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 GLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVBLKTPLGDTTHTCPRCPEPKSC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 IMISRIPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKIKPREEQYNSIYRVVSVLIVLH 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 315
                                  PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
                                                                                                                                                                                          322 STYRVVSVLTVIHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 381
                                                                                   262 PSVFLFFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 DIPPPCPRCPSPKSCDTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         325 LMISRIPEVICVVVDVSHEDPEVQFKWYVDGVEVHNAKIKPREEQFNSIPRVVSVLTVLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVK
                                                                                                                                         STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Sukaryota; Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi,
Mammalia; Butheria; Primates; Catarrhini, Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 91.5%; Score 1626.5; DB 4; Length 521; Local Similarity 81.7%; Pred. No. 2e-139; les 308; Conservative 11; Mismatches 11; Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

SEXULANCE FROM N.A.

Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitteed (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC033178, AH433178.1;
InterPro; IPR003306; Ig_-1.
InterPro; IPR003006; Ig_-1.
InterPro; IPR003596; Ig_-1.
InterPro; IPR003596; Ig_-1.
InterPro; IPR00406; Ig_-1.
InterPro; IPR00406; Ig_-1.
InterPro; IPR00406; IGV; I.
SYART; SM00406; IGV; I.
R SYART; SM00406; IGV; I.
R PROSITE; PS00290; IG_-HC; 2.
HYPOCHECICAL Protein.
SEQUENCE 521 AA; 57156 MW; ZAC7D22E72D6CAA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                    442 QGGNVFSCSVNHEALHNHYTQKSLSLSPGK 471
                                                                                                                                                                                                                                                                                                                                                        303 OCGNVFSCSVMHEALHNHYTOKSLSLSPGK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  521 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein
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                                  123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 APHPDELSKSKVSVTCLVKDFYPPEINIEWQSNGQPELETKYSTTQAQQDSDGSYFLYSK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDINE 21477448; PubMed=11593034; Hu Z., Garen A.; Garen A.; Fubmed=11593034; Hu Z., Garen A.; Garen A.; Fargeting tissue fact utmor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer."; Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185 (2001).
-i. SINITARITY: BELONGS TO PEPTIDASE FAMILY SI.
EMBI; AF272774; AAK58686.1; ---
HSSP; PO0761; IANI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GFYSLSSWYTVPASTWTSETYICNVVHAASNFKVDKRIEPIPDNHQKVCDMS-KCPKCPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 PELLGGESVFLEPPKPKDTLMISKTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 PELLGGPSVFIFPPNPKDTLMITRTPEVTCVVVDVSQENPDVKFNWYMDGVEVRTATTRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 KEEGPNSTYRVVSVLRIQHODWLSGKEFKCKVNNQALPQPIERTITKTKGRSQEPQVYVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ASTTAPKVFALAPGCGTTSDSTVALGCLVSGYFPEPVKVSWNSGSLTSGVHTFPSVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.2%; Score 1266.5; DB 6; Length 337; 69.2%; Pred. No. 6.3e-107; tive 43; Mismatches 52; Indels 9;
                                             Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q96PQ8 PRELIMINARY; PRT; 701 AA.
Q96PQ8;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2003 (TrEMBLrel. 23, Last annotation update)
Factor VII active site mutant immunoconjugate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Simil
Matches 234; (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                             OBTOGS;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Eukaryota: Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Eguus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
chain constant region (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

89.5%; Score 1590.5; DB 4; Length
Best Local Similarity 90.9%; Pred. No. 3.2e-136;
Matches 300; Conservative 12; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00196; COPPER BLUE; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; 3.
Hypothetical protein.
SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
                                                 473 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 QOGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               337. AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QEGNVFSCSVMHEALHNHYTQKSLSLGK 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2003 (TrEMBLrel. 23, Immunogobulin gamma 1 heavy IGHC1.
                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (MAR-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
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205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRBEQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 FNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPF 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               378 EQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKINVQKS 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGY?PEPVTVTWNSGSLSSGVHTFPAVLQSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 --SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTKPREEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY?PEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                            65.3%; Score 1161; DB 11; Length 469; 63.3%; Pred. No. 3.9e-97; tive 53; Mismatches 59; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11; Length 463;
                                                        to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC003435; AAH03435.1; --
HSSP; P01842; 7PAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; NGIS646; Igh-4.
INTERPOSTIO; IG-like.
INTERPOSTIO; Ig-like.
INTERPOSTIO; Ig-like.
INTERPOSTIO; Ig-MC.
INTERPOSTIO; Ig-V.
PEAM; PF00047; ig; 4.
PROSTITE; PS00835; IG-LIKE; 4.
PROSTITE; PS00290; IG-LIKE; 4.
PROSTITE; PS00290; IG-MC; 1.
SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
                                                                                                                                                                                                               Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; 1.
PROSITE; PS01290; IG MHC; 1.
SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q99LC4 PRELIMINARY; PRT; 463 AA.
Q99LC4;
01-JUN-2001 (Tremel. 17, Created)
01-JUN-2001 (Tremelrel. 17, Last sequence update)
01-MAR-2003 (Tremelrel. 23, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               438 NWEAGNIFICSVLHEGLHNHHTEKSLSHSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.0%; Score 1155;
                                                                                               InterPro; IPR007110; IG-11ke.
InterPro; IPR003006; IG-MHC.
InterPro; IPR00356; IG-WHC.
Pfam; PF00047; ic.
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 63.34
Matches 210; Conservative
                                Strausberg R.;
Submitted (MAR-2002) to t
EMBL; BC024405; AAH24405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       422 VSWGQGCATVG-----HFGVY-----TRVSQYIEWLQKLMRSEPRPGVLLRAPFP 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              467 GSAEPKSCDKTHTCPPCPAPBLLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        527 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS---NTKVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVWHEALHNHYTQKSLSLSPGK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-UUN-2002 (TrEMBLrel. 21, Created)
01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mypothetical 52.0 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria, Rodentia; Sciurognathi; Muridae; Murinae; Musinae; Musinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 71.1%; Score 1264; DB 4; Length 701; Best Local Similarity 82.4%; Pred. No. 2.9e-106; Matches 243; Conservative 4; Mismatches 30; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PSULIBS; BCF_CA; 1.
PROSITE; PSULIBS; BCF_CA; 1.
PROSITE; PSCO011; GLU_CRRBOXYLATION; 1.
PROSITE; PSCO290; IG_LIKE; 2.
PROSITE; PSCO240; TRYPSIN DOM; 1.
PROSITE; PSCO134; TRYPSIN HIS; 1.
PROSITE; PSCO135; TRYPSIN HIS; 1.
PROSITE; PSCO135; TRYPSIN HIS; 1.
BCF-11ke domaln; Hydrolase; Protease; Serine protease.
SEQUENCE 701 AA; 77826 MW; 94ACGCB842CC992F CRC64;
                                                                                         InterPro; IPR001438; EGF_II.
InterPro; IPR0026209; EGF_Iike.
InterPro; IPR002383; GLA_blood.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003264; Ser_protease_Iry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS00022; EGF 1; 1
PROSITE; PS01186; EGF 7; 1
                                                                                                                                                                                                                                                                                                                               Pfam; PP00008; EGF; 2.
Pfam; PP00008; EGF; 2.
Pfam; PP00004; 1g; 2.
Pfam; PP00049; trypsin; 1.
PRINTS; PR00010; EGFELODD.
PRINTS; PR00010; EGFELODD.
PRINTS; SM0010; EGFELODD.
SMART; SM00179; EGF_CA; 1.
SMART; SM00009; GLA; 1.
                                    InterPro, IPR00074
InterPro, IPR00188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218
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Exeron No. 1 Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa J., Fukunishi Y., Komo H., Adachi J., Fukuda S., Alzawa M., Isahi K., Kiyosawa H., Kondo S., Yamanaka I., RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Ra Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Rahl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Ra Fleischmann W., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Manger L., Washio T., RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Barke J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ringwald M., Rodriguez I., Sakamoto N., A Sasaki H., Sato K., Schoenbach C., Saya T., Shibata Y., Storch R.-F., Winner M., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L., Wanghia, Y., Kawaji H., Kohtsuki S., M. Wang K.H., Weltz C., Whittaker C., Wilming L., Wanghia, J., Kawaji H., Kohtsuki S.,
                                                                                   285
                                                                                                                              240
                                                                                                                                                                                                                300
                                                                                                                                                                                                                                       SOMANDE STATEMENT TO PEPEDIT VEW OWN GOPAEN Y KAN TOPIM DE SYFVY SKENVOKS 405
                                                               --SSVPIFPPREKDVLTITLTPRVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQ
                                                                                                                            181 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPQVYTLPPSR
                                                                                                                                                       FINSTFRSVSELPIMHQDMLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPK
                                                                                                                                                                                                                241 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                             GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 ASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYPPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 61.9%; Pred. No. 5.5e-95;
Matches 208; Conservative 53; Mismatches 68; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS50836; IG_MHC; 4.
SRGUTE; PS50230; IG_MHC; 1.
SEQUENCE 473 AA; $1699 NW; 9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                           406 NWEAGNTFTCSVLHEGLHNHHTEKNLSHSPGK 437
                                                                                                                                                                                                                                                                                                    RWOOGNVESCSVMHEALHNHYTOKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001).
EMBL; AK007918; BAB25349.1; -
HSSP; P01842; 7FAB.
MGD; MGI:96443; Igh-1.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-070-2001 (TrEMBLrel. 17, 01-070-2001 (TrEMBLrel. 17, 181006-00991k procesin. IGH-1 OR 1810060009RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashizaki Y.;
                                                                                   228
                                                                                                                                                                     286
                                                                                                                                                                                                                                                         346
                                                                                                                                                                                                                                                                                                  301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9D8L4
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
Q9D8L4
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                                                                                                                                                                     120
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                                                                                                                          199
                                                                                                                                                                                            200 -LYILSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCG----CKPCICTVPEV- 253
                                                                                                                                                                                                                                                                                                    311
                                                                                                                                                                                                                                                                                                                                        YNSTYRVVSVLTVLHODWINGKEYKCKVSNKALPAPIEKTISKAKGOPREPOVYTLPPSR 240
                                                                                                                                                                                                                                                                                                                                                                 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 EQMAKDKVSLTCMITDFFFEDITVEWQWNGQPAENYKNIQPIMDTDGSYFIYSKLNVQKS 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP--CPAPELL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                        140 AKTIPPSVYPLAPGSAAQINSMVILGCLVKGYPPEPVIVIMNSGSLSSGVHIFPAVLQSD
                                                                                                                                                                                                                                                    121 GGPSVFLFPPKFKDTLMISRTPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                             --SSVFIFPPREKDVLTILIFRVTCVVVDISKDDPBVQFSWFVDDVEVHIAQTQPREEQ
                                                                                                                                                                   63 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP--CPAPELL
                                                                                                                                                                                                                                                                                                                                                                                                                            DELIKNOVSLITCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                               3 ASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.; "Cloning of cDNAs encoding for anti-white pine blister rust monoc antibody (Mab 7, its light and heavy chains) and construction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.7%; Score 1151; DB 11; Length 437; 62.3%; Pred. No. 2.9e-96; ive 56; Mismatches 59; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single chain antibody (ScFV). ", Submitted (MAX-1999) to the EMBL/GenBank/DDBJ databases. EMBL; ABT5372; AAD40243.1; -. HSSP; P01842; TRAB. MGD; MGI:96446; Igh-4. TREEPPO; IPR00710; Ig-like. InterPro; IPR00710; Ig-like. InterPro; IPR003106; Ig-v. PROSITE; PS50835; IG_LIKE; 4. PROSITE; PS50835; IG_LIKE; 4. PROSITE; PS50835; IG_LIKE; 4. PROSITE; PS00290; IG_MHC; I. NON_TER 437 437
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48142 MW; 5C3A7BB3EE7D697C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Gammal heavy chain of Mab7 (Fragment).
               1.4e-96;
ches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    437 AA.
                                        Mismatches
                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
62.7%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 62.3 tes 207; Conservative
         Best Local Similarity 62.7
Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               437 4
437 AA;
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                                                                                                                                                                                                                                                                                                                                        181
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Matches
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63 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPP--CPAPELL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 GGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNVEVLTAQTQTHRED 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322 YNSTLRVVSALPIQHQDMMSGKEFKCKVNNKALPAPIERTISKPKGSVRAPQVYVLPPPE 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 ASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYPPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 AKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYPPEPVTLTWNSGSLSSGVHTPPAVLQSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MA2-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 51.9 kDa protein.
Hypothetical 51.9 kDa protein.
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.1%; Score 1122; DB 11; Length 473; 63.6%; Pred. No. 1.4e-93; ive 44; Mismatches 73; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (FRB-2001) to the EMBL/GenBank/DDBU databases.
EMBL; BCC003888; AAH03888.1; -.
HSSP; P01042; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; ..... 1g; 3.
SMan; SM00407; 1g; 3.
SMART; SM00406; ICV; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; 1.
PROSITE; A77 AA; 52449 MW; BE9889B7986DA155 CRC64;
                                                                                                                                                                                                                                                                                                                                                     Q99125;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
Mus musculus (Mouse)
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                                 301 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
                                                                           301 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
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                                                                                                                                                                                                                                                                                                               473 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like,
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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Local Sim-
211;
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Q91205;
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Matches
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AC (29120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMTKKQVTLTCMVTDFMPEDIXVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKK 436
                                                                                                                                                                                                                                                                                  258 PDLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 PPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 180
                                                                                                                                                   257
                                                                                                                                                                                                                                   117 PELLGGPSVFLFFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 176
                                                                                                                                                                                                                                                                                                                                                                                                177 REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318 HREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNRALPSPIEKTISKPRGPVRAPQVYVL 377
                                                                           63 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK-----SCDKTHTCPPCPA 116
139 AKTTAPSVYPLAPVCGGTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPALLQ-S 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - INTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIBPRG-PTIKPCPPCKCPAPNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 GGPSVFIFFPRIKDVLMISLSPRVTCVVVDVSEDDPDVQISWFVNNVEVLTAQTGTHRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                  198 GLYILSSSVTVTSNTWPSQTITCNVAHPASSTKVDKKIEPRVPITQNPCPPLKECPPCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (PEB-2001) to the EMBL/GenBank/DDBJ databases
EMBL; EC003878; AAH03878.1; -.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR007110; Ig-1ike.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003096; Ig_W.
Pfam; PF00047; ig; 3.
SWART; SW00406; IGV; 1.
PR0STIR; PS50835; IG_LIKE; 4.
PROSTIRE; PS500290; IG_MHC; 1.
SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0707-2001 (TrEMBLrel. 17, Created)
01-0707-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to RIKEN cDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 VDKSRWQOGNVFSCSVMHEALHNHYTOKSLSLSPGK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  438 VQKSTWERGSLFACSVVHEGLHNHLTTKTISRSLGK 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139
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Q99L31
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63 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT-HTCPP----CP 115
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                                                                                                                                                                                                                                                                                                                                                                                                                               318 THREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYI 377
                                                                                                                                                                                                                                                                                                                                116 APELLGGPSVFLFFPFKPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 175
                                                                                                                                                                                                                                                                                                                                                                                                          176 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---TKVDKKVEPK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 STKGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQ 60
                                                                                                                                                                                            198 GLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 SASAPTLFPLVSCENSPSDTSSVAVGCLAODFLPDSITFSWKYKNNSDISSTRGFPSVLR
                                                                                                                                                                         3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
25.0%; Score 444.5; DB 4; Length 597;
Best Local Similarity 26.5%; Pred. No. 8.8e-32;
Matches 116; Conservative 68; Mismatches 142; Indels 111; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                        Query Match 61.2%; Score 1088; DB 11; Length 474; Best Local Similarity 60.8%; Pred. No. 1.8e-90; Matches 205; Conservative 49; Mismatches 75; Indels 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Extraorberg R.;
Strauberg R.;
Strauberg R.;
Strauberg R.;
Submitteed (FEB-2011) to the EMBL/GenBank/DDBJ databases.
RMBL; BC002063; AAH02963.1; -
R InterPro: IPR00710; Ig-like.
R InterPro: IPR003006; Ig-WHC.
R InterPro: IPR003006; Ig-W.
R PRAM; PR00404; ig: 1.
R PROSITE; PS00296; IG-V.
R PROSITE; PS00296; IG-MC; 3.
R PROSITE; PS00296; IG-MC; 3.
R Hypotherical protein.
SEQUENCE 597 AA; 65274 MW; 2DAFABFB7E055851 CRC64;
                                     Hypothetical protein.
SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SSGLYSLSSVVTVPSSSL--GTQTY-ICNVNHKPSN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
PROSITE; PS50835; IG_LIKE; 4. PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN 2001 (TrEMBLrel, 17, 01-JUN-2001 (TrEMBLrel, 17, 01-MAR-2003 (TrEMBLrel, 23, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Q9BU10;
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Q9BU10
  8 % W B B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 GLYIMSSSSVIVPSSIWPSQIVICSVAHPASSITVDKKLEPSGPISIINPCPPCKECHKCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT-HTCPP----CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                        61.2%; Score 1088; DB 11; Length 473; 60.8%; Pred. No. 1.8e-90; ive 49; Mismatches 75; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025447, AAH25447, AAH25477, Ig-Ike.
InterPro; IPR0031006; Ig-WHC.
InterPro; IPR003596; Ig-V.
Pfam; PP00047; ig, 3
SWART; SM00406; IGV; 1.
                                                                                                 to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OBR3H6;
O1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 51.7 kDa protein.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 DIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 473
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                                                                          Strausberg R.;
Submitted (UUL-2001) to the EMBL/GenBa
EMBL, BC010327, AAH10327.1;
MOD; MGI:2144967, AU044919.
InterPro; IPR000345; CytC heme_bind.
InterPro; IPR000101; Ig-11xe.
InterPro; IPR000106; Ig-MHC.
InterPro; IPR005966; Ig-WHC.
InterPro; IPR005966; Ig-V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                   SMART; SM00406; ĪGV; 1.
PROSITE; PS00190; CYTOCHROME C; 1.
PROSITE; PS50835; IG_LKE; 4.
PROSITE; PS00290; IG_CHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 60.8
Matches 205; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                         SEQUENCE FROM N.A
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OBR3H6
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28-JAN-1993
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Active-site
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Zcytor 10::IgG gam
Human IgG gamma 1
Human death domain
Human immunoglobul
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Human IgG1 Fcgamma
Human immunoglobul
Human immunoglobul
                                                                                                 January 13, 2004, 12:18:44; Search time 77.4183 Seconds (without alignments) 680.681 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA41981.DAT:*
| SIDSI/gcgdata/geneseqg-embl/AA41982.DAT:*
| SIDSI/gcgdata/geneseqg-embl/AA41982.DAT:*
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| SIDSI/gcgdata/geneseqg/geneseqg-embl/AA2002.DAT:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                1107863 segs, 158726573 residues
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                                                                 OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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AAB04071
ABB1641
AAE21960
ABB05736
ABM77856
AAB71856
AAE32627
AAE32915
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match 1
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Perfect score:
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No.
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Humanised anti-Abe
Humanised anti-Abe
Humanised 26 anti
Humanised antibody
BIWA4/8 antibody
Human 1961 chain C
Humanised monocion
                                                                                             Completely humanis
Amino acid sequenc
Humanised 3D6 anti
Murine humanised mit
Human recombinant
Mucin (MUC-1) bi
Heavy chain sequen
45-3.1.1-84 antib
Anti-HIV-1 recombi
Humanised 10D5 ant
Anti-HIV-1 recombi
Humanised monoclon
Humanised cD4 antib
Reshaped CD4 antib
Human c510 antibo
Antibody C510 antibo
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Humanised 10D5 ant
Human type antihum
Human type antihum
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type antihum
chain of 3D6
Human kappa immuno
Sequence of the li
                  Heavy chain. Homo
Deglycosylated hea
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Reshaped CAMPATH-1
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AAY31669
AAM49203
AAR43339
AAR43339
AAE12733
ABC54713
AAE12715
        AAP91918
ABB80109
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ABP96295
ABP58287
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AAR22758
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AAU07745
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AAR20057
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ALIGNMENTS

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61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 PSVFLFPPKPKDTLMISRTPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor enables the production of recombinant cells expressing the receptor. Those cells can then be used to detect the presence of a modulator of zcytor10 protein by culturing the cells in the presence of a modulator of zcytor10 protein by culturing the cells in the presence of a test ligand and comparing levels of activity of mouse zcytor10 in the presence and absence of the test sample can be achieved. The method comprising contacting a test sample can be achieved. The method comprising contacting a test sample containing an amino cal sequence from Cys15 or Girs, of the zcytor 10 cytokine receptor and detecting the binding of the polypeptide to a ligand in the sample. Specified peptide fragments of the zcytor 10 cytokine receptor and the methods described are used to identify lagands that stimulate the proliferation and/or development of haematopoietic, lymphoid and myeloid cells. Peptide fragments of the cytokine receptor are useful for treating lymphoid, immune, inflammatory, splenic, blood or bone disorders and for generating antibodies directed against the receptor. A vector expressing a construct the extracellular cytokine binding domain of zottor 10 is fused to the heavy chain of IgG gamma and the extracellular construct the heavy chain of IgG gamma and the extracellular chain interleukin receptor subunit) is fused to human kappa light chain (See GBNESEQ record AAAS4475). The two sequences are fused to construct using two primers (AAAS4475).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                       New cytckine receptor mouse zcytor 10, useful for detecting ligands that stimulate proliferation or development of haematopoietic, lymphoid and myeloid cells
          cell; lymphoid cell; myeloid cell; lymph; blood; bone; inflammatory response; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 99.4%; Score 1767; DB 22; Length 330; Best Local Similarity 100.0%; Pred. No. 3.7e-125; Matches 330; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                              Lok S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 17; Page 120-121; 134pp; English.
                                                                                                                                                                                                                                                                                                                                            Presnell SR, Foster DC, Hammond AK,
                                                                                                                                                                                                                      11-MAY-2000; 2000WO-US12924.
                                                                                                                                                                                                                                                            11-MAY-1999; 99US-0309861
                                                                                                                                                                                                                                                                                                  (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-016096/02.
N-PSDB; AAA54473.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 330 AA;
        haematopoietic c
immune system; b
spleen; human.
                                                                                                                                          WO200068381-A1
                                                                                                       Homo sapiens
                                                                                                                                                                                16-NOV-2000
                                                                                      Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVDFPKSCDKTHTCPPCPAPELLG 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPSVFLFPPKPKDTLMISRIPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 FASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                                                                                                                                                                                                           The human CD4 cDNA is excised from the plasmid pSP6T4 and cloned into M13mp18. In order to excise a fragment containing the CH1 exon of the human gamma 1 heavy chain gene, the plasmid pBr gamma 1 is digested with SacII, and the SacII sites are then made flush using T4 DNA polymerase. The fragment containing the CH1 exon is then purified and ligated to the M13mp18 (CD4) vector. Oligonucleotide-mediated site-directed mutagenesis is then performed to juxtapose the CD4 and CH1 sequences in frame. The CD4-CH1 chimeric gene is then linearized and ligated to the Petl. Petl DNA fragment of the plasmid pBr gamma 1 containing the clessing CH2, and CH3 exons of the human gamma 1 chain gene designated CD4-IgGHKC-PRCCMV (ATCC 75192).

(Updated on 25-MAR-2003 to correct PN field.)
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binding; detection; modulation; recombinant cell;
                                                                                                                                                                                             ( I chimeric heavy chain homo-dimer and its expression for preventing and treating HIV infection useful as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.7%; Score 1773; DB 13;
100.0%; Pred. No. 2.4e-125;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WOOGNVFSCSVMHEALHNHYTOKSLSLSPGK 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zcytor 10:: IgG gamma fusion peptide.
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                                                        (PROG-) PROGENICS PHARM INC.
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                                                                                              Beaudry GA, Maddon PJ
                                                                                                                                  WPI; 1992-299758/36.
N-PSDB; AAQ27831.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 534 AA;
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diagnostic agent
                     08-FEB-1991;
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                                                                                                                                                                                               CD4-gamma 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and truncated zeytorig proteins. (I) has immunosuppressive, cytostatic, antirheumatic, artiarthritic, neuroprotective, antinflammatory, antirheumatic, approteins, (I) has immunosuppressive, cytostatic, antirheumatic, neptrotropic, dermatological, anti-HIV and hasmostatic activities, and can be used in vaccines. (I) or an antibody binding (I) can be used for suppressing the immune system for reducing rejection of leukaemias or lymphonas and grafts and for treating recil specific leukaemias or lymphonas and autoimmune diseases including rheumatorid arthritis, multiple sclerosis, diabetes mellitus, inflammatory bowel disease and sisease. The antibodies can also be used for treating immunologic renal diseases. Glomerulonephritis, mesangioproliferative disease, chronic lymphocytic leukaemia, secondary glomerulonephritis or vascuiltis associated with lupus, polyarteritis, scleroderma, HIV-related antibodies can also be used for treall or urological neoplasms and multiple myelomas, asthma, bronchitis, emphysema and other chronic
                                                                                                                                                                                                                                                                                                                                                                                 Human; zcytor19; cytokine receptor; immunosuppressive; cytostatic; antirinematic; antirinematic; antirinematic; antirinematic; antirinematic; antirinematic; antidabetic; nephrotropic; dermatological; anti-HV; haemostatic; vaccine; immune system; T-cell specific leukaemia; lymphoma; lupus; autoimmune disease; rheumatoid arthritis; multiple sclerosis; HIV; diabetes mellitus; inflammatory bowel disease; crohn's disease; asthma; immunologic renal disease; glomerulomephritis; vasculitis; polyarteritis; mesangioproliferative disease; chronic lymphocytic leukaemia; bronchitis; haemolytic uraemic syndrome; renal neoplasm; urological neoplasm; emphysema; chronic airway disease.
181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRBPQVYTLPPSRDE 240
                                      LIKNOVSLICLVKGFYPSDIAVEWESNGOPENNYKTIPPVLDSDGSFFLYSKLIVDKSRW 302
                                                                         241 LIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel Zcytor19 polypeptides and polynucleotides useful for stimulating immune responses in animals for producing antibodies, and for treating autoimmune diseases, leukemia and asthma -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention describes an isolated human zcytor19 protein (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grant FJ;
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                                                                                                                                   QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
                                                                                                            303 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
                                                                                                                                                                                                                                                                                                                                                Human IgG gamma 1 heavy chain SEQ ID NO:15.
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                                                                                                                                                                                                                                        ABB81641 standard; Protein; 330 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-NOV-2000; 2000US-253561P.
07-FEB-2001; 2001US-267211P.
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                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-527700/56.
N-PSDB; ABQ73076.
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and truncate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIKNQVSLICLVKGFYPSDIAVBWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; therapy; death domain containing receptor; DR6; receptor; anaemia; apploalist; rheumatoid arthritis; eczema; asthma; psoriasis; pancreatitis; diabetes; cancer; multiple sclerosis; Graves disease; glomerulonephritis; transplant rejection; systemic lupus erythematosus; hepatitis; cirrhosis; autoimmune; gastritis; dermatosis; cardiopathy; infertility; haemostatic; H. pylori-associated ulceration; antiinflammatory; vasotropic; virucide; acquired immunedeficiency syndrome; HUS; human immunodeficiency virus; HIV; haemolytic uraemic syndrome; HUS; immunodeficiency virus; adult respiratory distress syndrome; ARDS; cytostatic; thyromimetic; dermatological, hepatotropic; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                              GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                  121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                                                                                             3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                  1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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airway diseases. Human zcytor19 is located to chromosome 1, more specifically to chromosome 1p36.11. The present sequence represents a human IgG gamma 1 heavy chain protein, which is used in an example from the present invention
                                                                                                                                                                                          Gaps
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                                                                                                                                                Length 330;
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                                                                                                                                            99.4%; Score 1767; DB 23;
100.0%; Pred. No. 3.7e-125;
ive 0; Mismatches 0;
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                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ELIL ) LILLY & CO ELI.
                                                                                                                                            Query Match
Best Local Similarity
Matches 330; Conserv
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                                                                                                       330 AA;
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ABB05736;

or

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The invention relates to a method for treating or preventing a T cell mediated condition or, a Th2 cell mediated condition in a mammal. The method comprising a death domain containing receptor (DR6) agonist composition comprising a death domain containing receptor (DR6) agonist correction comprising a death domain condition in a mammal. A DR6 agonist is useful in the manufacture of a medicament for treating a T cell mediated condition in a mammal. A DR6 agonist is useful in the manufacture of a medicament for treating or preventing at least one symptom associated with abarrant apoptosis, graft-versus-host disease (GVHD), rheumatoid arthritis, eczemi, asthma, atopy, inflammatory bowel disease, vasculitis, psoriasis, pancretitis, inablandory stylendered mellitus, cancer, multiple selerosis, lashimoto's thyroiditis, Graves disease, transplant rejection, systemic unputs erythematosus, autoimmune daractosis, autoimmune gastritis, fibrosing lung disease, organ rejection after transplantation, thrombotic thrombocytopenic purpura (TYP), choonic alomentation, thrombotic thrombocytopenic purpura (TYP), adult respiratory distress syndrome (HNDS) adult respiratory distress syndrome (ANDS) crace condition or symptom related to the above mentioned diseases in a mammal. An DRS anteagonist is useful in the manufacture of a medicament for treating or preventing at laset one symptom associated with hypiciency syndrome (AIDS), fulminant viral hepatitis (HTV), HIV-induced lymphoma, HIV-induced acquired immunedeficiency associated uncertainned crace resource relating the pastitis of profession, crandoment viral hepatitis (ATV), HIV-induced lymphoma, HV-induced acquired immunedeficiency associated uncertainned repatiting of prience (AIDS), fulminant viral hepatitis (Brindicament relation or proposis, thuman immunodeficiency associated uncertainned according the partitis of prience (AIDS), fulminant viral hepatitis of prience (AIDS). Autoric distress syndrome (AIDS), fulminant viral hepatitis, derenciated ulceration or representation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     associated ulceration, cytoprotection during cancer treatment, recuperation from chemotherapy, recuperation from irradiation therapy, or a condition or symptom related to the above mentioned diseases in a mammal. The present sequence is human DR6 protein-related protein.
Treating or preventing T cell or Th2 cell mediated condition e.g., asthma or multiple sclerosis in mammal, comprises administering composition comprising death domain containing receptor, DR6 agonist
                                                                                                                                                                          Disclosure; Page 132-133; 133pp; English.
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330 AA; Sequence

ô 122 182 120 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEGYN 180 242 240 300 LIKNQVSLITCLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSDGSFFLYSKLIVDKSRW 302 62 9 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPBFVTVSWNSGALTSGVHTFPAVLQSS LTXNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE Gaps .; 0 Length 330; Indels 99.4%; Score 1767; DB 23; 100.0%; Pred. No. 3.7e-125; ive 0; Mismatches 0; 332 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK fatches 330; Conservative Local Similarity 121 63 61 123 183 181 243 241 Query Match 303 301 g à gg à a δ g $\stackrel{>}{\circ}$ 셤 g ò à

ABB05736 standard; Protein; 330

RESULT 5
ABB05736
ID ABB0

122 120

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PSVFLFPPKPEKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ecytor17 has immunomedilatory, antilifiammatory, antiviral, cytostatic, antirhemmatory antiviral, cytostatic, profilemmatic, antiathritic and muscular activities. The zcytor17 proteins are useful for treating and diagnosing lymphoid, immune, inflammatory, spheenic, blood or bone disorders. Agonists or antizorytor17 antibodies are useful in stimulating cell-mediated immunity and for stimulating lymphocyte proliferation, such as in the treatment of infections involving immunosuppression, including certain viral infections. They are also useful for inducting cytotoxicity and for treating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating autoimmune diseases (e.g. crohn's disease), cancer, pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to chromosome 5, specifically to the Sqil chromosomal region. ABA933767 to ABA93343 and ABA93361 to ABA93346 in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
                                                                                                                                antiinflammatory; antiviral; antirheumatic; antiarthritic; cytosfatic; muscular; lymphoid; immune; inflammatory; spleanic; blood; bone; infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease; autoimmune disease; rheumatorid arthritis; multiple sclerosis; cancer; inflammatory disease; pancreatitis; inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a cytokine receptor designated zcytor17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polynucleotide encoding a cytokine receptor zcytor17 which is useful for treating and diagnosing lymphoid, immune, inflammatory, spleenic, blood or bone disorders -
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                                                                                                                receptor; immunomodulatory;
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                                                                          Human immunoglobulin G gamma 1 protein sequence SEQ ID NO:38.
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100.0%; Pred. No. 3.7e-125;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 17; Page 187-188; 235pp; English.
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                                                                                                              Zcytor17; chromosome 5; 5q11; cytokine
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                                                                                                                                                                                                                                                                                                                                                                                                    26-JUN-2000; 2000US-214282P.
29-JUN-2000; 2000US-214955P.
08-FEB-2001; 2001US-267963P.
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Matches 330; Conservative
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N-PSDB; ABA93797.
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                                                                                                                                                                                                                                                     Homo sapiens.
                                     01-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for
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Wu H, Fung MSC;
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              330 AA;
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            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an immunoadhesin comprising:

(a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising a rhinovirus receptor protein linked to at least a portion of an immunoglobulin heavy chain, and

(b) optionally a J chain and secretory component associated with the chimeric ICAM-1 molecule. The immunoadhesin ls useful for chimeric ICAM-1 molecule. The immunoadhesin is useful for glycosylation and virucide activity. The immunoadhesin is useful for reducing infection by human rhinovirus (HRV) and hence the initiation or spread of the common cold by HRV. The immunoadhesin binds to HRV and compared to compare to the initiation or reduces its infectivity, competing with cell surface ICAM-1 for binding creduces its infectivity, competing with cell surface ICAM-1 for binding sites, interfering with virus entry or uncoating and directing premature release of viral RNA and formation of empty appsids. Expression of the immunoadhesin having multiple binding sites have a higher effective caffinity for the virus, thereby increasing the effectiveness of the immunoadhesin. Association of secretory component and immunoglobulin J chain coll culture and production in plants is safer for human use, constince plants are not known to harbor any animal viruses. The present the immunoglobulin protein sequence, useful to
           242
                   LIKNOVSLICLVKGFYPSDIAVEWESNGQPENNYKITPPVLDSDGSFLYSKLIVDKSRW 302
                                                                           241 LTKNQVSLTCLVKGFYPSDLAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300
                                                                                                                                                                                                                                                                                                         Human, immunoadhesin, intercellular adhesion molecule, ICAM-1,
human rhinovirus, immunoglobulin heavy chain, J chain, HRV; common cold,
    STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoadhesin for treating human rhinovirus infection comprises chimeric intercellular adhesion molecule-1, and optionally a J chain and secretory component in association
                                                                                                                                                                                                                                                                             Human Ig-gammal heavy chain constant region amino acid sequence
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                                                            Gaps
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Ouery Match 99.4%; Score 1767; DB 23; Best Local Similarity 100.0%; Pred. No. 3.7e-125; Matches 330; Conservative 0; Mismatches 0;
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/label= Hinge_region
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/label= CH2_region
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/label= CH3_region
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The invention relates to a novel fusion protein comprising an IgB Feepsilon fragment and an IgG Fegamma fragment, which binds to an FeepsilonRI and/Or FeepsilonRI receptor and an FegammaRIB receptor. The fusion protein of the invention may have a see in protein therapy. The fusion protein is useful in tracting or preventing IgB-mediated allergies and asthma, such as allergic asthma, allergic rhinitis, hay fever, food allergy, atopic dermatitis and drug allergy. The allergic response is particularly caused by peanut allergen. The present sequence represents the human IgG1 Fegamma fragment.
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                 FcgammakliB receptor, useful for treating or preventing allergies and asthma, comprises an IgE Fcepsilon fragment and an IgG Fcgamma fragment
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fusion protein which binds to PcepsilonRI or RII receptor and
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Pred. No. 3.7e-125;
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100.0%; Pre
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                                                                            Disclosure, Fig 5, 32pp; English.
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Matches 330; Conservative
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The present invention relates to a method of reducing the immunogenicity of a fusion protein. The method involves identifying a candidate T-cell epitope within a junction region spanning a fusion junction of a fusion protein and changing an amino acid within the junction region to reduce the ability of the candidate T-cell epitope to interact with a T-cell receptor. The method is useful for reducing the immunogenicity of fusion proteins for use in therapy. The present sequence is human immunoglobulin G1 (1gG1) heavy chain For region. This sequence is used to illustrate the method of the invention.
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                                            Reducing the immunogenicity of a fusion protein by changing an an acid within the junction region spanning a fusion junction of a forcein to reduce the ability of the candidate T-cell epitope to interact with a T-cell receptor
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             2003-111794/10
                                                                                                                                                                                                                                                                                                                     330 AA;
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The invention relates to a method for reducing the immunogenicity of a fusion protein which involves identifying a candidate T-cell epitope within a junction spanning a fusion junction of a fusion protein, and changing an amino acid within the junction region to reduce the ability of the candidate T-cell epitope to interact with a T-cell receptor. The method is useful for reducing the immunogenicity of a fusion protein. It is useful for analysing, changing or modifying one or more amino acids in the junction region of a fusion protein to identify a T-cell epitope and reduce its ability to interact with a T-cell receptor. The less immunogenic fusion proteins are useful in providing therapeutic treatment. The present sequence is human immunoglobuling therapeutic chain per cell need to illustrate the method of the invention.
                                                                                                        Reducing the immunogenicity of a fusion protein comprises changing a maino acid within the junction region to reduce the ability of the candidate T-cell epitope identified within the junction spanning to interact with T-cell receptor.
                                                                                                                                                                                                    Disclosure; Page 49-50; 68pp; English.
(LEXI-) LEXIGEN PHARM CORP
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ö 122 120 182 180 242 243 LIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 302 62 9 Human; immunoglobulin; constant; region; humanised; P-selectin; light; blocking; antibody; heavy; chain; variable; murine; thrombotic disease; monoclonal; PBL 3; CDR; comlementarity determining region; leukcoyte; expression vector; coexpression; pHCMV-1748RHA-gammalCi-dhfr; epitope; pHCMV-1748RLA-RR-neo; PBL;3/Humanised version A; vascular endothelium; 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREBOYN 3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG Gaps . 0 Length 330; 0; Indels Human kappa immunoglobulin light chain constant domain. 'Match 99.4%; Score 1767; DB 24; Local Similarity 100.0%; Pred. No. 3.7e-125; les 330; Conservative 0; Mismatches 0; 303 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332 301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330 ARR43685

ID AAR43685

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AC AR43685,

DT 25-MAR-2003 (updated)

DT 25-MAY-1994 (first entry)

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Human kappa immunoglobulin light chai:

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Human; immunoglobulin; constant; regit

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Human; immunoglobulin; regit

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Human; regit

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Human; regit

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Human; regit

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Human; regit

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123 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182

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142 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEGYN

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The sequences given in AAR43685-86 represent human immunoglobulin constant regions which were used in the production of the humanised resions which were used in the production of the humanised variable region coding sequences of the murine monoclonal antibody of pal.3, given in AAR43687-88. The CDRs from PBL.3 heavy and light chains were substituted for the CDRs of human heavy and light chains. CC The humanised variable regions were inserted into expression vectors. By coexpression of appropriate combinations of heavy and light chains, several humanised antibodies can be expressed. Coexpression of pHCWV-1748RHA-gammalCi-dhfr and pHCWV-1748RHA-RK-neo gives rise to the PBL.3/Humanised version A. Coexpression of pHCWV-1747CH-Gammacd-neo and pHCWV-1747-CL-KR-neo gives rise to the PBL.3/Humanised antibodies selectively bind epitopes on P-selectin and block adhesion of leukcyces to the vascular endothelium. They may be used to treat inflammatory and thrombotic diseases and other pathological coditions involving P-selectin and antibodies to it, esp. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 GLYSLSSWTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-P-Belectin antibody for ischaemia acute lung injury treatment useful to treat inflammation and pathological conditions of intercellular adhesion by competitive inhibition assays
 pHCMV-1747CH-gammaCi-neo; pHCMV-1747-CL-KR-neo; PB1.3 chimera;
acute lung injury; ischaemia reperfusion injury; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.4%; Score 1767; DB 14; Length 351; 100.0%; Pred. No. 3.9e-125; tive 0; Mismatches 0; Indels 0.
                                                                                                                                       120..134
/note= "Hinge region"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Polley MJ,
                                                                                        Location/Qualifiers
                                                                                                                        "CH1 domain"
                                                                                                                                                                                           /note= "CH2 domain"
                                                                                                                                                                                                                               /note= "CH3 domain"
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                                                                                                                                                                                                                                                                                                                                      93WO-US04274
pHCMV-1747CH-gammaCi-neo;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Chestnut RW, Paulson JC,
                                                                                                                                                                              135..244
                                                                                                                                                                                                              245..352
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Best Local Similarity 100.
Matches 330; Conservative
                                                                                                          22..119
/note= "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ51547.
                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                      04-MAY-1993;
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                                                                                                                                                                                                                                                                                                  11-NOV-1993
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WO2003015617-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
                                                                                                                                                                                                                                                                                                             13-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                        Home sapiens
                                                                                                                                                                                                                                                                                                                                  Heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-FEB-2003.
              42
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                                                                                                                                                                                                                                                                                          ABB80109;
                                63
                                                    102
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                                                                                                                                                                                                                                                  RESULT 12
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                     261
                                          302
                                                    LIKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 321
STYRVUSVLTVIHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
              STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               It may be fused to the first 180 N-terminal residues of CD4 at the C-terminus. The fusion protein may be used for antiviral of immunomodulatory therapy particularly in treatment of HIV
                                       LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
                                                                                                                                                                                                                                  Sequence of the linkered immunoglobulin gamma chain fragment.
                                                                                                                                                                                                                                                        Immunoglobulin gamma chain; IgG1 heavy chain constant region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Compsns. contg. ahdesion variants
- useful in therapy and diagnostics, eg CD4 variants
which are therapeutically useful for treating human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to add missing OS field.)
to correct PR field.)
to correct PI field.)
                                                                              QOGNVFSCSVMHEALHNHYTOKSLSLSPGK 332
                                                                                             QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 4a-4b; 36pp; English.
                                                                                                                                                                                                                                                                                                            42..43
/note= "Insert site"
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/note= "Insert site"
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                                                                                                                                                   AAP91918 standard; protein; 371 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                       87US-0104329
88US-0250785
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(updated)
(first entry)
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(Updated on 25-MAR-2003
(Updated on 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              which are therapeutical.
immuno-deficiency virus
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N-PSDB; AAN90779.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 AA;
                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                    03-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                        02-OCT-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                 28-SEP-1988;
                                                                                                                                                                                                      31-OCT-2002
14-MAY-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection.
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                                                                                                                                                                       AAP91918;
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242
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                                                                                                                                 123 PSYFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPBVKFNWYVDGVEVHNAKTKPREEQYN 182
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                                                                                                                                                                                                                                                                                                               LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 341
                                                                                  GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                162 PSVFLFPPKPKDTLMISKTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKFREEGYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequences given in AAG80104-09 represent preferred antibodies of the invention. This sequence represents the preferred heavy chain. The humanised antibody of the invention may be used for diagnosing preclinical or clinical Alzheimer's disease. The antibody specifically binds an epitope, preferably the amyloid beta peptide (Abeta). The antibodies sequester Abeta from its bound, circulating form in blood and alter clearance of soluble and bound forms of Abeta in central nervous system and plasma. The antibodies specifically bind an epitope representing amino acids 13-28 of the Abeta molecule.
                                                                                                                                                                                                                                                222 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagnosing preclinical or clinical Alzheimer's disease in a subject by administering an antibody which specifically binds an epitope
                                                       GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                           STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                      LIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complementarity determining region; CDR; humanised; mouse; 266; light; heavy; variable; domain; antibody; preclinical; clinical; Alzheimer's disease; epitope; amyloid beta peptide; Abeta; central nervous system; plassma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paul SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cummins DJ,
                                                                                                                                                                                                                                                                                                                                                                  QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
                                                                                                                                                                                                                                                                                                                                                                                                   OOGNVFSCSVMHEALHNHYTOKSLSLSPGK 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 15-16; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bales KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ŕ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-AUG-2001; 2001US-313221P.
17-AUG-2001; 2001US-313224P.
23-OCT-2001; 2001US-334987P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-AUG-2002; 2002WO-US26321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNIW ) UNIV WASHINGTON.
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Query Match 99.4%; Score 1767; DB 10; Length 371; Best Local Similarity 100.0%; Pred. No. 4.2e-125; Matches 330; Conservative 0; Mismatches 0; Indels 0;

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                                      Holtzman DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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            (UNIM ) (ELIL ) 1
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                                                                                                                              PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Any amino acid
/note= "Provided that if Xaa56 is Asn and Xaa57 is
neither Asp nor Pro, then Xaa58 is neither Ser nor Thr"
                                                                                                                                           GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVRPKSCDKTHTCPPCPAPELLGG
                                                                                                        GLYSLSSVVIVPSSSLGTQTYICNVNHKPSNTKVDKKVBPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                 LTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
                                                           ASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                          ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                                             293 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                                                                                 Complementarity determining region, CDR; humanised, mouse; 266; light; heavy; variable; domain; antibody; preclinical; clinical; Alzheimer's disease; epitope; amyloid beta peptide; Abeta; central nervous system; plasma.
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Any amino acid
/note= "Provided that if Xaa57 is neither Asp nor
Pro and Xaa58 is Ser or Thr, then Xaa56 is not Asn"
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           red. No. 5.38-125; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Any amino acid
/note= "Provided that if Xaa56 is Asn and
is Ser or Thr, then Xaa57 is Asp or Pro"
                                                                                                                                                                                                                                                 QGGNVFSCSVMHEALHNHYTQKSLSLSPGK 442
                                                                                                                                                                                                                                    303 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
                           Score 1767;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                     Pred
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                         99.4%; Scillarity 100.0%; P. Conservative 0;
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2001US-313224P.
2001US-334987P.
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                                                                                                                                                                                                                                                                                                                                                  Deglycosylated heavy chain,
                                                                                                                                                                                                                                                                                                                                 (first entry)
          AA;
                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
          442
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17-AUG-2001; 2
23-OCT-2001; 2
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Mus musculus
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                                 Best Local Sim
Matches 330;
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         Sequence
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                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                                          This sequence represents the preferred heavy chain from a deglycosylated version of the humanised mouse antibody 266 heavy chain of the invention. The antibody of the invention specifically binds an epitope, preferably the amyloid beta peptide (Abeta). The antibodies sequester Abera from its bound, circulating form in blood and alter clearance of soluble and bound forms of Abeta in central nervous system and plasma. The antibodies specifically bind an epitope representing amino acids 13-28 of the Abeta molecule. Deglycosylation of the heavy chain CDR2, as in this sequence, causes higher affinity for Abeta. The antibody of the invention may be used for diagnosing preclinical or clinical Alzheimer'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                    Diagnosing preclinical or clinical Alzheimer's disease in a su
administering an antibody which specifically binds an epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 442;
                                                                SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                Cummins DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.4%; Score 1767; DB 24;
100.0%; Pred. No. 5.3e-125;
ive 0; Mismatches 0;
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                                                                Bales KR,
                                                                                                                                                                                                                                                                                Claim 8; Page 20-22; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ź
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Best Local Similarity 100.
Matches 330; Conservative
                                                             Demattos
CO ELI
                                                                                                                       WPI; 2003-278505/27
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14-AUG-2002; 2002WO-US21324

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The invention relates to treating cognitive symptoms or reducing disease progression in a subject having a condition or disease associated with anyloid-beta peptide (Abeta). The method involves administering an amount of an anti-Abeta antichody that has greater affinity for soluble Abeta than 10^-.9 M, that has affinity (KD) for soluble Abeta 10 thigher than 10^-.9 M, or that has greater affinity for soluble Abeta than antichody 266 has. The method or the anti-Abeta antichody is useful in preparing a medicament for treating cognitive symptoms or reducing preparing a medicament for treating cognitive symptoms or disease associated with Abeta. The condition or disease is Alzheiner's diseases. Down's syndrome, cerebral amyloid angiopathy, vascular dementia, or mild cognitive impairment. The present sequence represents a humanised anti-Abeta antibody 266 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLYSLSSUVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 412
                                                                                                                                                                                                                                  Treating or reducing the progression of diseases associated with amyloid-beta peptide, e.g. Alzheimer's disease, vascular dementia or mild cognitive impairment, comprises administering an anti-amyloid-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 GLYSLSSVVTVPSSSLGTQTVICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 442;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.4%; Score 1767; DB 24;
100.0%; Pred. No. 5.3e-125;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                        Disclosure; Page 20-22; 84pp; English.
                                                                                                   2002US-383851P.
                                                                              17-AUG-2001; 2001US-313576P
28-MAY-2002; 2002US-383851P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 330; Conservative
                                                                                                                                  (ELIL ) LILLY & CO ELI
                                                                                                                                                                     Paul SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  442 AA;
                                                                                                                                                                                                                                                                                         peptide antibody
                                                                                                                                                                   Bales KR,
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The invention relates to treating cognitive symptoms or reducing disease any locabeta peptide (Abeta). The method involves administering an amount of an anti-Abeta peride (Abeta). The method involves administering an amount than 10^-9 M, that has affinity (KD) for soluble Abeta-40 or Abetal-42 higher than 10^-9 M, or that has greater affinity for soluble Abeta than antibody 266 has The method or the anti-Abeta antibody is useful in preparing a medicament for treating cognitive symptoms or reducing preparing a medicament for treating cognitive symptoms or reducing with Abeta. The condition or disease is Alzhaimer's disease, bown's syndrome, cerebral amyloid angiopathy, vascular dementia, or mild cognitive impairment. The present sequence represents a preferred heavy chain or a humanised anti-Abeta antibody 266 analogue that has a high
                                                                                                                                                                                                                                                                                                             /note= "Xaa is any amino acid, provided that if Xaa at position 57 is neither Asp nor Pro, then Xaa at position 58 is neither Asp nor Pro, then Xaa at position 58 is neither Ser nor Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 122
                                                                                                                                                                        /note= "Xaa is any amino acid, provided that if Xaa at position 57 is neither Asp nor Pro and Xaa at position 59 is Ser or Thr, then Xaa at position 56 is not Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating or reducing the progression of diseases associated with amyloid-beta peptide, e.g. Alzheimer's disease, vascular dementia or mild cognitive impairment, comprises administering an anti-amyloid-beta
                                                                                                                                                                                                                                           /note= "Xaa is any amino acid, provided that if Xaa a position 56 is Asn and Xaa at position 58 is Ser or then Xaa at position 57 is Asp or Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 GLYSLSSVVTVPSSSLGTQTYICHVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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                                                  Amyloid-beta, Abeta; antibody 266; nootropic; neuroprotective; CDR; immunostimulant.
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                Humanised anti-Abeta antibody 266 analogue heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.4%; Score 1767; DB 24;
100.0%; Pred. No. 5.3e-125;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 29-31; 84pp; English.
                                                                                                                           Location/Qualifiers
56
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100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-AUG-2002; 2002WO-US21324.
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28-MAY-2002; 2002US-383851P.
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affinity for Abeta.
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                                                                                                                                      Key
Misc-difference
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                                                                                                      Synthetic
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172

232

352

ABR39474 standard; protein; 442

(first entry)

12-JUN-2003

ABR39474;

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        QY
        123 PSVFLPPPREZDTLMISRTPEVTCVVDVSHEDPEVKFNMYUDGVEVHNAKTKPREEQYN 182

        Db
        233 PSVFLPPPREZDTLMISRTPEVTCVVUDVSHEDPEVKFNMYUDGVEVHNAKTKPREEQYN 292

        QY
        183 STYRVYSLTVLHQDMINGKEYKCKVSNKALPAPIEKTISKAKGQPREPQYYTLPPSRDE 242

        Db
        293 STYRVYSUTVLHQDMINGKEYKCKVSNKALPAPIEKTISKAKGQPREPQYYTLPPSRDE 352

        QY
        243 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENYKTTPPVLDSDGSFFLYSKLTVDKSRW 302

        Db
        353 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLXSKLTVDKSRW 412

        Db
        363 QGNVFSCSVHAFALHNHYTQKSLSSPG 332

        Db
        413 QQGNVFSCSVHAFALHNHYTQKSLSLSPGK 442
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Search completed: January 13, 2004, 12:38:27 Job time : 79.4183 secs

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1 EFASTKGPSVFPLAPSSKST......MHEALHNHYTQKSLSLSPGK 332
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| Cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06 PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06 PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06 PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06 PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08 NEW PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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| Cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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US-10	0 US-09-747-669-3	2 US-10-409-938-15	5 US-10-290-703-3	US-09-746-359A-54 Semience 5	0 US-09-825-561A-16 Sequence	US-09-746-359A-53	US-09-825-012-46 Sequence	0 US-09-825-012-55 Sequence	0 US-09-935-868-9 Sequence	2 US-10-282-162-9 Sequence	5 US-10-287-035-9 Sequence	US-09-740-002-27	0 US-09-948-429B-4 Sequence	0 US-09-948-429B-12	US-10-124-807-4	US-10-124-807-12	US-10-291-532-4	US-10-291-532-12	US-10-124-905-4	0-124-905-12 S	US-09-948-429B-8 Sequence	US-10-124-807-8 Sequence	2 US-10-291-532-8	US-10-124-905-8 Sequence	0 US-09-825-012-52	0 US-09-825-012-61 Sequence	2 US-10-159-006-22 Seguence	5 US-10-121-464-20 S	US-09-920-171-14 Sequence 1
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16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	32	36	37	38	. 39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 98, Application US/09990586;
Publication No. US20030109680A1
GENERAL INFORMATION:
APPLICANT: JIAO, JIN-AN
APPLICANT: WONG, HING
ITLE OF INVENTION: ANTHODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
ITLE DEPERENCE: 71758446943-CIP2
ITLE OF INVENTION: ANTHODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
ITLE REPRESENCE: 71758446943-CIP2
CURRENT APPLICATION NUMBER: 001-11-21
PRIOR APPLICATION NUMBER: 09/293,854
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 102
SOFTWARE PATENTIN Ver. 2.1
SEQ ID NO 98
LENGTH: 332
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 332; Conserv
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Query Match
Best Local a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 167, Application US/10310113
Publication No. US20030176664A1
GENERAL INFORMATION:
APPLICANT: JAGO, JUN-AN
APPLICANT: NGOG, HING C.
INTITE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
TITLE OF INVENTION UNMBER: US/10/310,113
CURRENT APPLICATION NUMBER: 09/990,586
PRIOR FILING DATE: 2001-11-21
PRIOR PLING DATE: 1999-0416
PRIOR APPLICATION NUMBER: 09/293,854
PRIOR FILING DATE: 1999-0416
PRIOR APPLICATION NUMBER: 09/293,864
PRIOR FILING DATE: 1999-0416
PRIOR APPLICATION NUMBER: 09/293,864
PRIOR FILING DATE: 1999-0416
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                                                     1 BFASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
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                                                                                                                                                                                                                                                                                    301 RWQQGNVPSCSVMHEALHNHYTQKSLSLSPGK 332
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                                                                                                    APPLICANT: WONG, HING C.
APPLICANT: WONG, HING C.
APPLICANT: STINSON, JEFFREY L.
APPLICANT: STINSON, JEFFREY L.
APPLICANT: STINSON, JEFFREY L.
TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
FILE REFERENCE: 71758/58066
CURRENT APPLICATION NUMBER: US/10/230,880
CURRENT APPLICATION NUMBER: 09/990,586
PRIOR PILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/343,306
PRIOR PILING DATE: 2001-10-29
PRIOR PILING DATE: 1099-04-16
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PALENTING DAYE: 1999-04-16
NUMBER OF SEQ ID NOS: 174
SEQ ID NO 98
LENGTH: 332
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100.0%; Pred. No. 6.6e-138;
tive 0; Mismatches 0;
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Publication No. US20030027253A1
GENERAL INFORMATION
APPLICANT: Presnell, Scott R.
APPLICANT: Two Wenfeng
APPLICANT: No. US20030027253A1ak, Julia E.
APPLICANT: No. US2001-11-28
PRIOR APPLICATION NUMBER: US 60/253,561
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 50
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Sequence 98, Application US/10230880
Publication No. US20030190705A1
GENERAL INFORMATION:
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Matches 332; Conservative
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US-10-230-880-98
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                         63 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
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78-20-112-582-1
Publication No. US20030166877A1
Publication No. US20030166877A1
GENERAL INFORMATION:
APPLICANTY Gillies, Stephen
TILLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
TILLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
CURRENT APPLICATION NUMBER: US/10/112,582
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: US 6/280,625
PRIOR APPLICATION DATE: 2001-03-30
PRIOR PLING DATE: 2001-03-30
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99.4%; Score 1767; DB 12;
Best Local Similarity 100.0%; Pred. No. 5.3e-137;
Matches 330; Conservative 0; Mismatches 0;
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SOFTWARE: Patentin version 3.0
SEQ ID NO 1
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                            Query Match 99.4%; Score 1767; DB 11; Length 330; Best Local Similarity 100.0%; Pred. No. 5.3e-137; Matches 330; Conservative 0; Mismatches 0; Indels 0
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Publication No. US20030096339A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Gao, Zeren
APPLICANT: Wilper, Jeen
APPLICANT: Wuiper, Joseph L.
APPLICANT: Waiper, Josep
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 15 LENGTH: 330 TYPE: PRT ORGANISM: Homo sapiens US-09-995-898A-15
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US-09-892-949-38
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Best Local Similarity
Matches 330; Conserv
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Query Match
Best Local Similarity 100
Matches 330; Conservative
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-320-231A-81
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// ORGANISM: Homo sapiens
US-10-047-542-20
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Publication No. US20030194405A1

GENERAL INFORMATION: Steven

APPLICANT: Neben, Steven

APPLICANT: Takeuchi, Toshihiko

TITLE OF INVENTION: Adrian

TITLE OF INVENTION: Treatment Of Agthma

TITLE OF INVENTION: Treatment Of Agthma

CURRENT PILING DATE: 2002-12-19

PRIOR FILING DATE: 2001-12-17

NUMBER OF SEQ ID NOS: 85

SOFTWARE: Patentin version 3.2
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                       Sequence 8, Application US/10110719
| Publication No. US20030166163A1
| Publication No. US20030166163A1
| GENERAL INFORMATION:
| APPLICANT: Gillies, Stephen
| TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
| FILE REFERENCE: LEX 020
| CURRENT APPLICATION NUMBER: US/10/310,719
| CURRENT APPLICATION NUMBER: 60/337,113
| PRIOR FILING DATE: 2002-12-04
| PRIOR FILING DATE: 2002-12-04
| PRIOR FILING DATE: 2002-04-12
| NUMBER OF SEQ ID NOS: 37
| SOFTWARE: Patentin version 3.1
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99.4%; Score 1767, DB 12; Length
Best Local Similarity 100.0%; Pred. No. 5.3e-137;
Matches 330; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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US-10-320-231A-81
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US-10-047-542-20

| Sequence 20, Application US/10047542 |
| Sequence 20, Application No. US20020168367A1 |
| Sequence 20, Application No. US20020168367A1 |
| SENDIAL INPORMATION: |
| APPLICANT: LARRICK, JAMES W. |
| APPLICANT: WYCOFF, KEITH L. |
| TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL |
| TITLE OF INVENTION: NATURE NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTION: APPLICATION NUMBER: US/10/047,542 |
| FILE REPERENCE: 030905,0004.CIPi |
| CURRENT APPLICATION NUMBER: US/10/047,542 |
| FRIOR PILING DATE: 2001-04-28 |
| PRIOR FILING DATE: 2000-04-28 |
| NUMBER OF SEQ ID NOS: 101 |
| SEQ ID NO 20 |
| LENGTH: 330 |
| LENGTH: SEQ ID NOS: 101 |
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| LENGTH: 340 |
| LENGT
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99.4%; Score 1767; DB 12; Length 330; 100.0%; Pred. No. 5.3e-137; ive 0; Mismatches 0; Indels 0
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63 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
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                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM FC computable
COMPUTER: IBM FC computable
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 28-May-2002
CLASSIFICATION: cUnknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
99.4%; Score 1767; DB 12;
Best Local Similarity 100.0%; Pred. No. 6.2e-137;
Matches 330; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: U5/08/457,918
FILING DATE: 1-UNN-1995
APPLICATION NUMBER: U5/08/236311
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: 07/84277
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: 07/250785
FILING DATE: 18-EB-1988
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEB-1988
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEB-1988
APPLICATION NUMBER: 07/250785
FILING DATE: 02-CCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0444P1C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 OQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
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TYPE: amino acid
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STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
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                                                                                                                                                                                                                                                                                                                                                                            Sequence 68, Application US/10269805
; Publication No. US2003012412941
; GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REPRENCES A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR PELING DATE: 2001-10-11
; NUMBER OF SEQ ID NGS: 76
; SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                    303 OOGNVESCSVMHEALHNHYTOKSLSLSPGK 332
                                                                                                                                                                                                                                                        301 ÓGGNVFSCSVMHEALHNHYTÓKSLSLSPGK 330
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Publication No. US20030143220A1
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-68
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US-10-097-044A-7
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LENGTH:

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APPLICANT: GILLIES, Stephen D
APPLICANT: IO, Kin-Ming
APPLICANT: LO, Kin-Ming
TITLE OF INVENTION: Enhancing the Circulating Half-life of Antibody-based
TITLE OF INVENTION: Pusion Proteins
TITLE OF INVENTION: Pusion Proteins
TITLE OF INVENTION: Pusion Proteins
TITLE APPLICATION WINBER: US/09/256,156A
CURRENT APPLICATION NUMBER: US 60/075,887
EARLIER APPLICATION NUMBER: US 60/075,887
EARLIER FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 447
                                                                                                                                                                                                                                                                                                                                                                                                                123 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
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NAME/KEY: VARIANT

LOCATION: (1). (117)

OTHER INFORMATION: The Xaa at positions 1 to 117 are non-conserved

OTHER INFORMATION: amino acids
US-09-256-156-1
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99.4%; Score 1767; DB 12;
Best Local Similarity 100.0%; Pred. No. 7.9e-137;
Matches 330; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
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                        ; OTHER INFORMATION: synthetic sequence US-10-320-231A-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09256156A Publication No. US20030105294A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Simil
Matches 330; C
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FEATURE:
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US-10-320-331A-79
US-10-320-331A-79
US-10-320-331A-79
Sequence 79, Application US/10320231A
Sequence 79, Application No. US2003019440EA1
GENERAL INFORMATION:
APPLICANT: Neben, Steven
APPLICANT: Takeuchi, Toshihiko
APPLICANT: Takeuchi, Toshihiko
APPLICANT: Takeuchi, Toshihiko
TITLE OF INVENTION: Artibody Inhibiting Stem Cell Factor Activity And Use For
TITLE OF INVENTION: Treatment of Asthma
FILLS REFERENCE: A430*163
CURRENT APPLICATION NUMBER: US/10/320,231A
CURRENT FILING DATE: 2002-12-19
FRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIKNQVSLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRM 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Humanised OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
        US-10-150-475A-6;

Sequence 6, Application US/10150475A;
Publication No. US20030103985A1;
GENERAL INPORMATION:
SAPPLICANT: Adolf, G. et al.
TITLE OF INVENTION: CYtotoxic CD44 Antibody Immunoconjugates;
FILE REFERENCE: 1/211
CURRENT APPLICATION NUMBER: US/10/150,475A;
PRIOR TILING DATE: 2002-05-17;
PRIOR FILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 99.4%; Score 1767; DB 15; Length 444; Best Local Similarity 100.0%; Pred. No. 7.8e-137; Matches 330; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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SEQ ID NO 79
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ORGANISM: Artificial
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Job time : 54.062 secs
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Patent No. US20020146750A1

Patent No. US20020146750A1

APPLICANT: Hoogenboom, Hendricus R.J.M.

APPLICANT: Henderikx, Maria P.G.

TILLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
FILE REFERENCE: DYX-015.1 WO/09/822,698A

CURRENT APPLICATION NUMBER: US/09/822,698A

CURRENT FILING DATE: 2000-03-30

PRIOR APPLICATION NUMBER: US 09/538,913

PRIOR APPLICATION NUMBER: US 09/538,913

PRIOR APPLICATION NUMBER: US 09/538,913

PRIOR APPLICATION OF SEQ ID NOS: 112

SOFTWARE: Microsoft Word

SEQ ID NO 26

LENGTH: 451
182
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                                                             PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKPNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
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ORGANISM: artificial sequence
FEATURE:
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US-09-822-698A-26
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Search completed: January 13, 2004, 13:13:45

Sequence Sequence Sequence

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Sequence Sequence

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Sequence Sequence Sequence

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COUNTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: 1BM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,311
FILING DATE: 02-MAY-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/84277
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/126785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION NUMBER: 07/126785
FILING DATE: 02-OCT-1987
ATTORNEY AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REGISTRATION NUMBER: 444PIC2
TELEPHONE: 415/225-1896
          US-09-282-846-2
US-09-680-145-2
US-09-026-985-71
US-09-021-9528-71
US-09-301-593-18
US-09-301-593-18
US-08-37-6222
US-08-146-2066-22
US-08-146-2066-22
US-09-98-6728-8
US-09-07-63-8
US-09-07-63-8
US-09-91-593-43
US-09-91-593-43
US-09-91-593-43
                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08236311
Patent No. 5565335
GENERAL INFORMATION:
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION:
AMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415/952-981
TELEX: 910/311-7168
INFORMATION FOR SEQ ID NO. 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acids
TOPOLOGY: linear
 RESULT 1
US-08-236-311-7
1761
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Sequence 7, Appli
Sequence 7, Appli
Sequence 13, Appli
Sequence 13, Appl
Sequence 10, Appli
Sequence 9, Appli
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                                                                                  January 13, 2004, 12:33:50; Search time 28.7057 Seconds (without alignments) 489.353 Million cell updates/sec
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                                                                                                                                                                 1 EFASTKGPSVFPLAPSSKST.......MHEALHNHYTQKSLSLSPGK 332
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6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-487-550-8
US-08-155-098-8
US-08-157-1011A-7
US-08-157-1011A-7
US-08-157-1011A-7
US-08-887-352B-16
US-08-887-352B-16
US-08-887-352B-16
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US-09-109-207C-14
US-09-109-207C-16
US-09-109-207C-18
                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-458-516-13
US-08-378-939-10
US-09-313-942A-7
US-09-740-002-27
US-09-740-002-27
US-08-487-550-4
US-08-487-550-12
US-09-526-098-4
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US-09-296-005-14
US-09-296-005-16
                                                                                                                                                                                                                                     328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                         protein - protein search, using sw model
                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                                                       US-09-990-586-98
1778
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Match Length DB
                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
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                                                                                  Run on:
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42 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 101
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; Sequence 7, Application US/08397411
; Patent No. 6129914
; Patent Neiner, George
APPLICANT: Gingrich, Reger
APPLICANT: Link, Brian
APPLICANT: Secondaria
; CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew
; STATE: California
; COMPUTRY: USA
; ZIP: 94105
; COMPUTRY: USA
; SOFTWARE: Patentin Release #1.0, Version #1.25
; COMPUTRY: APALICATION NUMBER: US/08/397,411
; PILICATION NUMBER: US/08/397,411
; PILICATION NUMBER: US/08/397,411
                                                                                                                                                                                                                                                                                                                                               Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                         Query Match
99.4%; Score 1767; DB 3;
Best Local Similarity 100.0%; Pred. No. 2e-160;
Matches 330; Conservative 0; Mismatches 0;
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APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
  REGISTRATION NUMBER: 36,575
REPERRICE/DOCKET NUMBER: P044;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
FELERAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acids
US-08-457-918-7
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                                                                                                                                                                                                                                                       63 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVBPKSCDKTHTCPPCPAPELLGG 122
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                                                                                                                                                     3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                   99.4%; Score 1767; DB 1; Length 371;
100.0%; Pred. No. 2e-160;
iive 0; Mismatches 0; Indels
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ZIP. 94080
ZIP. 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.5 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-JUN-1995
CLASSIFICATION NUMBER: 08/236311
FILING DATE: 08/236311
FILING DATE: 02-MAY-1994
PRICATION NUMBER: 07/336190
FILING DATE: 26-AUG-1992
PRICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
PRICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRICATION NUMBER: 07/250785
FILING DATE: 02-OCT-1987
APPLICATION NUMBER: 02-OCT-1987
ATTORNEY/AGRAT INFORMATION:
NAME: KUDINGC, JEFFERY S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OCGNVFSCSVMHEALHNHYTOKSLSLSPGK 332
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Patent No. 6117655
GENERAL INFORMATION:
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: California
CONTRY: USA
                                                 Query Match
Best Local Similarity 100.
Matches 330; Conservative
US-08-236-311-7
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 QOGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
            FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1182
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                             TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                               LENGTH: 449 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                            US-08-458-516-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-378-939-10
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APPLICANT: Co, Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIB/IIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                         99.4%; Score 1767; DB 3; L
100.0%; Pred. No. 2.6e-160;
live 0; Mismatches 0;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
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                                                                   011823-004901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 424
PRICR APPLICATION DATA:
APPLICATION NUMBER: 08 08/059,159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94105
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
ATTORNEY/AGENT INFORMATION:
NAME: Smith, william M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 01187
TELECOWNUICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEPHONE: 415-326-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/08458516
Patent No. 5777085
                                                                                                                                                                                   LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 330, Conservative
                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                               linear
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120 ASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 179
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                                                                                                                               3 ASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYPPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                        0; Gaps
          Length 449;
                                                                    Indels
Query Match 99.4%; Score 1767; DB 1; Best Local Similarity 100.0%; Pred. No. 2.6e-160; Matches 330; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/08378939;
Sequence 10, Se76561
GENERAL INFORMATION
GENERAL INFORMATION: PRODUCTION OF ANTIBODIES
ITILE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSER: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTERNTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
ZIP: 20044
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682 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 741
                                                                                                                                                                               742 PSVFLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 801
                                                                                                                                                                                                                        STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09289942A

Sequence 7, Application US/09289942A

Sequence 7, Application US/09289942A

GENERAL INFORMATION:
APPLICANT: Pai, Emil F.
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
TITLE OF INVENTION: MONOCLONAL ANTIBODY 2F5
TITLE OF INVENTION: MONOCLONAL ANTIBODY 2F5
TITLE OF INVENTION: MONOCLONAL ANTIBODY 2F5
CURRENT APPLICATION NUMBER: US/9/289,942A

CURRENT FILING DATE: 1999-04-13

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 7.
                                                                                                                                                                                                                                                                                                                                          862 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSVFLFPPKPXDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 182
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          PSVPLPPPKPKDTLMISRIPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                                                                                                                   253 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRESOYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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Pred. No. 6.7e-160;
0; Mismatches 1;
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ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                               303 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
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Best Local Similarity 99.7%;
Matches 329; Conservative
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US-09-289-942A-7
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WESUL: 6

Sequence 9, Application US/09313942

Sequence 9, Application US/09313942

Sequence 9, Application US/09313942

GENERAL INFORMATION:

APPLICANT: REGENERON PHARMACEUTICALS, INC.

TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

TITLE OF INVENTION: AND USING

FILE REFERENCE: REG 203-A

CURRENT APPLICATION NUMBER: US/09/313,942

PRIOR PRILING DATE: 1999-05-19

PRIOR FILING DATE: 1999-05-19

PRIOR FILING DATE: 1998-09-25

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 951
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99.4%; Score 1767; DB 2; I
Best Local Similarity 100.0%; Pred. No. 2.9e-160;
Matches 330; Conservative 0; Mismatches 0;
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FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: BRNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMUNICATION INFORMATION:
TELEFAX: (202) 783-604
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
                                                                                                                                                                                           LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-378-939-10
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ORGANISM: Homo sapiens
US-09-313-942-9
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RESULT 10

US-08-487-550-12
; Sequence 12, Application US/08487550
; Patent No. 6113896
; GENERAL INFORMATION:
; APPLICANT ANDERSON, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: "MANACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESANTS"
; TITLE OF INVENTION: IMMUNOSUPPRESANTS"
; MUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BUTNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 PSVFLFPPKPKDTLMISRTPEVICVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYN 326
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COMPUTER EADABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Elam PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 012712-131
TELEPHONE: 703-865-6620
TELEPHONE: 703-865-6620
TELEFEHONE: 703-865-6620
TELEFEHONE: 703-865-6620
TELEFERATION FOR SED ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.2%; Score 1763; DB 3;
99.7%; Pred. No. 7e-160;
tive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 99.73
Matches 329, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-487-550-4
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Patent No. 6113898
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION:
TITLE OF INVENTION: TO HUMBN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: IMMUNOSUPPRESANTS."
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                        Sequence 27, Application US/09740002

Sequence 27, Application US/09740002

Sequence 27, Application US/09740002

SENERAL INFORMATION:

APPLICANT: MORROW, PHILLIP

APPLICANT: MORROW, PHILLIP

TITLE OF INVENTION: BUFTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES

TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF

TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF

CURRENT APPLICATION NUMBER: US/09/740,002

PRIOR APPLICATION NUMBER: 08/488,376

PRIOR APPLICATION NUMBER: 08/488,376

PRIOR FILING DATE: 1999-06-17

NUMBER OF SEQ ID NOS: 27

SOFTWARE PARENTIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-740-002-27
                  RESULT 8
US-09-740-002-27
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 27
LENGTH: 475
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Gaps

182

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99.2%; Score 1763; DB 4; 99.7%; Pred. No. 7e-160; ive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 703-636-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Matches 329; Conserv
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US-09-526-098-12
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TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN BY.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 GLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG 122
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/Ms-DOS
SOFTWARE Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/487,550
FLING DATE: US/08/487,550
FLING DATE: US/08/487,550
ATORNEY/AGENT INPORMATION:
NAME: TESKINC, Robin L,
REGISTRATION NUMBER: 35,030
REFRENCE/COCKET NUMBER: 35,030
REFRENCE/COCKET NUMBER: 35,030
REFRENCE/COCKET NUMBER: 35,030
RELECOMMUNICATION INFORMATION:
TELEFACENCE/TOOKET NUMBER: 012712-131
TELEFACENCE/TOOKET NUMBER: 101211
TELEFACENCE TO 3-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
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Sequence 4, Application US/09526098
Patent No. 6492134
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.7
Matches 329; Conservative
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MOLECULE TYPE: protein US-08-487-550-12
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Patent No. 6492134
JENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS TITLE OF INVENTION: IMMUNOSUPPRESANTS"
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 476
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
FILING DATE:
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/POCKET UNMBER: 35,030
REFERENCE/POCKET UNMBER: 35,030
REFERENCE/POCKET UNMBER: 012712-131
TELEDPHONE: 703-936-6620
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COUNTRY:
ZIP: 2231
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Length 478;
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                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FLING DATE: 07-UN-1995
CLASSIFICATION: 435
ATTONINY AGENT INFORMATION:
NAME: TESKIN, RODIN L.
REGISTRATION NUMBER: 35,030
REPERENCE/POCKET NUMBER: 35,030
REPERENCE/POCKET NUMBER: 31,030
REPERENCE/POCKET NUMBER: 31,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.2%; Score 1763; DB 3, 99.7%; Pred. No. 7e-160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USB
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US-09-526-098-8
; Sequence 8, Application US/09526098
; Patent No. 6422134
; GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: PHARMACEUTIAL
ITLE OF INVENTION: PHARMACEUTIAL
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
; CALDERSSEE: BURNS, DOANE, SWECKI
                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.7
Matches 329; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-487-550-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
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Patent No. 6113898
General Information:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: INMUNES OF SEQUENCES:
I TOWNERS OF SEQUENCES:
CORRESSED: BURNS, DOWNE, SWECKER & MATHIS
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                                  COMPUTER: IEM PC_compatible
COMPUTER: IEM PC_COMPATIBLE
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303 OQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
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                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-4UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHRACTERISTICS: LENGTH: 476 amino acide TYPE: amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-526-098-12
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 329; Conserv
                                                                                                                                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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"MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
INMUNOSUPPRESANTS"
12
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                                                                                                                                 208
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                                                                                                                                                                                                                                                          209 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKABPKSCDKTHTCPPCPAPELLGG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 LIKNQVSLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 302
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                                                         3 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLOSS
                                                                                                       149 ASTKGPSVFPLAPSSKSTSGCTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                               123 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 328
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7e-160;
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Patent No. 5808032
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KURIHARA, TATSUYA
APPLICANT: TSURUOKA, NOBUO
APPLICANT: ARIMA, KENJI
APPLICANT: ARIMA, KENJI
APPLICANT: NISHIHARA, TATSURO
TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
TITLE OF INVENTION: PLASMIDS THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                SOFTHARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/526,098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
99.2%; Score 1763; D
Best Local Similarity 99.7%; Pred. No. 7e-1
Matches 329; Conservative 0; Mismatches
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                                                                                                                                            PRICA APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: 08/487,550
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: TERKIN, RODIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELEPHONE: 703-636-6620
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (03-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / MOLECULE TYPE: protein US-09-526-098-8
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COMPUTER: IBM PC
OPERATING SYSTEM:
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                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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US-08-157-101A-7
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                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/157,101A
FILING DATE: 05-APR-1994
CLASSIFICATION STARE: US/08/157,101A
FILING DATE: 05-APR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TITUS, MARLANA K
REGISTRATION NUMBER: 35433
REFERENCE/DOCKET NUMBER: 3437/204199
TELEPHONE: 202-861.3711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.7%; Pred. No. 8.2e-160;
Matches 329; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 332
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ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: January 13, 2004, 12:46:35
Job time : 30,7057 secs
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TELEX: 6714627 CUCH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 459 amino acidi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide
                                  STREET: 1100 NEW CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 13, 2004, 12:22:35; Search time 7.75633 Seconds (without alignments) 1326.664 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-990-586-99 553 1 RIVAAPSVFIFPPSDEQLKS.......EVIHQGLSSPVIKSFNRGEC 107

Scoring table:

283308 segs, 96168682 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Descripti	14 IQ	12 Iq kappa cha	13 Ig kappa cha	39 JC-kappa	Iq kappa	Ig kappa	Ig kappa cha	7 Ig kappa	PI	Ig kappa chain	Ig kappa	Ig kappa chain	Ig kappa	Ig kappa chain	Ig kappa chain	Ig kappa	monoclonal anti	Ig kappa c	Ig kappa	I kappa	gi	Ig kappa	PI 19	20 Ig kappa chain	58 Ig kappa chain	Ig kappa	32 gene Pvt-1a/Ig-		329 Iq kappa chai
•	ij	JE02	CEO	JE02	8520	K3HD	JE0241	A237	A375	3266	3060	KIR	PT0	K1R1	8427	2682	8388	302	PC42	3161	8520	A317	8374	8142	8013	S25(KIMS	154.		2010
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	Result No.		03	ю	4	Ŋ	φ	7	ω	σ																		27		

Ig kappa chain (Ma	kappa				kappa-	Ig kappa-1 chain C	Ig kappa-B9 chain		×	';;	Ig lambda chain C	Ig light chain pre	light chain	kappa-B5 chai	Ig kappa chain (WM
\$68212	A56169	G20907	K4RBBS	A20969	K4RB	F53275	K9RB	A49633	KSRBV	A46518	B26167	A21177	K3FG	KSRB	829593
	2 A56169	_								2 A46518					
N		N	-	ď	н	7	Н	7	Н	N	7	0	Н	Н	0
N	210 2	106 2	106 1	229 2	103 1	104 2	104 1	238 2	104 1	N	103 2	213 2	108 1	103 1	197 2
N	56.4 210 2	5 55.8 106 2 (5 55.4 106 1	229 2	5 46.6 103 1	5 46.3 104 2	44.6 104 1	44.3 238 2	43.6 104 1	118 2	41.8 103 2	41.8 213 2	40.7 108 1	40.4 103 1	197 2

ALIGNMENTS

RESULT 1 JE0244 Ig kappa chain NIG2 precursor - human C,Species: Homo sapiens (man) C,Species: Homo sapiens (man) C,Species: Os-Dec-1998 #sequence_revision Os-Dec-1998 #text_change 21-Jan-2000 C,Accession: JE0244 R,Alim, M.A.: Hara, Y.: Hossain, M.S.: Takeda, K.; Yamagata, F.: Yamaki, S.: Kazi, H.: T sipinfited to JTPID, November 1998 A;Reference number: JE0243 A;Reference number: JE0244 A;Reference number: JE0244 A;Residues: 1-215 < ALI>C,Superferent Homology C,Superferent Homology C,Superferent Homology C,Superferent Homology F:16-90/Domain: immunoclobulin homology	Query Match 100.0%; Score 553; DB 2; Length 215; Best Local Similarity 100.0%; Pred. No. 2.6e-47; O; Gaps O; Matches 107; Conservative O; Mismatches O; Indels O; Gaps O; Qy RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 168 Qy 61 SKDSTYSLSSTLTLSKADYEKHKYYACEVTHQCLSSPVTKSFNRGEC 107	RESULT 2 JE0242 Ig kappa chain NIG26 precursor - human C;Species: Home saplens (man) C;Species: Home saplens (man) C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000 C;Accession: JE0242 R;Alim, M.A.; Yamaki, S.; Hoseani, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T Submitted to JTPID; November 1998 A;Description: Structure relationship of kappatype light chains with AL amyloidosis: Mul A;Reference number: JE0241 A;Accession: JE0242 A;Molecule type: protein A;Residunes: 1-21s cALIP C;Superfamily: immunoglobulin V region; immunoglobulin homology F;16-91/Domain: immunoglobulin homology <imm></imm>	Query Match Best Local Similarity 100.0%; Score 553; DB 2; Length 215; Best Local Similarity 100.0%; Pred. No. 2.6e-47; Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-106 < GGCT.
A; Residues: 1-106 < GGCT.
A; Note: this sequence has the Inv (3) allotypic marker, 45-Ala and 83-Val
B; Gall, W.E.; Edelman, G.M.
B; Gall, W.E.; Edelman, G.M.
A; Balechemistry 9, 3188-3196, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfic
A; Reference number: A90565; MUID:71064027; PMID:4923144
A; Contents: annocation, Eu, disulfide bonds
B; Contents: annocation, Eu, Maranabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972
Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972
A; Title: Die Pritanerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sul
A; Reference number: A91651; MUID:72188439; PMID:5027703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Residues: 1-106 <SUT>
R,Hieter, P.A.; Max, E.B.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P.
Edli 22, 197-207, 1980
A;Title: Cloned human and mouse kappa immunoglobulin constant and J region genes conserva, Reference number: A90806; MUID:81042304; PMID:6775818
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Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967
Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967
Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1729, 1967
A;Title: Die volstaendige Aminosaeureseguenz des Bence-Jones-Proteins Cum. (kappa-Typ).
A;Contents: Bence Jones protein Cum
A;Accession: A31639
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A; Mesidues: 1-56, Q', 58.106 < HI2>

R; Titeni, K.; Shinoda, T.; Putnam, F.W.

J. Biol. Chem. 244, 3550-3560, 1969

J. AjTitle: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete A; Reference number: A92047; MUID:69234734; PMID:4893682

A; Contents: Bence Jones protein Ag
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A; Rough Charles and Full of the charles are considered as determined from the germline gene
A; Note: the sequence was determined from the germline gene
B; Hilschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayne, In Gamma Globulins: Structure and Function, Franck, F., and Shugar, D., eds., pp.57-74, A; Reference number: A94417
A; Accession: A94417
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A,Residues: 1-13, N',15-106 <TIT>
R;Kohler, H.; Shimizu, A.; Paul, C.; Putnam, P.W.
Science 169, 56-59, 1970
A;Title: Macroglobulin structure: variable sequence of light and heavy chains.
A;Reference number: A94242; MUID:70201507; PMID:5447531
A;Contents: Waldenstrom's macroglobulin Ou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Note: allotype Inv(3)
R;Steiner, V.; Chang, J.Y.
RESS Lett. 222, 6-10, 1987
A;Title: Chemical modification of the carboxyl groups of protein substrates
A:Reference number: S02572; MUID:88005152; PMID:3115831
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A;Residues: 1-13, 70, 15-106
A;Kurth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza,
Am. J. Hum. Genet. 48, 613-620, 1991
A;Title: Km typing with PCR: application to population screening.
A;Reference number: A37927; MUID:91150772; PMID:1900145
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A;Residues: 1-44,'A',46-56,'Q',58-82,'L',84-106 <HIL>
A;Note: this sequence has the Inv (1,2) allotypic marker, 45-Ala and
number: A90562; MUID:71064023; PMID:5489770
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C;Species: Homo sapiens (man)
C;Date: 31-Dec-1980 #sequence revision 02-Jul-1998 #text change 21-Jul-2000
C;Accession: B90562; A91651; A90806; A94417; A91639; A92047; A94242; B37927; A02116; S02
R;Gottlieb, P.D.; Cunningham, B.A.; Rutishauser, U.; Edelman, G.M.
Biochemistry 9, 3155-3161, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VI. Amino acid sequend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amy
                                                                                                                                                                                                                                                                                                                                        Ig Kappa chain NIG93 precursor - human (5.5pecies: Home sapiens (man) (5.5pecies: Home sapiens (man) (5.5pecies: Home sapiens (man) (5.5pecies: Home sapiens (man) (5.5pecies: Home sapiens) (6.5pecies:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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99.5%; Score 550; DB 2; Length 135;
Best Local Similarity 99.1%; Pred. No. 2.9e-47;
Matches 106; Conservative 1; Mismatches 0; Indels
                                          SKDSTYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC
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llarity 100.0%; Pred. No. 2.6e-47;
Conservative 0; Mismatches 0;
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Best Local Similarity
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Ig kappa chain C region - chimpanzee (fragment)
CjSpecies: Pan troglodytes (chimpanzee)
CjSpecies: Pan troglodytes (chimpanzee)
CjDate: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
CjAccession: 826653
Ribhrlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.
Hum. Antibodies Hybridomas 1, 23-26, 1990
A;Title: Potential of primate monoclonal antibodies to substitute for human antibodies:
A;Reference number: 826652; MUID:91355693; PMID:2129418
                                                                                                                                                                                                 109 RIVAAPSVFIFPPSDEQLKSGTASVVGLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 21-Jan-2000
C;Accession: A37927
Am. J. Hum. Genet. 48, 613-620, 1991
A;Rittle: Km typing with PCR: application to population screening.
A;Reference number: A37927; MUID:91150772; PMID:1900145
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   Score 520; DB 2; Length 215;
Pred. No. 4.7e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-99 «KUR»
C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: heteroteramer; immunoglobulin F;12-81/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 92.8%; Score 513; DB 2; Length 99; Best Local Similarity 99.0%; Pred. No. 9e-44; Matches 98; Conservative 1; Mismatches 0; Indels
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;19-68/Domain: immunoglobulin homology <IMM>
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100.0%; Pred. No. 3.5e-43;
Live 0; Mismatches 0;
                                                                      0; Mismatches
   94.0%;
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A;Molecule type: mRNA
A;Residues: 1-99 <EHR>
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                                   Best Local Similarity
Matches 104; Conserv
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Best Local Similarity
Matches 99; Conserv
       Query Match
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                                                                                A.Cross-references: GDB:12008B; OMIM:147200
A;Map position: 2p12-2p12
A;Map position: 2p12-2p12
C:Complex: an immunoglobulin heterotramer subunit consists of two identical light (kap hain disulfide bonds; in some cases, such as IQA and IGM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Superfamily: immunoglobulin homology <IMM>
F;19-8B/Domain: immunoglobulin homology <IMM>
F;26-86/Disulfide bonds: #status experimental
F;106/Disulfide bonds: interchain (to heavy chain) #status experimental
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: A23746
R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
A;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
A;Litle: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglascence number: A23746; MUDD:91131575; PMID:1993660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.1%; Score 537; DB 2; Length 216; 97.2%; Pred. No. 9.9e-46; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: JE0241
A;Molecule type: protein
A;Residues: -116 <ALI>-216 <ALI>-216 <ALI>-515 <ALI>-515 <ALI>-515 <ALI>-515 <ALI>-515 <ALI>-515 <ALI>-515 <ALI>-515 <ALI </ALI </a>
F:16-92/Domain: immunoglobulin homology <IMM>
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C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: heteroterramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 99.1%; Score 548; DB 1; I
Best Local Similarity 100.0%; Pred. No. 3.4e-47;
Matches 106; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 97.2
les 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: protein
Residues: 1-215 <LEO>
A; Contents: annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain V-C region (PLC18) - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jan-2000
                  3 AAPTVSIFPPSTEQLATGGASVVCLMNNPYPRDISVKWKIDGTERRDGVLDSVTDQDSKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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A.Molecule type: mRNA
A.Molecule type: manalated the codon CTC for residue 141 as Ser
A.Mole: the authors translated the codon CTC for residue 141 as Ser
C.Molec: the authors translated the codon CTC for residue 141 as Ser
C.Molec: the authors translated the codon CTC for residue 141 as Ser
C.Molec: the authors translated the codon CTC for residue 141 as Ser
C.Molecule translated the codon CTC for residue 141 as Ser
C.Molecule translated 
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R; Lammers, B.M.; Beaman, K.D.; Kim, Y.B.
Mol. Immunol. 28, 877-880, 199
A; Title: Sequence analysis of porcine immunoglobulin light chain cDNAs.
A; Title: Sequence number: PT0219; MUID:91342694; PMID:1715030
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                                                                                                                                                                                                                63 SIYSMSSTLSLIKADYESHNLYICEVVHKTSSSPVVKSFNRNEC 106
                                                                                                                                64 STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22; Indels
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63.5%; Pred. No. 1.6e-28;
iive 16; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;61-70/Region: framework 2
F;71-178/Domain: C region <CRG>
F;96-156/Disulfide bonds: #status predicted
F;176/Disulfide bonds: interchain #status predicted
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nes 69; Conservative
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Best Local
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C.Species: Rattus norvegicus (Norway rat)

C.Species: Rattus norvegicus (Norway rat)

C.Species: Rattus norvegicus (Norway rat)

C.Accession: A93301, A92807; A20217

R.Sheppard, H.W.; Gutman, G.A.

R.Sheppard, H.W.; Gutman, G.A.

A.7title: Allalic forms of rat kappa chain genes: evidence for strong selection at the le

A.7title: Allalic forms of rat kappa chain genes: evidence for strong selection at the le

A.Accession: A93901, MUD: 82082587; PMID: 6273908

A.Accession: A93901

A.Accession: A93901, MUD: 82082587; PMID: 6273908

A.Accession: A93901

A.Accession: A1 mmunoglobulin heterotetramer subunit consists of two identical light (kap caper and a self and self a
                                                                                                                                                                                                                                                                 Ig Kappa chain precursor - rat

C.Species: Rattus norvegicus (Norway rat)

C.Species: Rattus norvegicus (Norway rat)

C.Species: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000

C.Accession: 806084

R.Crowe, J.S.; Smith, M.A.; Cooper, H.J.

Nucleic Acids Res. 17, 7992, 1989

A.Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain CDNA

A.Reference number: 806084; MID:90016888; PMID:2508067

A.Molecula type: mRNA

A.Molecula type: mRNA

A.Molecula type: mRNA

A.Molecula type: mRNA

A.Residues: 1-240 <CRO>
A.Cross-references: EMBL:X16129; NID:956457; PIDN:CAA34256.1; PID:956458

C.Superfamily: immunoglobulin V region; immunoglobulin homology

C.Superfamily: signal sequence #status predicted <BIG>

F.11-240/Poroduct: Ig kappa chain #status predicted <MAT>

F.153-222/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Indels
KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK 99
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N.Alternate names: immunoglobulin light chain
C.Species: Mus musculus (house mouse)
C.Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C.Accession: 868241; 868214
C.Accession: 868241; 868214
R.Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T. submitted to the EMBL Data Library, March 1994
A.;Description: Specific peroxidase activity by formation of an antibody L-chain-porphyri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-218 <TAX>
A;Acsar = references: BMBL:D29670; NID:g473962; PIDN:BAA06141.1; PID:g473963
A;Crosar = references: EMBL:D29670; NID:g473962; PIDN:BAA06141.1; PID:g473963
B;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T. FEES Lett. 375, 273-276; 1995
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin A;Reference number: S68211; MUID:96085223; PMID:7498516
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                                                                                                                                                                                                                                                                                               Species: Mus musculus (house mouse)
Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
Accession: 542772
AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Cross-references: EMBL:X75536; NID:g414143; PIDN:CAA53226.1; PID:g414144 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F:14-93/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.7%; Score 358; DB 2; Length 217; 61.7%; Pred. No. 4.8e-28; ive 15; Mismatches 26; Indels
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A;Residues: 'NI',3-212 <TAM>
A;Cross-references: EMBL:D29670
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
                                                                                                                                 STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
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64.7%; Score 358; DB 2;
Best Local Similarity 61.7%; Pred. No. 4.9e-28;
Matches 66; Conservative 15; Mismatches 26
                                                                                                                                                                                                                                                                                                                             Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 61.78
Matches 66; Conservative
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A Molecule type: mRNA
A, Residues: 1-217 <SCH>
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DD 112 RADAAPTVSIPPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD 171

QY 61 SKDSTYSLSGTLTLSKADYEKHKVYAGEVTHOGLSSPVTKSFNRGEG 107
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172 SKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFURGEC 218

Search completed: January 13, 2004, 12:44:42 Job time: 7.75633 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

January 13, 2004, 12:19:34; Search time 4.67249 Seconds (without alignments) 1076.912 Million cell updates/sec Run on:

US-09-990-586-99 553 1 RTVAAPSVFIFPPRDEQLKS......EVTHQGLSSPVTKSFNRGEC 107

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	homo s	rattu	rattue		P01839 oryctolagus	P01840 oryctolagus		oryg		rana	oryg		P01842 homo sapien			P15814 homo sapien		P01846 sus scrofa	mus		cavi		mus	P01863 mus musculu	P01865 mus musculu	P01859 homo sapien	homo	mus m	P01860 homo sapien	рошоц	m snm	01866 mus	01867 mus
S OF THE S	KAC HUMAN	KACB RAT	KACA RAT	KAC MOUSE	KACB RABIT	KAC4_RABIT	KAC9_RABIT	KAC6 RABIT	LAC CHICK	KAC_RANCA	KACS RABIT	LAC1_MOUSE	LAC_HUMAN	LAC RABIT	LACI RAT	ILL1_HUMAN	LAC2 RAT	LAC PIG	LAC3 MOUSE	LAC2 MOUSE	GC2 CAVPO	LACS_MUSSP	EPC_MOUSE	GCAA_MOUSE		GC2_HUMAN	GC4_HUMAN	GCAB MOUSE	GC3 HUMAN	GC1_HUMAN	LACS MOUSE	GCB MOUSE	GCBM_MOUSE
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GC_RABIT MUC_MESAU MUC_SUNMU MUC_SUNMU ESC_RAT GCC_RAT GCC_RAT GCCI_M MOUSE MUC_MOUSE MUCM_MOUSE GCA_RAT GC3_MOUSE GCA_RAT GC3_MOUSE
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                                                                                                     3. The
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=69234734; PubMed=4893682;
Titani K., Shinoda T., Putnam F.W.;
"The amino acid sequence of a kappa type Bence-Jones protein. 3
complete sequence and the location of the disulfide bridges.";
J. Biol. Chem. 244:3550-3560(1969).
                                                                                                                                                                                             MEDIJINE=70201507; PubMed=5447531;
Kohler H., Shimizu A., Paul C., Putnam F.W.;
"Macroglobulin structure: variable sequence of light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin C region, 3D-structure
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V -> L (IN INV(1,2) MARKER).
/FTId=vAR_003897.
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E -> Q (IN REF. 5 AND 6).
51984D1FDD372CE8 CRC64;
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Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
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GO; GO:0006855; F:immune response; NAS.
InterPro; IPR003597; Ig-like.
InterPro; IPR003597; Ig_c1.
PROF0047; Ig_11.
SMART; SM00407; IGc1; 1.
PROSITE; PSS0835; IG_HKC; 1.
PROSITE; PSS0835; IG_HKC; 1.
Immunoglobulin domain; Immunoglobulin C region; 3D-
                                                                                                                                                                                SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
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                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-33; 38-41 AND 62-80. TISSUE=Abdominal adipose tissue; PubMed=9588180;
                                    SEQUENCE (BENCE-JONES PROTEIN AG)
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EMRL, V00557; CAA23823.1; --
PIR, B90562, K3HU.
PDB, IDSB, 09-FEB-00.
PDB, IDSI, 09-FEB-00.
PDB, IDSI, 09-FEB-00.
PDB, IHEZ, 10-ACC-00.
PDB, IHEZ, 12-MAR-97.
PDB, IHEZ, 12-MAR-97.
PDB, IMIX, 15-MAR-97.
PDB, IMIX, 15-MAR-97.
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57 E
11609 MW;
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83
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106 AA;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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MEDLINE-7521238; PubMed=807630;

MEDLINE-7521238; PubMed=807630;

Starace V., Ouerinjean P.;

"The primary structure of a rat kappa Bence Jones protein: phylogenetic relationships of V- and C-region genes.";

"The primary structure of a rat kappa Bence Jones protein: phylogenetic relationships of V- and C-region genes.";

"Instanty: LSS-62(1975).

"Instanty: Contains 1 immunoglobulin-like domain.

PIR; A93901; KIRTB.

R HSSP, PO1842; 2MCG.

InterPro; IPR003109; Ig_c1.

InterPro; IPR003509; Ig_c1.

InterPro; IPR003006; Ig_MHC.

PEam; PF0047; Ig_C1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sheppard H.W., Gutman G.A.; "Albelic forms of rat kappa chain genes: evidence for strong selection at the level of nucleotide sequence."; Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
                                                                                       61 KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 106
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                                               62 KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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E -> Q (IN REF. 2).
E -> Q (IN REF. 2).
V -> VW (IN REF. 2).
S -> N (IN REF. 2).
( + 4CPA7CA820DICA36 CRC64;
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D -> N (IN REF. 2
N -> K (IN REF. 2
                                                                                                                                                                                                                                                                21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig kappa chain C region, B allele.
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MEDLINE=82082587; PubMed=6273908;
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SMART, SM00407, IGG1; 1.
PROSITE, PS00835; IG LIKE; 1.
PROSITE, PS00290; IG MHC, 1.
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                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat)
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P01835;
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Query Match 99.1%; Score 548; DB 1; Length 106; Best Local Similarity 100.0%; Pred. No. 4.5e-48; Matches 106; Conservative 0; Mismatches 0; Indels

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                                                                                                                                                  Ig kappa chain Cregion, A allele.
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butharia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutebria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE (MOPC 21).
MEDLINE-73053310; PubMed=4638343;
Svasti J. Milstein C.;
"The complete amino acid sequence of a mouse kappa light chain.";
Biochem. J. 128:427-444(1972).
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MEDLINE=73008889; PubMed=5073237;
Svaeti J., Miletein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Biochem. J. 126:837-850(1972).
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106 106 INTERCHAIN (WITH A HEAVY CHAIN).
106 AA; 11732 MW; B7E120D9700DDD66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       Sheppard H.W., Gutman G.A.;
"Allelic forms of rat kappa chain genes: evidence for strong selection at the level of nuclectide sequence.";
Proc. Natl. Acad. Sci. U.S.A. 78;7064-7068(1981).
-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02118; KIRTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.9%; Score 359; DB 1; Length 106; llarity 63.5%; Pred. No. 3.3e-29; Conservative 16; Mismatches 22; Indels
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                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1g kappa chain C region:
                       106 AA.
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                 STANDARD;
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Best Local Similarity
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P01837;
                 KACA RAT
P01836;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licenseeisb-sib.ch/sww.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch/.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=81191915; PubMed=6262318;
MAX E.E., Maizel J.V. Jr., Leder P.;
MAX E.E., Maizel J.V. Jr., Leder P.;
"The nuclectide sequence of a 5.5-kilobase DNA segment containing the mouse kappa immunoglobulin J and C region genes.";
J. Biol. Chem. 256:5116-5120(1981).
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MEDLINE=88329081; PubMed=3138116;
de Wacle P., Feys V., van de Voorde A., Molemans F., Fiers W.;
de Wacle P., Feys V., van de Voorde A., Molemans F., Fiers W.;
"Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed against the tumour marker human placental alkaline phosphatase.";
phosphatase.";
Eur. J. Biochem, 176:287-295(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Altenburger W., Neumaier P.S., Steinmetz M., Zachau H.G.; "DNA sequence of the constant gene region of the mouse immunoglobulin Kappa chain."; Nucleic Acids Res. 9:971-981(1981).
                                                                                                                                                                                                                                                                                                                                MEDITNE-82059477; PubMed-6170937; Hamlyn P.H., Gait M.J., Milstein C.; "Complete sequence of an immunoglobulin mRNA using specific priming and the dideoxymucleotide method of RNA sequencing."; Nucleic Acids Res. 9:4485-4494(1981).
SEQUENCE FROM N.A., AND REVISIONS TO 53-59.
SEQUENCE 79064137; PubMed=103625,
Hamlyn P.H., Brownlee G.G., Cheng C.-C., Gait M.J., Milstein C.;
"Complete sequence of constant and 3' noncoding regions of an immunoglobulin mRNA using the dideoxynucleotide method of RNA immunoglobulin mRNA using the dideoxynucleotide method of RNA
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SNART; SN0407; IGC; 1.
PROSITE; PS50835; IG_LKE; 1.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
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PDB; IXCV; 11.MAY-02.
PDB; IXCV; 11.MAY-02.
PDB; IXCV; 11.MAY-02.
PDB; 25C8; 09-UUL-99.
MGD; MGI:96495; IGK-C.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-c1.
InterPro; IPR003506; Ig-MHC.
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1IGC, 03-JUN-95.
1KB5, 08-APR-98.
1KCR, 11-MAY-02.
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106 AA;
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P01840;
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                                                                                        62
                                                             63
                                                       4 AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD
                                                                            -!- MISCELLANEOUS: IN BASILEA RABBITS, THE MAJOR TYPE OF LIGHT CHAIN IS LAMBDA. THE KAPPA CHAIN SHOWN IS A MINOR COMPONENT. ALL OTHER RABBIT B ALLOTYPES HAVE 64-CYS.
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Bukarycta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
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63.3%; Score 350; DB 1; Length 106; 61.5%; Pred. No. 2.6e-28; 1ve 15; Mismatches 25; Indels
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AF9B928DDA853849 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 kappa-B4 chain C region.
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SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG MHC; PALSE NEG.
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EMBL; V00885; -; NOT_ANNOTATED_CDS.
PIR; A01121; K4RBBS.
HSSP; P01842; 7FAB.
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87
106
11279 MW;
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
                              64; Conservative
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hes 56; Conservative
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              Similarity
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P01839;
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"Primary structure of the L chain from a rabbit homogeneous antibody to streptococcal carbohydrate. II. Sequence determination of peptides from tryptic and peptic digests.";
J. Biol. Chem. 250:3289-3296(1975).
-!- MISCELLANBOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO THE SPECIFIC CARBOHYDRATE OF GROUP C STREPTOCOCCI & WAS ISOLATED FROM THE SERUM OF A SINGIL RABBIT.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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MEDIJLE=8330036; PubMed=6412231;
MEDIJLE=8330036; PubMed=6412231;
"Rabbit immunoglobulin kappa genes: structure of a germline b4
allotype J-C locus and evidence for several b4-related sequences in
the rabbit genome.";
Proc. Natl. Acad. Sci. U.S.A. 80:5709-5713(1983).
                                                                                                                                                                                                                                                                                                                                       21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
17-SEP-2003 (Rel. 42, Last annotation update)
18-SEP-2003 (Rel. 42, Last annotation update)
19-SEP-2003 (Rabbit)
19-SEP-2003 (Rabbit)
19-SEP-2003 (Rabbit)
19-SEP-2003 (Relection)
19-SEP-2003 (Relecti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=82060334; PubMed=6795636; Heidmann O., Auffray C., Cazenave P.-A., Rougeon F.; Wouleotide sequence of constant and 3' untranslated regions of kappa immunoglobulin 11ght chain mRNA of a homozygous b4 rabbit.' Proc. Natl. Acad. Sci. U.S.A. 78:5802-5806(1981).
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58 N -> D (IN REF. 3)
11043 MW, 5FC5ACC8B60E68DB CRC64;
46.6%; Score 257.5; DB 1; Length 48.5%; Pred. No. 4.4e-19; ive 21; Mismatches 29; Indels
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SMARY; SM00407; IGC.; 1.
PROSITE; PS00290; IG_MRC; FALSE NEG.
Immunoglobulin domain; Immunoglobulin C region.
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1 IGC. 166.
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InterPro; IPR003597; Ig cl.
InterPro; IPR003006; Ig MHC.
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103 AA;
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50; Conserv
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65 TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107

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Query Match
Best Local Similarity
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NCBI_TaxID=9031;
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                                                                                       APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALGSGNSQESVTEQDSKDS 64
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, East annotation update)
17 Kappa-B9 chain C region.
18 Kappa-B9 chain C region.
19 Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
19 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Oryctolagus chainat (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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                                                                                                                                                                                                             65 TYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPYTKSFNRGEC 107
                                                                                                                                                                                                                                                                               63 TYNLSSTLTLTSTQYNSHKEYTCKVT-QGTTS-VVQSFNRGDC 103
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P01838;
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P03984;
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5 APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS
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01-FEB-1991 (Rel. 17, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16 lambda chain C region.
6allus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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MEDLINE=87218480; PubMed=3107981;
Parvarī R., Ziv E., Lencner F., Tel-Or S., Burstein Y., Schechter I.;
"Analyses of chicken immunoglobulin light chain cDNA clones indicate a few germline V lambda genes and allotypes of the C lambda locus.";
EMBO J. 6:97-102(1987).
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HSSP, F01842, ZMCG.
InterPro; IPR00310; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR00306; Ig_MHC.
SMAPP; SM00407; Ig., 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS50835; IG_LIKE; 1.
IMMINGIODULIN domain; Immunoglobulin C region.
NON_IER
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PIR, A02124; K5RBV.
HSSP; P01842; 2MCG.
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Biochemistry 22:993-998(1983).
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                                                                                                                                                                                                                                           49; Conservative
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          13
28
47
108 AA,
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P01841;
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KACS_RABIT
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MIKOTYAK C.A., Steiner L.A.;
MOI. Immunol. 25:695-703(1968).
MOI. Immunol. 25:695-703(1974).
MOI. Immunoglobulin domain; Immunoglobulin C region.
MON. TER.
MON. TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rāna čatesbeiana (Būll frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.8%; Score 231; DB 1; Length 103;
43.3%; Pred. No. 1.9e-16;
iive 19; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERCHAIN (WITH HEAVY CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 STYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N -> D.
77BF341B511B91B2 CRC64;
-!- SIMILARITY: Contains 1 immunoglobulin-like domain
                                                                                                                                                                                                                                                                                                                       EMBL, X04768; CAA28461.1; -.
PIR; B26167; B26167.
HSSP, POLSA, 7 FRAB.
INTERPRO; IPRO(310); Ig-like.
INTERPRO; IPRO(3557); Ig-c1.
INTERPRO; IPRO(3067); Ig-d1.
SMART; SMO407; Ig1.
PROSITE; PSSO(835); IG_LIKE; I.
PROSITE; PSSO(835); IG_LIKE; I.
IRMUNDGlobulin domain; Immunoglobulin C region.
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01-JUL-1989 (Rel. 11, Last sequence update)
15-SEP-2003 (Rel. 22, Last annotation update)
1fg light chain C region.
Rana catesbelana (Bull frog).
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11361 MW;
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Best Local Similarity 43.3%
Matches 45; Conservative
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103
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103
90
103 AA;
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P11272;
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DISULFID
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SEQUENCE
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KAC_RANCA
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Chersi A., Alexander C.B., Mage R.G.;
Chersi A., Alexander C.B., Mage R.G.;
Chersi A., Alexander C.B.

T. Contains alorype.";

Mol. Immunol. 17.1515-1523 (1980).

E. Single rabbit of b5 allorype.";

Mol. Immunol. 17.1515-1523 (1980).

R. RSSP; Polda42, 7RRB.

R. RSSP; Polda42, 7RRB.

R. RICEPTO; IPRO0110; Ig-like.

R. InterPro; IPRO01106; Ig-like.

R. RART; SM00407; IgC.1.

R. RART; SM00407; IgC.1.

R. RART; SM00407; IGG.1.

R. RART; SM00407; IGG.1.

R. RART; SM00407; IGG.1.

R. RAMRT; SM00407; IGG.1.

R. DOMÄIN

T. DISULPID

26 85
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                                                                                                                                                                                                                                    7 FIVSIXCPSLEQRNSGSASTVCLVDKFYPGGAQVTWKGDNKVISSGVDTSDKIKD-KDNT
                                                                                                                                                                                                       6 PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALOSGNSQESVTEQDSKDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 APSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS
                                                                                                                                               2; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Lagomorpha, Leporidae, Oryctolagus.
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K -> R (IN HALF OF THE MOLECULES)
6 60B18F7AF1411F6C CRC64;
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MISSING (IN REF. 2).
P -> S (IN REF. 2).
A -> T (IN REF. 2).
E -> Q (IN REF. 2).
VA -> LP (IN REF. 2).
WA -> LP (IN REF. 2).
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                                                                                    Length 108;
                                                                              40.7%; Score 225; DB 1; Length 10
48.0%; Pred. No. 8.1e-16;
ive 16; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                     66 YSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
                                                                                                                                                                                                                                                                                                                                                       66 YSMSSTLTMSSEEF-KYSTWTCEVTHPTLTPALAKSFQTSEC 106
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig kappa-B5 chain C region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Appella E.;
"Amino acid sequences of two mouse immunoglobulin lambda chains.";
Proc. Natl. Acad. Sci. U.S.A. 68:590-594(1971).
-!- MISCELLANBOUS: THE MOPC 315 CELL LINE PRODUCES 2 LIGHT CHAINS, 1
NORMAL LAMBDA-2 CHAIN & 1 ABNORMAL LAMBDA-1 CHAIN THAY IS MISSING
A LARGE PART OF THE V REGION. THE C REGION SEQUENCE (SHOWN HERE)
APPEARS COMPLETELY NORMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=82220143; PubMed=6283385;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
Baltimore D.; M. Paskind M. Reth M., Imanishi-Kari T., Rajewsky K.,
"Somatic variants of murine immunoglobulin lambda light chains.";
Nature 298:380-382 (1982).
                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=81148806; PubMed=6259534;
Bothwell A.L.M., Paskind M., Schwartz R.C., Sonenshein G.E.,
Gefter. M.L., Baltimore D.;
"Dual expression of lambda genes in the MOPC-315 plasmacytoma.";
Nature 290:65-67(1981).
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PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS02209; IG_MHC; 1.
Immunoglobulin domaiñ; Immunoglobulin C region; 3D-structure.
DONĀIN 6 100 IG-LIKE.
            TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
                                           63 TYNLSSTLTLQKSNYNSHNEYTCQVA-QGAGS-VVQSFSRKNC 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-83014953; PubMed=6812053; Storb U.; Selsing E., Miller J., Wilson R., Storb U.; "Evolution of mouse immunoglobulin lambda genes."; Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685(1982).
                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
11-SEP-2003 (Rel. 42, Last annotation update)
19 lambda_1 chain C region.
                                                                                                                                                                                                                            105 AA.
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MEDLINE=71107854; PubMed=5276767;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
Pfam; PP00047; ig; 1.
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EMBL; JO0587; AAB59672.1; -.
PIR; A93922; LIMS.
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                                                                                                                                                                                                                      STANDARD;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                             LAC1 MOUSE
P01843;
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                                                                                                                                                  RESULT 12
LAG1_MOUGE
LAG1_MOUGE
LAG1_MOUGE
LAG1_MOUGE
LAG1_MOUGE
DT 21-JUL
DT 21-JUL
DT 21-JUL
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OC Mammal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=70166723; PubMed=4909564; Titchi K., Shinoda T., Putnam F.W.; "The amino acid sequence of a lambda type Bence-Jones protein. 3. The complete amino acid sequence and the location of the disulfide
                                                                                                                                                                                                              Gaps
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MEDLINE-74109253; PubMed=4814727;
MEDLINE-74109253; PubMed=4814727;
MEDLINE-74109253; Polymed R.J.;
"Amino acid sequence of the (lambda) light chain of a human myeloma immunoglobulin (IgG New).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE (BENCE-JONES PROTEIN X), AND DISULFIDE BONDS.
MIDLINES-6089380. Pubmed-4889841;
Milatein C., Clegg J.B., Jarvis J.M.;
"Immunoglobulin lambda-chains. The complete amino acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Comparative studies on the structure of the light chains of human immunoglobulins. IV. Assignment of a subsubgroup."; J. Biochem. 93:421-429(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE (BENCE-JONES PROTEIN KERN).
MEDLINES-1150336; Pubmed=5549568;
Ponsting1 H., Hess M., Hilschmann N.;
"Structural rule of antibodies. Primary structure of a monoclonal immunoglobulin-L-chain of the lambda type, subgroup IV (Bence-Jones protein Kern). V. The complete amino acid sequence and its genetic interpretation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBL_TaxID=9606,
                                                                                                                                                                                                              7;
                                                                                                                                                                  / Match 38.1%; Score 210.5; DB 1; Length 105; Local Similarity 42.5%; Pred. No. 2.2e-14; Nes 45; Conservative 20; Mismatches 34; Indels 7
                                                                                                                                                                                                                                                                                                                    64 ST--YSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 107
                                                                                                                                                                                                                                                                                                                                              61 SNNKYMASSYLTLTARAWERHSSYSCQVTHEG--HTVEKSLSRADC 104
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Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
      INTERCHAIN (WITH HEAVY CHAIN).
104 INTERCHAIN (WITH HEAVY CHAIN
20 ET -> TE (IN REF. 4).
56 Q -> B (IN REF. 4).
75 MISSING (IN REF. 4).
82 HS -> SH (IN REF. 4).
85 S -> SS (IN REF. 4).
96 B -> Q (IN REF. 4).
96 E -> Q (IN REF. 4).
96 B -> Q (IN REF. 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1g lambda chain C regions.
IGLCI AND IGLC2 AND IGLC3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bridges.";
J. Biol. Chem. 245:2171-2176(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE (BENCE-JONES PROTEIN SH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bence-Jones protein.";
Biochem. J. 110:631-652(1968).
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  104
19
56
75
75
81
85
96
105 AA;
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DISULFID
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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LAC_HUMAN
ID _ LAC H
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-!- MISCELLANBOUS: THE SEQUENCE SHOWN IS THE KERN-/OZ-/MCG- CHAIN FOUND IN PROTEINS 8H, X, AND NIG-64. THE KERN PROTEIN HAS THE KERN PROTEIN HAS THE OZ+ MARKER, THE NEW PROTEIN HAS THE OZ+ MARKER, THE MCG PROTEIN HAS THE KERN+ MARKER, AND THE MCG+ MARKER.

-!- MISCELLANBOUS: SIX TANDEM LAMBDA-TYPE GENES WERE IDENTIFIED & THE 3 MOST S' WERE SEQUENCED. THESE CORRESPOND TO THE MCG SEQUENCE (LAMBDA-1), THE KERN-/OZ- SEQUENCE (LAMBDA-2) & THE KERN-/OZ+ SEQUENCE (LAMBDA-3).

-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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MEDLINE-82080680; PubMed-6273747;
Hieter P.A., Hollis G.F., Korsmeyer S.J., Waldmann T.A., Leder P.;
"Clustered arrangement of immunoglobulin lambda constant region genes
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Ely K.R., Herron J.N., Harker M., Edmundson A.B.;
"Three-dimensional structure of a light chain dimer crystallized in.
water. Conformational flexibility of a molecule in two crystal
                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEWM.
MEDLINE-75046825; PubMed=4215080;
Poljak R.J., Amzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
Saul F.;
                                                                                                                MEDLINE-95255298; PubMed-7737190; Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri "Characterization of the two unique human anti-flavin monoclonal immunoglobulins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saul F.;
"The three-dimensional structure of the fab' fragment of a human yeloma immunoglobulin at 2.0-A resolution.";
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Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
Panagiotopoulos N.;
Rotational allomerism and divergent evolution of domains in
immunoglobulin light chains.";
Biochemistry 14:3953-3961(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=75013804; PubMed=4415202;
Fett J.W., Deutsch H.F.;
Farimary structure of the Mog lambda chain.";
Blochemistry 13:4102-4114(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG)
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EMBL, X31754, CAB38569.1, ALT_INIT.
EMBL, X31755, CAA.6049.1, -.
EMBL, X51755, CAA.6049.1, -.
                                                                                                                                                                                                                                                                           3ur. J. Biochem. 228:886-893(1995)
Biochemistry 13:1295-1302(1974)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . Mol. Biol. 210:601-615(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K-RAY CRYSTALLOGRAPHY OF MCG
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PDB; 7FAB; 31-JAN-94.
PDB; 1AQK; 04-FEB-98.
PDB; 1LIL; 15-MAY-97.
Genew; HGNC:5855; IGLC1.
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                                                                                   SEQUENCE
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4 AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA-LQSGNSQESVTEQDSK 62
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                                                     Gaps
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
1711_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE.
MEDILINE=82091105, PubMed=6797414;
Garcia I., Jaton J.-C.;
"The primary structure of the constant region of Basilea-rabbit
                                                                                                                                                                                                                                                                                                                                                                           'n,
                                                                                                                                                                                                                                                                                                                                                        37.7%; Score 208.5; DB 1; Length 105; 40.0%; Pred. No. 3.5e-14; ive 27; Mismatches 31; Indels 5
                                                                                                                                       INTERCHAIN (WITH HEAVY CHAIN)
A -> N (IN MCC+ MARKER).
/FITGEVAR 003898.
S -> T (IN MCC+ MARKER).
/FITG=VAR_003899.
                                                                                                                                                                                                                                                                                                                                                                                                                           63 DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                    62 NNKYAASSYLSLTPEQWKSHRSYSCQVTHEG--STVEKTVAPTEC 104
                                                                                                                                                                     /FTId=VAR 003899.
S -> G (IN KERN+ WARKER).
T TId=VAR 003900.
T -> K (IN WGC+ WARKER).
/FTId=VAR 003901.
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              FTId=VAR 003902
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01-FEB-1991 (Rel. 17, Last sequence update)
15-SEP-2003 (Rel. 22, Last annotation update)
11g lambda chain C region.
Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                          42; Conservative
Genew; HGNC:5856; IGLC2.
Genew; HGNC:5857; IGLC3.
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104
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                              6 PSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS--QESVTEQDSKD 63
                                                                                                                                                                                                                                                                                                                                                                                                                                    6 PSVILFPPSSEELKDNKATLVCLISDFYPRIVKVNWKAD-----GNSVTQGVDTTQPSKQ 60
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01-FBB-1991 (Rel. 17, Last sequence update)
15-SBP-2003 (Rel. 42, Last annotation update)
1g lambda-1 chain (2 region.
Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                           ch 36.8%; Score 203.5; DB 1; Length 105;
l Similarity 44.3%; Pred. No. 1.1e-13;
47; Conservative 15; Mismatches 33; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-87305594; PubMed-3114047; Steen M.L., Hellman L., Pettersson U.; Steen M.L., Hellman L., Pettersson U.; "The immunoglobulin lambda locus in rat consists of two C lambda genes and a single V lambda gene.";
immunoglobulin lambda-chains.";
Biochem. J. 197:177-183(1981).
-!- MISCELLANBOUS: THIS LAMBDA CHAIN EXPRESSES THE C7 ALLOTYPIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 ST--YSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 107
                                                                                                                                                                                                                                                                                          104 104 INTERCHAIN (WITH HEAVY CHAIN)
105 AA; 11484 MW; B427513272E8663D CRC64;
                                                                    -!- SIMILARITY: Contains 1 immunoglobulin-like domain HSSP; P01842; 7FAB.
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-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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InterPro; IPR00110; Ig-like.
InterPro; IPR001369; Ig_Cl.
InterPro; IPR001369; Ig_MHC.
InterPro; IPR0047; Ig_1.
INTERPO; IRR0407; IG_1.
INTERPO; IRR0407; IG_1.
INTERPOSITE; PS50835; IG_LIKE; I.
INTERPOSITE; PS00290; IG_MHC; I.
INTERPOSITE; PS00290; IG_MHC; I.
INTERPOSITE; PS00290; IG_MHC; I.
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HSSP; P01842; 7FAB.
                                                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
Pfam; PP00047; Ig_1.
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Matches 47,
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4 AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA-LQSGNSQESVTEQDSK 62
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                                                                                         ch 34.4%; Score 190; DB 1; Length 104; Similarity 39.0%; Pred. No. 2.4e-12; 41; Conservative 20; Mismatches 38; Indels
                                        INTERCHAIN (WITH HEAVY CHAIN)
CBF71811F4EC878A CRC64;
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104 AA, 11565 MW; (
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ALIGNMENTS

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128 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVOWKVDNALQSGNSQESVTEQD 187
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QNUECT-2002 (TTENBIREL 22, Created)
01-OCT-2003 (TTENBIREL 22, Last sequence update)
01-MAR-2003 (TTENBIREL 23, Last annotation update)
Hypothetical protein.
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Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Score 553; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.7e-49;
Matches 107; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
                                                                                                                                                                                                                                                                                                                                    TISSUB-Lung;
TISSUB-Lung;
TISSUB-Lung;
Strausberg R.;
Strausberg R.;
Submitted (UUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC030813; AAH30813.1;
InterPro; IPR00710; Ig-like.
InterPro; IPR003597; Ig-d.:
InterPro; IPR003597; Ig-d.:
InterPro; IPR003597; Ig-d.:
InterPro; IPR003597; Ig-d.:
SMART; SM00407; IG-1.
SMART; SM00407; IG-1.
SMART; SM00406; IG-V.
PROSITE; PSS0835; IG-IKKE; 2.
PROSITE; PSS0835; IG-IKKE; 2.
PROSITE; PSS08290; IG-MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 234 AA; 25530 MW; 6316E8DEF8D132F8 CRC64;
      234 AA
      PRT;
PRELIMINARY;
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239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Mammary gland;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rissum=colon;
                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q91WS9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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QBR028
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Q91WS9
ID Q9
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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193 SKDSTYSLSSTLTLSKADYEKHKVYAČEVTHQGLSSPVTKSFNRGEČ 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Ling;
Straubberg R.;
Straubberg R.;
Submitteed (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO22352; AH22362.1; -
R InterPro; IPR007110; Ig-11ke.
R InterPro; IPR00306; Ig-W.
R PROPORTY; SW00406; Ig-V.
R PROSITE; SW00406; IG-V: 1.
R PROSITE; PS00399; IG-LIKE; 2.
R PROSITE; PS00399; IG-LIKE; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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TISSUE=Prostate;
Strausberg R.;
Submitted (UUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC030814; AAH30814.1;
InterPro; IPR003101, 19.1ike.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003596; Ig.MHC.
                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lery Match
100.0%; Score 553; DB 4;
ist Local Similarity 100.0%; Pred. No. 1.8e-49;
tches 107; Conservative 0; Mismatches 0;
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SMART; SM00407; 1Gc1; 1.
SMART; SM00407; 1Gc1; 1.
PROSITE; PSC0815; 1G LIKE; 2.
PROSITE; PSC0290; 1G MHC; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2003 (TrEMBLrel. 23,
Hypothetical protein.
                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                       RESULT 2
CONTODO
CONTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                          61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 SKDSTYSMSSTLILITKDEYERHNSYTCEATHKISTSPIVKSFNRNEC 233
Query Match 99.3%; Score 549; DB 4; Length 239; Best Local Similarity 99.1%; Pred. No. 4.7e-49; Matches 106; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SKDSTYSLSSTLTLSKADYBKHKVYACEVTHQGLSSPVTKSFNRGEC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.7%; Score 352; DB 11; Length 22
60.7%; Pred. No. 1.3e-28;
ive 15; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013496; AAH13496.1; -.
InterPro; IPR007110; Ig-11ike.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF0047; ig; 2.
SWART; SM0046; IGV.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NÔN TER 1
SEQÜENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OBR028 PRELIMINARY; PRT; 234 AA. 08R028; CHENBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2003 (TrEMBLrel. 21, Last annotation update) Hypothetical 25.7 kDa protein. Mus musoulus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                             Q91WS9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence)
01-WAR-2003 (TrEMBLrel. 23, Last annotatic
Hypothetical 25.8 kbs protein (Fragment).
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1 RIVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVOWKVDNALQSGNSQESVTEQD
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.7%; Score 352; DB 11; Length 234; Best Local Similarity 60.7%; Pred. No. 1.36-28; Matches 65; Conservative 15; Mismatches 27; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.,
Strausberg R.,
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC027418; AAH57418.1;
InterPro; IPR00710; Ig-like.
InterPro; IPR007006; Ig_MHC.
InterPro; IPR003006; Ig_W.
Pfan; PF0047; Ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00935; IG_MHC; 1.
PROSITE; PS00939; IG_MHC; 1.
PHypothetical protein.
SEQUENCE 234 AA; 25887 MW; 4EB08C91426AEABI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25.7 Kba protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
63.7%; Score 352; DB 11;
Best Local Similarity 60.7%; Pred. No. 1.3e-28;
Matches 65; Conservative 15; Mismatches 27;
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TISSUE=Colon;
                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                   Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 SKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 63.7%; Score 352; DB 11; Length 234; Best Local Similarity 60.7%; Pred. No. 1.3e-28; Matches 65; Conservative 15; Mismatches 27; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
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EMBL; BCD28540; AAH28540.1; -
InterPro; IPR003506; Ig_WHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 2.
SMART; BM00406; IGW; 1.
PROSITE; PR00259; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 234 AA; 25702 MW; 148377F9CICDOABE CRC64;
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; aco15292; AAAH15292.1; ...
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_V.
InterPro; IPR003596; Ig_V.
Flan; PF00047; ig; 2.
SMART; SM00406; IGV; 1.
PROSITE; PS002290; IG MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al protein.
234 AA; 25929 MW; BODOBOEGEB7812D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ol-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25.9 kba protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8R062;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rissum=Colon;
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SEQUENCE 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O91WF8
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Q91WF8
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Q8R062
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 SKDSTYSMSSTLTLTKDBYBRHNSYTCBATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27; Indels
                                                                                                                                                                    Strausberg R.; Submitted (DEC 2001) to the EMBL/GenBank/DDBJ databases. Submitted (DEC 2001) to the EMBL/GenBank/DDBJ databases. InterPro; IPR003006; Ig_MHC. InterPro; IPR003006; Ig_WHC. InterPro; IPR003366; Ig_V. Pfam; PP00047; ig; Z. SMARI; SM00406; IGV; I. PROSITE; PS00290; IG_MHC; I.
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192 SXDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 238

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129 RADAAPTVSIFPPSSEQLISGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 RADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                               Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia: Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.7%; Score 352; DB 11; Length 238; 60.7%; Pred. No. 1.3e-28; ive 15; Mismatches 27; Indels. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 235;
                                                                                                                                                                                                               A Straubberg R.,
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BCO06643, AAH06643.1, -
R InterPro; IPR003100; Ig-like.
R InterPro; IPR003006; Ig-MHC.
R InterPro; IPR003596; Ig-V.
R InterPro; IPR003596; Ig-V.
R Effect; IPR00406; IGV:
R SWART; SW00406; IGV:
R SWART; SW00406; IGV:
R PROSITE; PS00835; IG LIKE; 2.
R PROSITE; PS00290; IG-MHC; 1.
R PROSITE; PS00290; IG-MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strauberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC019760; AAH19760.1; -... InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; 1g; 2. SMART; SM00406; 1Gv; 1. PROSITE; PS02909; 1G MHC; 1. Rypochetical protein. SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;
                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Unknown (Protein for MGC:6582).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 26.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
63.7%; Score 352; DB 11;
Best Local Similarity 60.7%; Pred. No. 1.3e-28;
Matches 65; Conservative 15; Mismatches 27;
 235 AA
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 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 60.79
Matches 65; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                  NCBI_TaxID=10090;
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QBVCI6;
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Q8VCI6
ID Q8VCI6
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1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 SKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ECO020335, AAH02035.1; -.
HSSP; P01679; 2PBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.; Strausberg R.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC021781. AAH21781.1; InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26344 MW; FB2B06A0B801330A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26303 MW; C16119CACA25C337 CRC64;
                                                                                                                   (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8VC55 PRELIMINARY; PRT; 239 AA.
Q8VC55;
Q1-MAR-2002 (TrEMELrel. 20, Created)
O1-MAR-2003 (TrEMELrel. 20, Last sequence update)
O1-MAR-2003 (TrEMELrel. 23, Last annotation update)
Hypothetical 26.3 kDa protein.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.7%; Score 352; DB 11;
60.7%; Pred. No. 1.3e-28;
ive 15; Mismatches 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003056; Ig MHC.
Pfam; PF00047; ig; 2,
SMART: SMORIO; Ig; 1.
PROSITE; PS50335; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                     Hypothetical 26.3 kDa protein.
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SMART, SM00406, IGV; 1.
PROSITE, PS00290, IG MHC; 1.
HYDOCHELICAL Procein.
SEQUENCE 239 AA; 26303 MM
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les 65, Conservative
                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 238 AA; 2
                                                                                                                                                                                                                                                       Mus musculus (Mouse)
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TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                   WCBI_TaxID=10090;
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                                                                                    099M37;
01-JUN-2001 (
01-JUN-2001 (
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                                                             099M37
RESULT 11
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                              099M3
                                                                                              A PACA SERVICE OF THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
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Search completed: January 13, 2004, 12:43:10 Job time : 20.1572 secs
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NON TFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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SEQUENCE
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                                                                   1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVOWKVDNALQSGNSQESVTEQD
          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2002 (TrEMBLrel. 22, Created)
1-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 107
                                                                                                                                                                                                                                            Match 63.7%; Score 352; DB 11; Length 239; Local Similarity 60.7%; Pred. No. 1.4e-28; es 65; Conservative 15; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Breat tumor;

A Strausberg R.,

Strausberg R.,

Submitted (JUN 2002) to the EMBL/GenBank/DDBJ databases.

B Submitted (JUN 2002) to the EMBL/GenBank/DDBJ databases.

EMBL; BC031498; AAH31498.1; -..

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig.

R SMART; SM00409; IG; 2.

R SMART; SM00409; IG; 2.

R SMART; SM00406; IGV; 1.

R PROSITE; PS00260; IGV; 1.

R PROSITE; PS00290; IG MHC; 1.
       27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 239 Aa, 26366 MW, D7BE84398AA341F0 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Kappa light chain of Mab7 (Fragment).
   15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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Best Local S
Matches 65
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QSKOF8
Matches
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108 RADAAPTVSIPPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQD 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OBTCJS PRELIMINARY, PRT; 106 AA.
OBTCJS. (TEMBLrel. 21, Created)
O1-JUN-2002 (TEMBLrel. 21, Last sequence update)
O1-MAR-2003 (TEMBLrel. 23, Last annotation update)
O1-MAR-2003 (TEMBLrel. 23, Last annotation update)
D1-MAR-2003 (TEMBLrel. 23, Last annotation update)
D1-MAR-2003 (TEMBLrel. 23, Last annotation update)
DRESP66J0810.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Eutherla; Primates; Catarrinin; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 SKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKCFNRNEC 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Lymph node;
TISSUE-Lymph node;
Duesterhoeft A., Lauber J., Newes H.W., Weil B., Wiemann Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL713800; CAD28551.1;
InterPro; IPR003110; Ig-like.
InterPro; IPR003597; Ig c1.
single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFF152371; AAD40242.1;
HSSP; P01679; 2PBJ.
                                                                                                                                                                                                                                                                                                                                                                                                214 214
214 AA; 23922 MW; 52BA205FDE995E2A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tch 62.7%; Score 347; DB 11; al Similarity 59.8%; Pred. No. 3.9e-28; 64; Conservative 15; Mismatches 28;
                                                                                                                      InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003506; Ig_V.
Pfam; PF00047; Ig, 2.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00390; IG_MHC; 1.
NON_TER 214 214
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PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
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fusion printiple pot high pot

RSV RSV RSV

RSV RSV

RSV RSV RSV

Title: Perfect score:

Sequence:

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OM protein

Run

Scoring table:

Searched:

DB DB

Minimum | Maximum |

Database

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin G; IgG molecule; human; Fc region; LFA-1 receptor;
disorder; salvage receptor binding epitope; cell adherence interaction;
lymphocyte; T cell inflammatory response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polypeptide(s) that are not Fc fragments and have an increased half-life - are useful for the treatment of LFA-1 mediated disorders
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                                                                     AAE10514
AAE10516
AAE10516
AAE10520
AAE10522
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ABP66583
ABP66585
                                                                                                                                                                                                                                                                                                                                                                    ABP66587
ABP66589
ABP66591
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ABP66595
ABP66597
ABP66601
ABP66605
ABP66605
ABP66605
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AAB83157
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AAW40578;
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Human kappa CL dom
Human kappa light
Human Kappa CL dom
Human kappa protei
Human kappa CL dom
Human kappa CL dom
Sequence of human
Human kappa light
Sequence of human
                                                                                           January 13, 2004, 12:18:44; Search time 24.9511 Seconds (without alignments) 680.681 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                    A Geneseq 19Jun03:*

| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/genseqp-embl/AA1982.DAT:*
| SIDSI/gcgdata/geneseq/genseqp-embl/AA1982.DAT:*
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| SIDSI/gcgdata/geneseq/genseqp-embl/AA1982.DAT:*
| SIDSI/gcgdata/geneseq/genseqp-embl/AA1986.DAT:*
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553
1 RIVAAPSVFIFPPSDEQLKS.......EVTHQGLSSPVTKSFNRGEC 107
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            5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                              1107863 seqs, 158726573 residues
           GenCore version
Copyright (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                   using sw model
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AAW92425
AAB27000
ABG31883
ABB98755
AAP93559
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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                                                                   protein search,
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Result No.

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This protein fragment is derived from a human immunoglobulin kappa CL domain and is used to describe a novel method to produce polypeptides which contain an repitope from the Pc region of an IgG molecule and a mutated salvage receptor binding epitope. They are useful for the treatment of LFA-1 mediated disorders. These are conditions caused by cell adherence interactions involving the LFA-1 receptor on lymphccytes, e.g. rell inflammatory responses. The mutated salvage receptor sequence in the polypeptides means that they have increased in vivo circulatory half-lives when compared to normal Fc regions of IgG molecules.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y protein, useful for treating cancer and for imaging activated stromal fibroblasts in healing wound or inflamed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIVARAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 100.0%; Score 553; DB 19; Length 107; Local Similarity 100.0%; Pred. No. 6.4e-49; es 107; Conservative 0; Mismatches 0; Indels 0.
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                                Disclosure, Fig 2; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY50152 standard; Protein; 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                        107 AA;
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activation protein alpha (RAP). FAP is a cell surface molecule activation protein alpha (RAP). RAP is a cell surface molecule of reactive stronal fibroblast, and its induction is a highly consistent molecular trait of the reactive strona of many types of epithelial cancer. Although F19 may be useful in vitro, e.g., for diagnosis, its applications for in vivo use in humans are problematic as it elicits a human anti-mouse response which reduces the efficacy of the antibody in patients and impairs continued administration. The novel human reshaped F19 was humanised by grafting the murine complementarity determining regions (CDRs) of F19 onto human variable regions to human constant regions. These modifications also result in the improved producibility in eukaryotic cell culture systems as compared to a chimexic antibody having the entire variable regions of F19 joined to human constant regions. The human reshaped F19 antibody has low immunogenicity for humans and is useful for treating cancers e.g., colorectal cancers, non-small cell lung cancers, breast cancers, head and neck cancers and metastatic cancers, bladder cancers, continued standard in the indiamed become of the concers and metastatic cancers. It is also useful for the concert of the concers and metastatic cancers. It is also useful for the concert of the concers and metastatic cancers. It is also useful for the concert of the concert 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       skin or a tumour in a human patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY08745 standard; protein; 107
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97US-0788800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 AA;
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This invention describes a method for preparing a variant Fab or F(ab')2 polypeptide having increased half-life in vivo, where the polypeptide contains an Ig or Ig-like domain comprising a CH1 and/or CL region, is cleared from the kidneys and does not contain an IgG For region. The method involves altering the polypeptide within the CH1 or CL region to incorporate a salvage receptor binding epitope taken from two loops of a CH2 domain of an IgG For region. The polypeptides have a reduced renal Production of antibody fragments with reduced renal clearance - by introducing salvage receptor binding epitope into CH1 or CL region Disclosure; Column 55-58; 38pp; English. (GETH) GENENTECH INC. WPI; 1999-152694/13. Query Match Best Local Simi: Matches 107; (Homo sapiens 14-APR-1995; 14-APR-1995; 23-APR-1999 JS5869046-A 09-FEB-1999 Presta LG, invention AAW92425; Sequence AAW92425 RESULT 쉱 à

95US-0422092

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1 RTVAAPSVEIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWRVDNALQSGNSQESVTEQD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salvage receptor binding epitope; immunomodulator; LFA-1 agonist; mutagenesis; anti-CD18 Fab H52; immunoglobulin; Ig; Crohn's disease; psoriasis; meningitis; allergy; eczema; B-cell lymphoma; wound repair;
                                                                                                                                                                                   1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
clearance rate and an increased circulatory half-life. This sequence represents a human kappa protein CL domain used in the method of the
                                                                                                                                                                                                                                                            61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 107
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                                                                                                           100.0%; Score 553; DB 20;
100.0%; Pred. No. 6.4e-49;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                             AAB27000 standard; Protein; 107
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                                                                                                                                                 Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human kappa CL domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammation, vaccine
                                                                                                                             Similarity
                                                                         107 AA;
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                                     invention
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                                                           focal ischaemic stroke by administering novel anti-CD18 antibody which has cerebroprotective properties. The invention particularly describes a method of treating focal ischaemic stroke caused by the obstruction of a main cerebral artery which comprises administering an anti-CD18 antibody to increase the blood flow or reduce the infarct size, where: (1) the antibody binds to an extracellular domain of CD18 and inhibits or reduces the ability of the cell expressing CD18 too bind too adothellum, (2) the antibody binds CD18 with an affinity of less than 4 nm, or (3) the antibody dissociates CD11b/CD18 complex. This sequence represents the human Kappa-CL domain which is used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody; salvage receptor binding epitope; Fab; F(ab')2; immunoglobulin; CH region; CL region; Kidney; Fc region; CH1 domain; CH2 domain; IgG; kappa protein; renal clearance rate; circulatory half-life.
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                                                                                                                                                                                                                                                                                                                                                                                                       1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
                                             This invention describes a method for improving the clinical outcome in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKDSTYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSPNRGEC 107
                                                                                                                                                                                                                                                                                                                                100.0%; Score 553; DB 20; llarity 100.0%; Pred. No. 6.4e-49; Conservative 0; Mismatches 0;
       Disclosure, Fig 4A-B, 25pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW92425 standard; peptide; 107 AA
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                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                        107 AA;
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half-life of polypeptides The polypeptides comprise an ignorant domain, and a salvage receptor binding opinope within the Igor Ig-like domain, and a salvage receptor binding epitope within the Igor Ig-like domain. The salvage receptor binding taken from two loops of the CTF domain of an Fo region of an Ig molecule. The modified polypeptides are useful for preventing or treating allergic conditions (e.g. eczema), antigen-antibody complex mediated disorders, e.g. Crohn's disease, psoriasis, meningitis, allergic conditions (e.g. eczema), antigen-antibody complex mediated reducing inflammatory responses and inducing tolerance to immunostimulants. They may also be used in diagnostic assays. The nucleic acids and modified polypeptides are useful for the passive immunisation of patients, as well as for affinity purification of an antigen from recombinant cell culture or natural sources.
                                                                                                           New nucleic acid encoding new modified polypeptides with increased circulatory half-life useful for preventing/treating LFA-1-mediated disorders, e.g. reducing inflammatory responses or inducing tolerance to immunostimilans -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence was used in a method for improving the in vivo
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WPI; 2000-610925/58.
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1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC

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(first entry)

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ABB98755 standard; Protein; 107
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                                           RTVAAPSUFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
                                                                RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Increasing cerebral blood flow and/or reducing infarct size in focal ischaemic stroke using anti-CD18 antibody and tissue plasminogen activator is useful to improve clinical outcome in acute ischaemic
                                                                                                                                                                                                                                                                      focal ischaemic stroke; main cerebral artery;
tissue plasminogen activator; anti-CD18 antibody; stroke;
acute ischaemic stroke; thrombolytic therapy; thromboembolic stroke.
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  Length 107;
                                                                                      SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
                                                                                                   SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
                                                                                                                                                                                                                                                            cerebral blood flow; infarct size;
                      Indels
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0; Mismatches 0;
100.0%; Score 553; DB 21;
100.0%; Pred. No. 6.4e-49;
iive 0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 107; Conservative 0;
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99US-0251652.
97US-0788800.
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                                                                                                                                                                                                               (first entry)
          al Similarity 100.
107; Conservative
                                                                                                                                                                                                                                                          Human; kappa CL domain;
focal ischaemic stroke;
                                                                                                                                                                                                                                    Human kappa CL domain.
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Query Match
Best Local S:
Matches 107
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                                                                                                                                                                                         ABG31883;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of a humanized antibody which specifically binds to fibroblast activation protein alpha for manufacturing a medicament for treating
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                                                                 Human, cytostatic; antitumour; immunosuppressive; antiallergic; humanised; antibody; fibroblast activation protein alpha; FAPalpha; cancer; monoclonal antibody F19; colorectal cancer; non-small cell lung carcinoma; breast cancer; pancreatic cancer; tumour; systemic autoimmune disease; allergy; light chain;
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100.0%; Score 553; DB 24;
Best Local Similarity 100.0%; Pred. No. 6.4e-49;
Matches 107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INGELHEIM INT GMBH.
INGELHEIM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tanswell P;
Human kappa light constant chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 55; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-APR-2002; 2002WO-EP04041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-APR-2001; 2001US-283868P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amelsberg A, Scott A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-058609/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BOEH ) BOEHRINGER
(BOEH ) BOEHRINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABV74601
                                                                                                                                                                                                                                                                                                                                                                                                       WO200283171-A2
                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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The invention relates to a compound which comprises a target cell-specific portion, comprising an humanised monoclonal antibody, having specificity for polymorphic epithelial mucin (FBM) or its antigen binding fragment and a cyctoxic portion having endonucleolytic activity, exemplified by AAMS2184-AAMS2188 and encoded by ABA02682-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 146
                                                                                                                                                                                                                                      Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel compound used to treat cancer has target cell-specific portion comprising humanised monoclonal antibody having specificity for polymorphic epithelial mucin, and cytotoxic portion having endonucleolytic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; P-selectin ligand; glycoprotein; fusion protein; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-selectin ligand and kappa chain constant region fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKDSTYSLSSTLTLSKADYBKHKVYACEVTHQGLSSPVTKSFNRGEC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNKGEC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 100.0%; Score 553; DB 22; Local Similarity 100.0%; Pred. No. 1.3e-48; les 107; Conservative 0; Mismatches 0;
                                                                                  AAM52145 standard; Protein; 193 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Figure 3; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY29770 standard, Protein, 201 AA
                                                                                                                                                                                                 Humanised HMFG1 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-APR-2000; 2000GB-0008049.
02-OCT-2000; 2000US-237159P.
                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2001; 2001WO-GB01324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ANTI-) ANTISOMA RES LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-662969/76
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                                                                                                                                                                                                                                                                                                                                    WO200174905-A1.
                                                                                                                                                              05-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                           11-0CT-2001
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                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                       AAM52145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Young RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                             RESULT 9
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ID AAY2
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AC AAY2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           It is employed in the prepn. of CD4 fusions. The insert site is given in the Features Table. CD4 fusion proteins can have antiviral and fimunomodilatory activity are esp. useful for treating HIV infections, regardless of genetic variation within the virus. They and antibodies raised against them can also be used diagnostically for assaying adhesons and their ligands.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid sequences encoding adheson, esp. CD4, variants -
partic. with trans-membrane domain inactivated or fused to other
peptide, useful esp. for treating HIV infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 143;
                      SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="light variable and joining"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 553; DB 10;
100.0%; Pred, No. 9.2e-49;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                       Sequence of human kappa light chain fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and their ligands. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38..38
/note="light constant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example, Figure Fig 5, 78pp, English
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37..38
/note="insert site"
                                                                                                                                 AAP93559 standard; protein; 143 AA
                                                                                                                                                                                                                                                                                                          HIV; antiviral; therapy; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88WO-US03414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87US-0104329
88US-0250785
                                                                                                                                                                                                             (updated)
(first entry)
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/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gregory TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1989-114397/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAP93559.
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-OCT-1987;
28-SEP-1988;
                                                                                                                                                                                                           25-MAR-2003
28-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO8902922-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Capon DJ,
61
                                                                                                                                                                        AAP93559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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diabetes; transplant rejection; myocardial infarction; thermal injury; metastratic condition; autoimmune thyroiditis; multiple sclerosis; Reynaud's syndrome; neutrophilic dermatosis; Sweet's syndrome; Grave's disease; glomerulonephritis; gingivitis; periodontitis; Crohn's disease; necrotising enterocolitis.
                                                                                                                                                                                                                                                   New P-selectin ligand fusion proteins, used for treating e.g. inflammation, infections, asthma, diabetes, ulcerative colitis or
inflammation; intercellular adhesion; ulcerative colitis;
                                                                                                                                                                                            Kumar
                                                                                                                                                                                           Camphausen R, Chang X, Cumming D, Davis M,
Larsen GR, Sako DS, Shaw G, Veldman GM;
                                                                                                                                                                                                                                                                                         Claim 66; Page 128-129; 145pp; English
                                                                                                                                                      98US-0032080.
                                                                                                                                    99WO-US04302.
                                                                                                                                                                        (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                       transplant rejection
                                                                                                                                                                                                                      WPI; 1999-527628/44.
                                                                                                                                                                                                                                N-PSDB; AAZ08843
                                                                   sapiens.
                                                                                             WO9943834-A2.
                                                                                                                                                     27-FEB-1998;
                                                                                                                02-SEP-1999
                                                                            Synthetic.
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The present invention describes P-selectin ligand fusion proteins comprising amino acids 42-60, 42-402, 42-310, 42-88, 42-118 or 42-189 or february amino acids 42-60, 42-402, 42-310, 42-88, 42-118 or 42-189 or february amino acids 42-60, 42-402, 42-310, 42-88, 42-118 or 42-189 or february amino acids a ligand for P-selectin number ondothelial cells and platelets. The isolated P-selectin ligand proteins may be useful in treating conditions characterized by P., E. or L-selectin mediated intercellular adhesion e.g. myocardial infarction, metastatic conditions, inflammatory disorders, thermal injury such as burns or frostbite, autoimmune thyroiditis, experimental allorgic encephalomylelits, multiple sclerosis, multiple organ injury syndrome secondary to trauma, diabetes, Reynaud's syndrome, corgan injury syndrome secondary to trauma, diabetes, Reynaud's syndrome, neutrophilic dermatosis (Sweet's syndrome). Inflammatory bowel disease, drawe's disease, glomerulomephitis, gingivitis, periodonitis, haemolytic uraemic syndrome, ulcerative colitis, crohn's disease, or cytokine-induced toxicity. Isolated P-selectin ligand proteins may also be useful in organ transplantation, both to prepare organs for transplantation and to quell organ transplant rejection. Peslectin ligand proteins can be used to treat haemodialysis and leukophoresis patients or used as an antimetastatic agent. The fusion proteins can also be used to treat haemodialysis and leukophoresis patients or used as an antimetastatic agent. The fusion proteins can be used for the production of antibodies for use in therapy, detection, diagnosis and drug screening. AAZ08839 to AAZ08850 enocde specifically alven in AAZ0866 to AAX29777.

201 AA; Sequence

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95 RIVAAPSVFIFPPSDEQLKSGTASVVCLLINNFYPREAKVQWKVDNALQSGNSQESVTEQD 154
                                                                                                         1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
                                                        .
0
100.0%; Score 553; DB 20; Length 201; 100.0%; Pred. No. 1.4e-48; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                            61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 107
Query Match
Best Local Similarity 100.
Matches 107; Conservative
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155 SKDSTYSLSSTLTLSKADYEKHVYACEVTHQGLSSPVTKSFNRGEC

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The present invention describes an Bscherichia coll strain (I) deficient in Chromosomal deep and prc encoding protease DegP and Prc, respectively, and harbouring a mutant spr gene, the product of mutant spr gene suppresses growth phenotypes exhibited by strains harbouring prc mutants. Coll is useful for producing a polypeptide, by culturing (I) comprising nucleic acid encoding the polypeptide, by culturing (I) comprising nucleic acid that the nucleic acid is expressed, and recovering the pertach such that the nucleic acid is expressed, and recovering the heterologous polypeptide from the strain. The heterologous polypeptide is proteolytically sensitive. Culturing of (I) is performed in a fermentor under conditions of high- or low-cell density fermentation. The polypeptide is an antibody (humanised or full-length artibody) or Apo2 ligand. The antibody (humanised or full-length anti-vascular endothelial growth factor (VBGF), anti-tissue factor, 2C4, anti-tasue antibody is also an antibody is an antibody is also an antibody fragment having a light chain (kappa light chain). The antibody fragment having a light chain (kappa light chain). The antibody fragment tayer fusion, anti-CD1a antibody is also an antibody fragment taying a light chain (kappa light chain). The antibody fragment tissue factor Fab'. Pab', anti-tissue factor Fab'2 or                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel Escherichia coli strain useful for producing polypeptide, deficient in degP and prc encoding protease, and harboring mutant spr gene, product of gene suppresses growth phenotypes of strains harboring
                                                                                                                                                                                                                                     Bacterial host, protease, degP, prc, spr, anti-VEGF antibody, anti-Dody, humanised, Apo2 ligand, anti-CD18, anti-tissue factor, 2C4, anti-CD20, anti-vascular endothelial crowth factor;anti-Her-2, anti-CD40, Fab, anti-CD11a, Fab'; Fab'2, Fab'2-leucine zipper fusion, anti-VEGF Fab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 553; DB 23; Length 212; Best Local Similarity 100.0%; Pred. No. 1.5e-48; Matches 107; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                     Humanised anti-CD18 kappa LC sequence SEQ ID NO:5.
                            ABP51955 standard; Protein; 212 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 10; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-DEC-2001; 2001WO-US47581.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-DEC-2000; 2000US-256162P
                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-583522/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200248376-A2.
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                    09-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prc mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                             ABP51955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen CY;
ABP51955
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1 RIVAAPSVFIFPFSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD

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RESULT 12

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High potency recombinant antibody, useful for preventing and treating diseases induced or caused by viruses, especially respiratory syncytial virus and parainfluenza virus, has high kinetic association rate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a high potency antibody including its immunologically active portions, fragments and segments other than vitaxin. The antibody has increased potency, high rate constant for antibody-antigen complex formation and high affinity for any desirred antigen. The high potency antibody is also useful for nullifying or ameliorating the effects of addictive drugs, such as cocaine. The high potency has specificity for antigenic determinants found on microbes such as viruses, bacteria or fungi, antigens found on cancer cells and toxic substances or product of toxic substances. The high potency antibody is useful for preventing or treating a disease caused by a virus such as respiratory syncytial virus (RSV) and parantilemenza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 RTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RTVAAPSVFIFPPSDEQLKSGTASVVCLINNFYPREAKVQWKVDNALQSGNSQESVTEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   virus (PIV). The present sequence is humanised high potency antibody full length light chain variable region.
                                                                                                                                                                                                                         Human, light chain; respiratory syncytial virus infection; virucide
parainfluenza virus; therapy; high potency antibody; drug; cocaine;
cancer cell; toxic substance.
                                                                                                                                                                                 Humanised high potency antibody clone 25 full length light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wu H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 553; DB 22; Best Local Similarity 100.0%; Pred. No. 1.5e-48; Matches 107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Huse WD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 23; Page 75-76; 98pp; English.
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                                                  AAE10510 standard; Protein; 213
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ID AAE10512 standard, Protein; 213
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AC AAE10512;
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                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Young JF, Koenig S,
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         RESULT 13
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106 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Production of recombinant antibodies (Ab), Ab fragments or Ab fragment/enzyme fusion proteins can be used for tumour therapy, cospecially when the fusion protein comprises a tumour specific of the fragment and an enzyme capable of converting a non-toxic prodrug to a toxic drug. The fusion proteins are constructed in expression converting an expression proteins are constructed in expression products to be isolated in a soluble functional allowing expression products to be isolated in Soluble functional form without renaturation. The Ab fragment is an PAb fragment or an antigen binding region. In the fusion protein, the Ab component is humanised and the enzyme component is a human cytoplasmic enzyme. This fusion protein comprises the antibody constant and variable light chain regions.
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protein - by cytoplasmic expression in thio.redoxin.reductase
deficient E. coli
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                                                                       166 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 212
                                             SKDSTYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 107
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(first entry)
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14-FEB-1997
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AAW04301

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Watkins JD;

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Gaps

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Indels

Length 213;

166 9

Best Loca Matches

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High potency recombinant antibody, useful for preventing and treating diseases induced or caused by viruses, especially respiratory syncytial virus and parainfluenza virus, has high kinetic association rate
                                                                                                                                                       Human, light chain, respiratory syncytial virus infection, virucide, parainfluenza virus; therapy, high potency antibody; drug; cocaine; cancer cell; toxic substance.
                                                                              Humanised high potency antibody clone 26 full length light chain.
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    10-DEC-2001 (first entry)
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NAME OF THE PROPERTY OF THE PR
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Watkins JD;

Wu H,

Huse WD,

The invention relates to a high potency antibody including its immunologically active portions, fragments and segments other than vitaxin. The antibody has increased potency, high rate constant for antibody-antigen complex formation and high affinity for any desired antigen. The high potency antibody is also useful for nullifying or meliorating the effects of addictive drugs, such as cocaine. The high potency has specificity for antigenic determinants found on microbes such as viruses, bacteria or fungi, antigens found on cancer calls and toxic substances or product of toxic substances. The high potency antibody is useful for preventing or treating a disease caused by a nitus (PUV). The present sequence is humanised high potency avirus (PUV). The present sequence is humanised high potency antibody full length light chain variable region. 213 AA; Sequence Query Match

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Gaps • 100.0%; Score 553; DB 22; Length 213; 100.0%; Pred. No. 1.5e-48; ive 0; Mismatches 0; Indels 0; Best Local Similarity 100. Matches 107; Conservative

1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60

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AAE10514 standard; Protein; 213 AA.

AAE10514;

10-DEC-2001 (first entry)

Humanised high potency antibody clone 18 full length light chain.

Human; light chain; respiratory syncytial virus infection; parainfluenza virus; therapy; high potency antibody; drug;

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107 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
                                                                                                                                                                                                                                                                                                                                                         High potency recombinant antibody, useful for preventing and treating diseases induced or caused by viruses, especially respiratory syncytial virus and parainfluenza virus, has high kinetic association rate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a high potency antibody including its immunologically active portions, fragments and segments other than vitaxin. The antibody has increased potency, high rate constant for antibody-antigen complex formation and high affainty for any desired antigen. The high potency antibody is also useful for unliking or potency has specificity for antigenic determinants found on microbes such as viruses, bacteria or fungi, antigens found on cancer cells and toxic substances or product of toxic substances. The high potency antibody is useful for preventing or treating a disease caused by a viruse such as respiratory syncytial virus (RSV) and parainfluenza virus (PIV). The present sequence is humanised high potency antibody light chain variable region.
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Job time : 24.9511 secs
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                                                                                                                                                                                                                                                                                  Johnson LS,
cancer cell; toxic substance
                                                                                                                                                                  01-MAR-2001; 2001WO-US06815.
                                                                                                                                                                                                         01-MAR-2000; 2000US-0186252
                                                                                                                                                                                                                                           (MEDI -) MEDIMMUNE INC
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                                      sapiens
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Sequence 42, Appl Sequence 44, Appl Sequence 46, Appl Sequence 50, Appl Sequence 51, Appl Sequence 21, Appl Sequence 213, Appl Sequence 213, Appl Sequence 213, Appl Sequence 213, Appl Sequence 219, Appl Sequence 219, Appl Sequence 221, Appl Sequence 221, Appl Sequence 221, Appl Sequence 223, Appl Sequence 223, Appl Sequence 231, Appl Sequence 251, Appl

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APPLICANT: Bednar, Martin M.
Thomas, G. Roger
Gross, Cordell E.
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: Winbatin (Genericch)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/811,384
FILING DATE: 20-DGC-200
CLASSIFICATION ED ATA:
APPLICATION NUMBER: 09/251652
FILING DATE: 17-FEB-200
APPLICATION NUMBER: 08/788800
FILING DATE: 22-JAN-1997
APPLICATION NUMBER: 60/093038
FILING DATE: 23-JAN-1996
ATTORNEY/AGRIT INFORMATION:
US-09-796-848A-44

US-09-796-848A-44

US-09-796-848A-46

US-09-796-848A-50

US-09-796-848A-50

US-09-796-848A-50

US-09-796-848A-51

US-09-996-288-213

US-09-996-288-213

US-09-996-288-213

US-09-996-288-213

US-09-996-288-223

US-09-996-288-223

US-09-996-288-223

US-09-996-288-223

US-09-996-288-223

US-09-996-288-233

US-09-996-288-245

US-09-996-288-245

US-09-996-288-245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Love, Richard B.
REGISCHATTON WUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1729C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09811384
Patent No. US20020081294A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      001
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   Sequence 97, Appl Sequence 99, Appl Sequence 166, Appl Sequence 168, Appl Sequence 99, Appl Sequence 18, Appl Sequence 18, Appl Sequence 17, Appl Sequence 77, Appl Sequence 77, Appl Sequence 77, Appl Sequence 38, Appl Sequence 18, Appl Sequence 1
                                                                                                                    ; Search time 17.1013 Seconds (without alignments) 1260.812 Million cell updates/sec
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1 RTVAAPSVFIFPPSDEQLKS......EVTHQGLSSFVTKSFNRGEC 107
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US -09-990-586-99
US -10-190-586-99
US -10-113-168
US -10-310-113-168
US -10-310-880-99
US -10-36-709-54
US -10-36-709-54
US -10-36-805-67
US -10-320-231A-77
US -10-320-231A-77
US -09-796-848A-38
US -09-796-848A-38
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Maximum Match 100%
Listing first 45 summaries
                                                                                    protein search, using sw model
                                                                                                                    January 13, 2004, 12:43:20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match ]
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Perfect score:
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No.
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Length 107;

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APPLICANT: Park, John E.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Bamberger, Use
APPLICANT: Saldanta, Jose W.
APPLICANT: Saldanta, Jose W.
APPLICANT: Saldanta, Jose W.
TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility
TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility
FILE REFERENCE: 0562.1890002
CURRENT APPLICATION NUMBER: US/10/159,006
CURRENT FILING DATE: 1090-04-29
PRIOR FILING DATE: 1990-04-29
PRIOR PELICATION NUMBER: EP 98107925.4
PRIOR PELICATION NUMBER: US 60/086,049
PRIOR PELING DATE: 1990-04-30
PRIOR PELING DATE: 1990-05-18
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1958 OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
THROMBOSES
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100.0%; Score 553; DB 11;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0;
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APPLICANT: WONG, HING C.
APPLICANT: NIEVES, ESPERANZA LILIANA
APPLICANT: MOSQUERA, LUIS A.
TITLE OF INVENTION: USE OF ANTI-TISSUE
TITLE OF INVENTION: THROMBOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 166, Application US/10310113 Publication No. US20030176664A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/10159006 Publication No. US20030143229A1
; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 99; LBNGTH: 107; TYPE: PRT; TYPE: PRT; CRGANISM: Homo sapiens US-09-990-586-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 107
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ORGANISM: Homo sapiens
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Publication No. US20030109680A1
GENERAL INFORMATION:
APPLICANT: JIAO, JIN-AN
APPLICANT: WONG, HING C.
TITLE OF INVENTION: ANTIBIOLIES FOR INHIBITING BLOOD COAGULATION AND METHODS
TITLE OF INVENTION: OF USE THEREOF
FILE REFERENCE: 71758/46943-CIP2
CURRENT APPLICATION NUMBER: US/09/990,586
CURRENT FILING DATE: 2001-11-21
PRIOR PPLICATION NUMBER: 09/293,854
PRIOR APPLICATION NUMBER: 09/293,854
PRIOR PELING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PALENTIN Ver. 2.1
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Publication No. US20030109680A1
GENERAL INFORMATION:
APPLICANT: JIAO, JIN-AN
APPLICANT: WONG, HING C.
TITLE OF INVENTION: OF USE THEREOF
FILE REFERENCE: JTAS946434-CIP2
CURRENT APPLICANTION: OF USE THEREOF
FILE REFERENCE: JTAS946434-CIP2
CURRENT APPLICATION UMBER: US/09/990,586
CURRENT FILING DATE: 2001-11-21
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                                                                                                                                                                                                                                                                                            Length 107;
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100.0%; Score 553; DB 9;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0;
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Pred. No. 6
                                                                                                                                                                              TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                   LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
   TELEPHONE: 650/225-5530
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                               TELEFAX: 650/952-9881
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al Similarity 100.0%;
107; Conservative 0
                                                        INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS
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PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 102
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TYPE: PRI
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 107; Conserv
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Length 107;

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Sequence 99, Application US/10230880 Publication No. US20030190705A1 GENERAL INFORMATION:
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US-10-230-880-97
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US-10-230-880-99
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Publication No. US20030176664A1

GENERAL INFORMATION:

APPLICANT: JIAO, JIN-AN

APPLICANT: MONG, HING C.

APPLICANT: NIEVES, ESPERANZA LILIANA

APPLICANT: NIEVES, ESPERANZA LILIANA

TITLE OF INVENTION: THROMBGSE

TITLE OF INVENTION UNDER: 00/990,586

PRIOR FILING DATE: 2001-11-21

PRIOR APPLICATION NUMBER: 00/343,306

PRIOR APPLICATION NUMBER: 09/990,416

PRIOR PILING DATE: 1999-04-16

PRIOR FILING DATE: 1999-04-16

PRIOR FILING DATE: 1999-03-10

NUMBER OF SEQ ID NOS: 169

SOFTWARE: PRECHIN Ver. 2.1

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Pred. No. 6.5e-53;
Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 107;
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FILE REFERENCE: 58122(71758)
CURRENT APPLICATION NUMBER: US/10/310,113
                           CURRENT APPLICATION NUMBER: US/10/310, 1
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 09/990,586
PRIOR FILING DATE: 2001-11-21
PRIOR PELING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-29
PRIOR PILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 09/293,854
PRIOR APPLICATION NUMBER: 09/10-06
PRIOR PILING DATE: 1997-03-10
NUMBER OF SEQ ID NOS: 169
SOFTWARE: PREENTIN Ver: 2.1
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Best Local Similarity 100.0%;
Matches 107; Conservative 0
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CRGANISM: Homo sapiens
US-10-310-113-166
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US-10-310-113-168
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1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
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APPELICANT: WINGON, JEFPER L.

APPLICANT: STINSON, JEFPER L.

APPLICANT: STINSON, JEFPER L.

APPLICANT: STINSON, JEFPER L.

TITLE OF INVERTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES

FILE REFERENCE: 71758/58066

CURRENT APPLICATION NUMBER: US/10/230,880

CURRENT PAPLICATION NUMBER: 09/990,586

PRIOR FILING DATE: 2001-11-21

PRIOR FILING DATE: 2001-11-21

PRIOR FILING DATE: 2001-11-21

PRIOR FILING DATE: 2001-11-22

PRIOR PILING DATE: 1999-04-16

NUMBER OF SEQ ID NOS: 174

SOFFWARE: Patentin Ver. 2.1

SEQ ID NO 99

TENNITH: 107
APPLICANT: WONG, HING C.
APPLICANT: WONG, HING C.
APPLICANT: WONG, HING C.
APPLICANT: STINSON, JEFFREY L.
APPLICANT: MOSQUERA, LUIS A.
TITLE OF INVENTION: MITHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
FILE REFERENCE: 71759/5806
CURRENT APPLICANTON NUMBER: 03/990,886
PRIOR PILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-11-21
PRIOR PLLING DATE: 2001-11-29
PRIOR PLLING DATE: 2001-10-29
PRIOR PLLING DATE: 2001-10-29
PRIOR PLLING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PATENTIN VET: 2.1
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100.0%; Score 553; DB 12;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0;
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100.0%; Score 553; DB 12;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 107; Conservative
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US-10-269-805-67
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ORGANISM: Artificial
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; Publication No. US200301039681
; Publication No. US200301039681
; APPLICANT: Boehringer Ingelheim International GmbH
APPLICANT: Boehringer Ingelheim Pharmaceuticals, Inc.
TITLE OF INVENTION: Cancer treatment by using FAP-alpha specific antibodies
FILE REFERENCE: 1.1203f; US/10/121,464
; CURRENT FILING DATE: 2002-11-15
; PRIOR PLICATION NUMBER: US 60/283,868
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 107
                                                                                                                                                                                                                           Sequence 54, Application US/10366709

Publication No. US2030219433A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HANSEN, HANS
APPLICANT: QCLENBERG, DAVID M.
TITLE OF INVENTION: MATH-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
TITLE OF INVENTION: MATH-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
TITLE OF INVENTION: MATH-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
TITLE OF INVENTION: MATH-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
TITLE OF INVENTION: MATH-CD20 ANTIBODIES AND FUSION PROTEINS THEREOF AND
TITLE OF INVENTION NUMBER: US/10/366,709
CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 60/356,132
PRIOR APPLICATION NUMBER: 60/416,232
PRIOR APPLICATION NUMBER: 60/416,232
NUMBER OF SEQ ID NOS: 55
SOCTUMENT PLING DATE: 2002-10-07
SEQ ID NO 5: 55
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1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 107;
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                                                       61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
                                                                                                      SKDSTYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 107
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100.0%; Score 553; DB 15;
Best Local Similarity 100.0%; Pred. No. 6.5e-53;
Matches 107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 553; DB 12;
100.0%; Pred. No. 6.5e-53;
tive 0; Mismatches 0;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 107; Conservative
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CRGANISM: Homo sapiens
US-10-366-709-54
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US-10-121-464-18
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Sequence 71, Application US/10320231A
| Sequence 71, Application No. US20030194405A1
| Publication No. US20030194405A1
| Publication No. US20030194405A1
| GENERAL INFORMATION:
| APPLICANT: Nobem, Steven
| APPLICANT: Tomkinson, Adrian
| TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For TITLE OF INVENTION: Treatment Of Asthma | TITLE OF INVENTION: Treatment Of Asthma | FILE REFERENCE: 7430*163 | CURRENT APPLICATION NUMBER: US/10/320,231A | CURRENT APPLICATION NUMBER: US/0/342,174 | PRIOR FILING DATE: 2001-12-17 | NUMBER OF SEQ ID NOS: 85 | SOFTWARE: Patentin version 3.2 | SEQ ID NO 77 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | LEARTH APPLICATION NUMBER OF SEQ ID NOS: 85 | 
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                                                                                                  1 RIVAAPSVFIFFPEDBOLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
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1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
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                                                                                                                                                                                                                              61 SKDSTYSLSSTLTLSKADYBKHKVYACEVTHQGLSSPVTKSFNRGEC 107
                                                                                                                                                                                                                                                                                                                                       61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NESOUR IN THE REPERBY OF A PAPLICATION US/10269805
; Sequence 67, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INPORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERBNCE: A-722
CURRENT FILING DATE: 2002-10-10
; PRIOR PILICATION NUMBER: US 60/328,604
; PRIOR PILICATION NUMBER: US 60/328,604
; ROWERRE POF SEQ ID NOS: 76
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 67
; LENGTH: 107
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Best Local Similarity 100.0%; Pred. No. 1.5e-52;
Matches 107; Conservative 0; Mismatches 0;
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167 SKDSTYSLSSTLTLSKADYEKHKVYACEVIHQGLSSPVTKSFNRGEC 213
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Sequence 38, Application US/09796848A

Settle No. US20020098189A1

GENERAL INFORMATION:
APPLICANT: Young, James F.
APPLICANT: Huse, William D.
APPLICANT: Wu, Herren
APPLICANT: Wu, Herren
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
TITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
TITLE OF INVENTION WIMBER: US-001-10-00
FILE REFERENCE: 469201-52
CURRENT FILING DATE: 2000-10-03-01
SEQUENCE PRICATION NUMBER: US-001-10-03-01
SEQUENCE PRECOMBINE P
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US-09-796-848A-38
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Best Local Similarity 100.0%; Score 553; DB 9; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.5e-52;
Matches 107; Conservative 0; Mismatches 0; Indels C
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                                                                                                  61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
                                                                                                                                         166 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 212
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                                                                                                                                                                                                                                                                                                                 US-10-011-125-5
; Sequence 5, Application US/10011125
; Sequence 5, Application US/10011125
; Publication No. US20020142388A1
; Publication No. US2002014238BA1
; APPLICANT: Chen, Christina Yu-Ching
APPLICANT: Chen, Christina Yu-Ching
; TITLE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125
; PRIOR FILING DATE: 2001-12-07
; PRIOR FILING DATE: 2000-12-14
; SEQ ID NO 5
; LENGTH: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sequence is synthesized.
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106 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 165

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RESULT 15	
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; Sequence 40, Application US/09796848A	
; Patent No. US20020098189A1	
; GENERAL INFORMATION:	
Young, James F.	
, APPLICANT: Johnson, Leslie S.	
; APPLICANT: Huse, William D.	
, APPLICANT: Wu, Herren	
OF INVENTION: B	
; TITLE OF INVENTION: Producing Them	
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APPLICATION N	
; PRIOR FILING DATE: 2000-03-01	
; NUMBER OF SEQ ID NOS: 59	
; SOFTWARE: Patentin Ver. 2.1	
; SEO ID NO 40	
LENGTH: 213	
ORGANISM: Artificial Sequence	
COTHER INFORMATION: Description of Artificial Sequence: Light chain of	
OTHER INFORMATION: high potency antibody.	
US-109-140	
100.0%; Score 553;	
Best Local Similarity 100.0%; Fred. No. 1.56-52; Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps	0
ON THY A PSYPIPPSDBOLKSGTASYVCLLNNFYPREAKVOWKYDNALQSGNSQESVTEQD 60	_
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DD 107 RIVAAPSVFIFP?SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166	
Ov 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107	
DD 167 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213	
Search completed: January 13, 2004, 13:13:46	

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1 RIVAAPSVPIFFPSDEQLKSGTASVVCLINNFYPREAKVQWKVDNALQSGNSQESVIEQD
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Sequence 8, Application US/08422101

GENERAL INFORMATION:

APPLICANT: Leonard Presta

CORRESPONDERS: 31

CORRESPONDERS: 31

COUNTRY: California

COUNTRY: USA

ZITP: 94080

COUNTRY: USA

ZITP: 94080

CONFUTER: LBW PC compatible

COMPUTER: LBW PC compatible

CORPUTER: Datin (Genenech)

CURRATING SYSTEM: USA/MS-DOS

SOFTWARE: DATIN (Genenech)

CURSIFICATION NUMBER: US/08/422,101

FILING DATE: LA-ARR-1995

CURASIFICATION: SAN
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100.0%; Score 553; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels
                   US-09-680-148-1
US-09-280-942A-6
US-09-210-2417-264-11
US-09-417-264-11
PCT-US93-07832-24
PCT-US93-07832-39
PCT-US93-07832-39
US-08-887-3528-13
US-08-887-3528-17
US-08-887-3528-19
US-08-887-3528-19
US-08-887-3528-19
US-08-887-3528-19
US-08-466-151-9
US-08-466-151-9
US-09-109-207C-13
US-09-109-207C-13
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFRENCE/DOCKET NUMBER:
REFRENCE/DOCKET NUMBER:
TELESPHONE: 415/225-1994
TELESPX: 910/371-7168
INPORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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US-08-422-101-8
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Agentence 8, Agentence 8, Agentence 20, Agentence 12, Sequence 12, Sequence 13, Sequence 11, Sequence 11, Sequence 11, Sequence 12, Sequence 24, Sequence 24, Sequence 26, Agentence 26
                                                                                                                                                                                                                                                                                 RTVAAPSVFIFPPSDEQLKS......EVTHQGLSSPVTKSFNRGEC 107
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Sequence 24,
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                5.1.6
Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-437-642B-39
US-08-437-642B-40
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                                                                                                                                                                                                                                                                                                                                                                                            328717 segs, 42310858 residues
                version -
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Maximum Match 100%
Listing first 45 summaries
                                                                                                      protein search, using sw model
                                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                GenCore (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
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553
1 RTVAAPSVFIFPPSI
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Perfect
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No.
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ынык: US/08/788,800
22-Jan-1997
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08788800 Patent No. 5914112
                                                                                                                                                                                                                                                                                                                                                                                                                                          TANAME: LEE, WEIGY M.
REGISTRATION NUMBER: 932
REFERENCE/DOCKET NUMBER: 932
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/252-994
TELERA: 415/252-9981
TELERA: 910/371-7168
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 107 amino acids
amino acid
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Best Local Similarity 100.
Matches 107; Conservative
NUMBER OF SEQUENCES:
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  1 RTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
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                                                                                                                                                                        Sequence 8, Application US/08422091
; Sequence 8, Application US/08422091
; Patent No. 5747035
; GENERAL INFORMATION:
    APPLICANT: Leonard Presta
    APPLICANT: Leonard Presta
    APPLICANT: Leonard Presta
    APPLICANT: Altered Polypeptides with Increased
    TITLE OF INVENTION: Altered Polypeptides with Increased
    TITLE OF INVENTION: Half-Life
    NUMBER OF SEQUENCES: 31
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Genentech, Inc.
    STREET: 460 Point San Bruno Blvd
    CITY: South San Francisco
    STATE: California
    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 107;
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                                               61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
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APPLICANT: Brad Snedecor
TITLE OF INVENTION: Altered Polypeptides with Increased
TITLE OF INVENTION: Half-Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 553; DB 1;
; Pred. No. 4.9e-57;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATIN (Genentech)
APPLICATION DATA:
APPLICATION NUMBER: US/08/422,091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UMBER: US/08/422,091
14-APR-1995
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Patent No. 5869046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 932
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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ATTORNEY/AGENT INFORMATION
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Best Local Similarity 100.
Matches 107; Conservative
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 14-APR-1
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
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APPLICANT: Bednar, Martin M.
APPLICANT: Thomas, G. Roger
APPLICANT: Gross, Cordell E.
TITLE OF INTENTION: ANTI-CD18 ANTIBODIES IN STROKE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE 15
CORRESPONDENCE ADDRESS:
ADDRESSES: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; DB 2;
4.9e-57;
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: Gouth San Francisco
COUNTRY: Gouth San Francisco
COUNTRY: Gouth San Francisco
COUNTRY: Gouth San
EDING TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: DATIN (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 14-APR-1995
CLAGSIFICATION DATA:
APPLICATION NUMBER:
FILING DATE: H-APR-1995
FILING DATE: FILING DATE:
ATTORNEY AGENT THORMATION:
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-422-112-8
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US-08-422-112-8
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                  Indels 0; Gaps
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APPLICANT: Leonard Presta
APPLICANT: Brad Snedecor
TITLE OF INVENTION: Altered Polypeptides with Increased
TITLE OF INVENTION: Half-Life
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
                                                                                                                                                                                                                                                                                                                                                          Length 107;
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Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94080
COMPUTER READABLE FORM:
MEDINA TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: patin (Geneticel)
SUSTINARE: patin (Geneticel)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,093
FILING DATE: 14-APR-1995
CLASSIFICATION: 536
PRIOR APPLICATION NATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 932
TELECHONE: 415/22-1994
TELECHONE: 415/22-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5-08-422-093-8
Sequence 8, Application US/08422093
Patent No. 6096871
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
                                                                                     REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                          LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acid
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                                                                                                                                                                                       1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
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100.0%; Score 553; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.9e-57;
Matches 107; Conservative 0; Mismatches 0; Indels (
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    Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08422112
Patent No. 6121022
GENERAL INFORMATION:
APPLICANT: Leonard Presta
APPLICANT: Brad Snedecor
TITLE OF INVENTION: Altered Polypeptides with Increased
TITLE OF INVENTION: Half-Life
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTY.

ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/422,112
APPLICATION NUMBER: US/08/422,112
APPLICATION NUMBER: US/08/422,112
APPLICATION NUMBER: US/08/422,112
APPLICATION NUMBER: US/08/422,112
APPLICATION NUMBER: US/08/422,112
APPLICATION NUMBER: SPRICK APPLICATION DATA: APPLICATION NUMBER: REFERENCY/DOCKET NUMBER: US/08/41/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11/08/11
100.0%; Score 553; DB 3;
illarity 100.0%; Pred. No. 4.9e-57;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
US-09-301-593-20
; Sequence 20, Application US/09301593A
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                 Best Local Similarity
Matches 107; Conserv
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1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
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APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Link, Brian
APPLICANT: Tso, J. Yun
TITULE OF INVANTION: Baspecific Antibody Effective to Treat
TITULE OF INVANTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
ADDRESSEE: Townsend and Townsend and Crew
ATRET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
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100.0%; Score 553; DB 3; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 107; Conservative '0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
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                                                                                                                                                                                                                                                                                                                                                                                      Length 213,
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOUTHARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSITCATION 1424
PRIOR APPLICATION 1424
PRIOR APPLICATION 1424
FILING DATE: 27-MAR-1992
ATFORNEY/AGENT INPORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/POCKET UNBER: 31,223
REFERENCE/POCKET UNBER: 011823-004901
TELLEPHONE: 415-325-2400
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 553; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/08397411
Patent No. 6129914
GENERAL INFORMATION:
                                                                                      TYPE: amino acide TOPOLOGY: ):-COLOGY: (COLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 amino acids
(202) 672-5399
                                  TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: peptide US-08-397-411-12
                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-630-820-6
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    TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
                                                                                                                                                           APPLICANT: Bamberger, Uwe
APPLICANT: Bamberger, Olivier
APPLICANT: Leger, Olivier
APPLICANT: Leger, Olivier
APPLICANT: Saldanha.
APPLICANT: Saldanha.
APPLICANT: Rettig, Wolfgang J.
TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
FILE REFERENCE: 0652.189001
CURRENT APPLICATION NUMBER: US/09/301,593A
CURRENT APPLICATION NUMBER: EP 98107925.4
BARLIER APPLICATION NUMBER: US 60/086,049
EARLIER PELLING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn Ver. 2.0
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLANNFYPREAKVOWKVDNALQSGNSQESVTEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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4.9e-57;
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IN PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,820
FILING DATA:
APPLICATION NUMBER: US/08/630,820
FILING DATA:
APPLICATION NUMBER: DE 19513676.4
FILING DATA:
APPLICATION NUMBER: DE 19553676.4
FILING DATA:
APPLICATION NUMBER: 13.468363
ATTORNEY/AGBNT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/306
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08630820
| Sequence 6, Application US/08630820
| Patent No. 6008023
| GENERAL INFORMATION:
| APPLICANT: CPEER, Martin
| APPLICANT: COZECH, OGORG
| TITLE OF INVENTION: CYTOPLASMIC EXPRESSION: TITLE OF INVENTION: ANTIBODY FRAGMENTS AND TITLE OF INVENTION: IN B. COLI NUMBER OF SEQUENCES: ADDRESS: ADDRESSE: ADDRESSE: Foley & Lardher STREET: 3000 & Street, N.W., Suite 500 CITY: Washington STATE: D.C.
| COUNTRY: USA ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 553; D
Best Local Similarity 100.0%; Pred. No. 4.9
Matches 107; Conservative 0; Mismatches
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US-09-301-593-20
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US-07-934-373C-24
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                                        107 RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 166
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1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60
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                                                                                        61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 107
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                                                                                                                                   167 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
                                                                                                                                                                                                     RESULT 10
US-08-458-516-12
Sequence 12, Application US/08458516
Fatent No. 5777085
GENERAL INFORMATION:
APPLICANT: Co, Man Sung
APPLICANT: To, Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
CORRESPONDENCE MILLIAM M. Smith
ADDRESSE: William M. Smith
ADDRESSE: William M. Smith
ADDRESSE: William M. Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATE:
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENY INFORMATION:
NAME: Smith, Millam M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/07934373C; Patent No. 5821337
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 107; Conservative
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US-07-934-373C-24
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108 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 167
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                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-006/MS-005
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION NUMBER: PCT/US92/05126
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 15-JUN-1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 40,378
REGISTRATION NUMBER: 40,378
REGISTRATION NUMBER: 40,378
REGISTRATION NUMBER: POTO9P2
TELECOMMUTICATION NUMBER: POTO9P2
REGISTRATION NUMBER: AO,378
REGISTRATION NUMBER: AO,378
REGISTRATION NUMBER: AO,378
REGISTRATION NUMBER: POTO9P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 553; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94080
COMPUTER READABLE FORM:
MEDIVER: 15 1nch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                         G. Presta
Immunoglobulin Variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-934-373C-39
; Sequence 39, Application US/07934373C
; Patent No. 5821337
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Prester
TITLE OF INVENTION: Immunogl
NUMBER OF EXCUBNICES: 48
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DAN Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JUNE OF THE OFFICE OFFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 214 amino acids
Amino Acid
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Gaps

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Sequence 6, Application US/08480753

Sequence 6, Application US/08480753

Patent No. 5830675

GENERAL INFORMATION:
APPLICANT: Targan M.D., Stephan R.
APPLICANT: Targan M.D., Alda M.
TITLE OF INVENTION: PERINUCLEAR ANTI-NEUTROPHIL CYTOPLASMIC ANTIBODY OF TITLE OF INVENTION: ULCERATIVE COLITIS, PRIMARY SCHEROSING CHOLANGITIS, OR TITLE OF INVENTION: TYPE I AUTOIMMUNE HEPATITIS
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ADDRESSEE: Wendy A. Whiteford, Esq.
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 ŘÍVAAPSVPIPPPSDEQIKSCTASVVCLIANPYPŘEAKVOWKYDNALOSGNSQESVTEQD 167
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                                                                                                                                                                                                                                                                                                                                       1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
                                                                                                                                                                                                                                                                                                                                                                                    108 RIVAAPSVPIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
                                                                                                                                                                                                                                     Length 214;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,753
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Whiteford, Wendy A.
REGISTRATION NUMBER: 36,964
REFERENCE/DOCKET NUMBER: P07 33571
TELECONMUNICATION INFORMATION:
                                                                                                                                                                                                                                        ; Score 553; DB 2;
; Pred. No. 1.2e-56;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%;
Matches 107; Conservative 0;
TELECOMMUNICATION INFORMATION:
                                                                       TYPE: Amino acids

TOPOLOGY: Linear
US-07-934-373C-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 107; Conservative
                                               TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inear
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US-08-480-753-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 107; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMITTE USAGE
ZIP: 94080
COMPUTER READABLE FORM:
MEDLUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genetech)
CURRAN APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN 1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: O7/15272
FILING DATE: 14-JUN 1992
FILING DATE: 14-JUN 1992
FILING DATE: 14-JUN 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 40, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION NUMBER: US/07/934,373C
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-AUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REPERSICE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REPERSICE/DOCKET NUMBER: P0709P2
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
             WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Genentech, Inc
STREET: 1 DNA Way
CITY: South San Francisco
STATE: Callfornia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: Linear
US-07-934-373C-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-934-373C-40
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Gaps

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Query Match
100.0%; Score 553; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 107; Conservative 0; Mismatches 0; Indels
61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107
                                          168 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
                                                                                                                                                                                                                                                    APPLICANT: Thomas, G. Roger
APPLICANT: Thomas, G. Roger
APPLICANT: Thomas, G. Roger
APPLICANT: Thomas, G. Roger
APPLICANT: Thomas, G. Roger
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
NUMBER OF SEQUENCES: 15
CORRESPEDINCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COMMIRY: USA
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WINPATIN (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,800
FILING DATE: 22-Jan.1997
CLASSIFTATION: 42-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P09971
TELECOMMUNICATION INFORMATION:
TELEPAX: 415/925-9801
TELEFAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
                                                                                                                                                                             Sequence 11, Application US/08788800
Patent No. 5914112
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-788-800-11
à
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108 RIVAAPSVPIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 167 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107 168 SKOSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214 .. අධ ò

1 RIVAAPSVFIFPPSDEQLKSGTASVVCLLANNFYPREAKVQWKVDNALQSGNSQESVTEQD

0; Gaps

Search completed: January 13, 2004, 12:46:35 Job time : 9.25153 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 13, 2004, 12:22:35 ; Search time 23.8489 Seconds (without alignments) 1326.664 Million cell updates/sec

US-09-990-586-100 1754 1 EFASTKGPSVFPLAPCSRST......MHEALHNHYTQKSLSLSLGK 329 Title: Perfect score: Sequence:

Scoring table:

283308 seqs, 96168682 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description			chain	chain	chain	ø	Ω		chain	Д.	Ig gamma-1 chain -	hain pr	Ig gamma-2 chain C	hain C		chain	hain C	b chain			amma-3h	g gamma-2c chain	g gamma-1 c	g gamma-2a	g gamma-2a chain	g gamma-2 chain	g gamma-1 chai	g gamma-2a cha	g gamma-2a
SUMMARIES	ID	G4HU	GZHU	CHHI	10	_	147159		10	10	GHRB	S31459	S22080	G2GP	C30554	869339	831866	PT0207	PS0018	PS0017	PC4436	G3HUWI	S00847	GIMS	G2MSA	S37483	806611	GIMSM	G2MSAM	G2MSAB
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U	Ig gamma-2a chain		Ig gamma 4 chain c	Ig gamma-2a chain	Ig gamma-2b chain	Ig gamma-2b chain	Ig gamma-2b chain	Ig gamma heavy cha	epsilo	Ig heavy chain VHI	heavy chain p	Ig heavy chain (DO	Ig gamma-1 chain C	Ig heavy chain V-I	Ig epsilon chain C
G3MSC	840295	G3MSM	147162	PS0019	GZMSBM	GSMS11	\$01321	I46732	S38864	S69340	S04845	S69131	S14236	A36040	EHRT
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329	446	398	277	322	405	474	475	180	548	249	549	241	152	218	429
62.6	62.2	62.2	61.9	61.8	59.8	58.8	58.6	39.0	36.7	32.4	32.3	31.6	31.4	31.3	28.3
1098.5	1091.5	1090.5	1085.5	1084.5	1049.5	1032	1027.5	684	644	568.5	566.5	553.5	551	549	496
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4 5

ALIGNMENTS

```
A, Modecule type: DNA
A, Residues: 1-327 < ELL>
A, Note: the sequence was determined from the germline gene
R, Anote: Lt. i. Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A, Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant r
A, Reference number: A90249; MUID:70207560; PMID:4192699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A) Map position: 14q32.33-14q32.33
A) Introns: 99/A: 111/1/; 221/1
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin C resjon; immunoglobulin C resjon; immunoglobulin to resjon; heterotetramer; immunoglobulin P: 20-85/Domain: immunoglobulin to Monology cIMI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                            Gramma-4 chain C region - human C;Species: Homo sapiens (man) C;Accession: A90933; A90249; A02150 C;Accession: A90933; A90249; A02150 R;Ellison, J.; Buxbaum, J.; Hood, L. DNA 1, 11-18, 1981 A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene. A;Reference number: A90933; MUID:83187104; PMID:6299662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F)134-203/Domain: immunoglobulin homology <IM2>
F)24-203/Domain: immunoglobulin homology <IM3>
F)240-307/Domain: immunoglobulin homology <IM3>
F)14/Disulfide bonds: interchain (to light chain) #status experimental
F)27-83,141-201,247-305/Disulfide bonds: #status predicted
F)105,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F)107/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ASTKGPSVFPLAPCSRSTSBSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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100.0%; Pred. No. 7e-115;
iive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GDB:119340; OMIM:147130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 327; Conservative
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A, Residues: 1-30,81-326 <PIN>
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123 FLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY 182

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A;Cross-references: GDB:119338; OMIM:147110
A;Cross-references: GDB:119338; OMIM:147110
A;Nap position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kay being the cases; and mean as 1gA and 1gM, the subunits associate into legistical subulitation; some cases; such as 1gA and 1gM, the subunits associate into legistical subulication; glycoprotein; heterotetramer; immunoglobulin cregion; immunoglobulin homology <IMI>F;20-85/Domain: immunoglobulin homology <IMI>F;239-306/Domain: immunoglobulin homology <IMI>F;239-306/Domain: immunoglobulin homology <IMI>F;239-306/Domain: immunoglobulin homology <IMI>F;219-3106,109/Disulfide bonds: interchain (to light chain) #status experimental F;27-83,140-200,246-304/Disulfide bonds: interchain (to heavy chain) #status experimental F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A; Residues: 1330 <ELL>
A; Residues: 1330 <ELL>
A; Residues: 1330 <ELL>
A; Cross-references: EBLS-21370
A; Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) markers, A; Note: Lys-330 is removed after translation
A; Note: Lys-330 is removed after translation
B; Harris, Lu'
submitted to the EMBL Data Library, October 1992
A; Reference number: S33904
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A;Residues: 2-330 <HAR>
A;Residues: 2-330 <HAR>
A;Crose-references: BMBL:217370
A;Crose-references: BMBL:217370
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of
A;Reference number: $33887; MUID:83001943; PMID:6811139
A;Accession: $33887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299
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Cispecias: Homo sapiens (man)
Cispecias: Homo sapiens (man)
Cispecias: Judan-1981 #sequence revision 18-Aug-1982 #text_change 16-Jul-1999
Ciscession: A33433; S36881; S33887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQG
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92.4%; Pred. No. 3e-105;
ive 10; Mismatches 14; Indels
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                                           A, Gene: GDB: IGHG2
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Cippecies: Homo sapiens (man)
Cipate: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 21-Jul-2000
Cipate: 30-Apr-1981 #sequence revision 13-Jun-1988, 1982
Rilison, J.; Hood, L.
Rydon, J.; Hood, L.
Rydolecule tyne: DNA
A; Reference number: A93906, MUID:82197621; PMID:6804948
A; Reference number: A93906
A; Residues: 1-326 *CELL
A; Cross-references: GB:V00554; GB:J00230; NID:g32789; PIDN:CABS8438.1; PID:g6066056
A; Residues: Lyge: DNA
A; Residues: Lyge: DNA
A; Reference number: A92809; MUID:81007873; PMID:6774012
A; Reference number: A92809; MUID:81007873; PMID:6774012
A; Residues: Try-156 is at or near the complement-binding site
A; Residues: Lip-156 is at or near the complement-binding site
Connell, G. B: Parr, D. M.; Hefmann, T.
Can. J: Biochem: A92809
A; Title: The amino acid sequences of the three heavy chain constant region domains of a A; Reference number: A90752; MUID:80001357; PMID:113060
A; Reference number: A90752; MUID:80001357; PMID:113060
A; Reference number: A90752; MUID:80001357; PMID:113060
A; Reference number: A90808
A; Reference number: A90808
A; Reference number: A90809
A; Title: The amino acid sequences of the three heavy chain constant region domains of a A; Reference number: A90808
A; Reference number: A90808
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A; Residues: 1-24, E', 26-57, EV', 60-85;132-171, ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
A; Residues: 1-24, E', 26-57, EV', 60-85;132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
A; Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
Mol. Immunol. 16, 923-925, 1979
A; Reference number: A93132; MUD:80114419; PMID:118920
A; Reference number: A93132; MUD:80114419; PMID:118920
A; Reference number: A93132
A; Molecule type: protein
A; Accession: A93132
A; Molecule type: Drotein
A; Residues: 238-275 c+Mor-
B; Molecule type: Drotein
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RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK 242
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Rimilstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
Biochem. J. 121, 217-225, 1971
Arithe: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
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1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFFAVLQSS
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-96, TX', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A; Residues: 1-96, TX', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A; Cate: this sequence has the GIm(3) and GIm(non-1) markers
B; Gall, W.E.; Edelman, G.M.
B; Chemistry 9, 3188-3196, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A; Reference number: A90565, MUID: 71064027; PMID: 492344
A; Contents: annotation; disulfide bonds
A; Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A; Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A; Contents: annotation; disulfide bonds
A; Contents: annotation; disulfide bonds
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A,Residues: 136-154, Q',156-165, Q',167-176, Q',178-194, N',196-197, D',199-238, B',240,
A;Note: this sequence has the GIM(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H.; Hilschmann, WH.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen 1gG1-Immunglobulins (Myelomprotein Nie),
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A interns: 99/1; 114/1, 2244

C interns: 9/1, 250-308/Disulfide bonds: #status experimental

F internal internal internal (to light chain) #status experimental

F internal internal (to light chain) #status experimental
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-34, (°, 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E'
A; Note: this sequence has the Glm(17) and Glm(1) markers
A; Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A; Title: Die Primaerstruktur des kristallieierbaren monoklonalen Immunglobulins IgGl
A; Reference number: A91723; MUID: 83289131; PMID: 6884994
A; Contents: myeloma protein KOL; disulfide bonds
A; Accession: A91723
                                                                                                                                                                                                                                                                                      A, Molecule type: protein
A,Residues: 1-96, Kr, /98-135 < CUN>
A,Residues: 1-96, Kr, /98-135 < CUN>
A,Note: this sequence has the Gim(3) marker, 97-Arg
R,Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 317-3181, 1970
Biochemistry 9, 317-3181, 1970
A,Fitele: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid a A,Reference number: A90564; MUID:71064025; PMID:5530842
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A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
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Best Local Similarity 90.9
Matches 300; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 ODWINGKEYKCKVSNKGLPSSIEKTISKAKGOPREPOVYTLPPSQEEMTKNOVSLTCLVK
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                                                                                                120 PSVFLEPPKEKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN
                                                                                                                                                                                                                                              181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
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                                                GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                   STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE
GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESK---YGPPCPSCPAPEFLGG
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 cHUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin homology <1MM>
P;20-88/Domain: immunoglobulin homology <1MM>
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80.6%; Pred. No. 9.9e-104;
iive 8; Mismatches 15;
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C,Accession: 147160
R,Kacskovics, 1.; Sun, J.; Butler, J.E.
R,Kacskovics, 1.; Sun, J.; Butler, J.E.
A,Timunol, 153, 3565-357, 1994
A,Title: Five putative subclasses of swine 1gG identified from the cDNA sequences of a shafetence number: 147159; MUD:95015845; PMID:7930579
                                                                                                                                                                                                                                                                                                                                                                                                                                           182
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C,Species: Sus scrofa domestica (domestic pig)
C,Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLQSS
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residuss: 1-328 «KAC>
A;Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C;Genetics:
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                      A, Gene: 1gG2a C; Superfamily: immunoglobulin C region; immunoglobulin homology F_1133-202/Domain: immunoglobulin homology <IMM>
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C,Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                  73.2%; Score 1283.5; DB 71.7%; Pred. No. 1.1e-82; ive 39; Mismatches 51
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147159
R;KacsKovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 356-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a sheference number: 147158; MUID:95015845, PMID:7930579
                                                                                    Iggamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Apecies: 28-De-21987 #sequence_revision 28-De-1987 #text_change 23-Jul-1999
C;Accession: A22511
R;Huck, S; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Mucleic, Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: 0
A;Reference number: A23511; MUID:86148507; PMID:3081877
                                                                                                                                                                                                                                                                                                 A;Accession: A23511
Modecule type: DNA
A;Reaidues: 1-377 cNUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GLYSLSSVVTVPSSSLGTQTYTCNVNHKPBNTKVDKRVELKTPLGDTTHTCPRCPEPKSC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----YGPPCPSCPAPEFLGGPSVFLFPPKPKDT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 DIPPPCPRCPERSCOTPPPCPRCPERSCOTPPPCPRCPAPELLGGPSVFLFPPKPKDT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LMISRIPEVICVVVDVSQEDPEVQFNWYVDGVEVHNAKIKPREEQFNSIYRVVSVLTVLH 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 LMISRIPEVICVVVDVSHEDPEVQFKMYVDGVEVHNAKIKPRERQYNSIFRVVSVLIVZH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ODWINGKEYKCKVSNKGLPSSIBKTISKAKGQPREPQVYTLPPSQEEMTKNGVSLTCLVK 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSRBEMTRNQVSLTCLVK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHE 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 GFYPSDIAVEWESSGOPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVNHE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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A, Molecule type: mRNA
A, Residues: 1.328 cKAC>
A, Ctoss-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.8%; Score 1575; DB 2; Length 377; 79.6%; Pred. No. 5e-103; tive 12; Mismatches 15; Indels 5(
                                                                                                                                                                                                                                                                                                                                                                     A/Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA277C96netics:
CyGenetics: GB:IGHG3
A/Genetics: GB:IGHG3
A/Genetics: GB:IGHG3
A/GENETICS: GAB:IGHG3
A/AMap position: 14q32.33-14q32.33
A/INTCAS: 98/33, 115/3; 130/3; 145/3; 160/3; 270/3
CyUperfamily: immunoglobulin C_region; immunoglobulin homology
C;Keywords: immunoglobulin homology <IMM>
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Best Local Similarity 79.6*
Matches 300; Conservative
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A,Accession: A93328
A,Accession: A93228
A,Rocession: A93228
A,Rocession: A93228
A,Rocession: A93228
A,Rocession: A93228
A,Crose-references: Gs:Maf6426, MID:9165111, PIDN:AAA31289.1, PID:9165112
A,Crose-references: Has the dil allotypic marker, 104-Met, and the el5 allotypic marker. A,Note: this sequence has the dil allotypic marker, 104-Met, and the el5 allotypic marker. Biochem. J. 116, 249-259, 1970
A,Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin (A,Reference number: A90245; MUD:70110015; PMID:5461106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Accession: A90290
A,Molacule type: protein
A;Residues: 1-47, E',49-71,'PV',72-128 <PRA>
R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Muld. 19329; Muld. 19329; Muld. 193512
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A,Residues: 1-323 cBRN-
A,Residues: 1-323 cBRN-
A,Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
R,Pratt, D.M.; Mole, L.E.
R,Pratt, D.M.; Mole, L.E.
B, Pratt, D.M.; Mole, L.E.
A,Title: Sequence studies on the constant region of the FG sections of rabbit immunoglobi
A,Reference number: A90290; MUID:76135469; PMID:1243651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig gamma chain C region - rabbit (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 24-Apr-1984 #sequence revision 15-Nov-1984 #text_change 16-Jul-1999
C;Accession: A91749; A90290; Ā93928; A90245; A94416; A02161
E;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
A;Ritle: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I
A;Reference number: A91749; MUD:84030930; PMID:6313520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 NQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PID:g433122 C;Genetics: A;Gene: ICA C;Genetics: A;Gene: ICA C;Gene: ICA C;Superfamily: immunoglobulin C region; immunoglobulin homology F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                     61 GLYSLSSMYTVPASSLSSKSYTCNVNHPATTTKVDKRVGIHQPQTCPICPGCE-VAGPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK
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М
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A;Residues: 132-143,'E',145-161 <PRU>
R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney,
                                                                                                                                                                  70.7%; Score 1240.5; DB 2; 70.2%; Pred. No. 1.1e-79; ive 37; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 HGDKFECAVMHEALHNHYTQKSISKTQGK 328
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                                                                                                                                                                                            Best Local Similarity 70.2 Matches 231; Conservative
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147161

147161

15 gamma 3 chain constant region - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Species: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C;Accession: 147161

R;Kacsesion: 147161

A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of shifterence number: 147158; MUD:95015845; PMID:7930579

A;Sterus: preliminary; translated from GB/EMBL/DDBJ
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19 annual chain constant region - pig (fragment)

2) species: Sus scrofa domestica (domestic pig)

C, Species: Sus scrofa domestica (domestic pig)

C, Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C, Accession: 147158

R, Kacskovics, I.; Sun, J.; Butler, J.E.

A, Timmunol. 153, 3565-3573, 1994

A, Title: Five putative subclasses of swine IgG identified from the cDNA sequences (A), Reference number: 147158; MUID:9501845; PMID:730579

A, Accession: 147158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 RVVSVLPIQHQDWLKGKEFKCKVNNVDLPAPITRTISKAIGQSREPQVYTLPPPAEELSR 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 SKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKFSVDKASWQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
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                                        NQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQ 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APKTAPSVYPLAPCGRDTSGPNVALGCLASSYFPEPVTMTWNSGALTSGVHTFPSVLQPS
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Pred. No. 2.4e-81;
9; Mismatches 54; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-328 <KAC>
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A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
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                                                                                                                                                EGNVFSCSVMHEALHNHYTQKSLSLSLGK 329
                                                                                                                                                                                         300 GGGIFQCAVMHEALHNHYTQKSISKTPGK 328
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70.8%; Fil
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Best Local Similarity 70.81
Matches 233; Conservative
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Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N.Alternate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Accession: S22080; S06610; A31303
R;Sanders, P.G.
Submitted to the EMBL Data Library, November 1991
A;Reference number: S22080
A;Accession: Cattle Cat
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Ajfene: Ig CH gamma-1
Ajintrons: 98/1; 111/1; 221/1
Ajintrons: 98/1; 111/1; 221/1
Cjsuperfamily: immunoglobulin C region; immunoglobulin; membrane protein C; Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein F;161-225/Domain: immunoglobulin homology <1MM>
F;161-225/Domain: immunoglobulin homology <1MM>
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                               318 OFNSTERVVSALPIQHQDWTGGKEFKCKVHNRALPAPIVRTISRTKGQAREPQVYVLAPP
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                                    LGGPSVPLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE
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larity 67.6%; Pred. No. 1.4e-75;
Conservative 35; Mismatches 68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            438 DINSWOEGDIYACUVMHEALHNHYIQKSISKPPGK 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 DKSRWOEGNVFSCSVMHEALHNHYTOKSLSLSLGK
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A,Residues: 142-470 <SYM>
A,Cross-references: EMBL:X16701
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                                    A; Reference number: A34416
A; Accession: A94416
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J., ed., pp.109-127, Almqvist and Wiksell,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGN 303
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Dacte: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999

C;Accession: S3459

R;Patri, S.; Nau, F.

submitted to the EMBL Data Library, December 1992

A;Reference number: S31459

A;Reference number: S31459

A;Retus: preliminary

A;Molecule type: mRNA

A;Residues: 1-472 < PAT>

A;Residues: 1-472 < PAT>

A;Cross-references: EMBL:X69797
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larity 67.5%; Pred. No. 1.5e-76;
Conservative 34; Mismatches 63;
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C; Keywords: immunoglobulin
F;277-346/Domain: immunoglobulin homology <IMM>
            Nobel Symp. 3, Killander,
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Best Local Similarity 69.0
Matches 225; Conservative
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Matches 226; Conserv
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61 61	OY 118 GGPSVETFPERMINITALISM FOR THE POLICY OF THE POLICY	Db 237 DELSKSKVSVTCLINFFPADIHVENTNPVSEKEYRYTPFTEDADGSYFLYSKLTVD 296 QY 296 KRANDEGNYSCSVMHEALHNHYTTQKSLSLSLS 328 Db 297 KSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG 329 RESULT 14	C30554 Ig heavy chain C region - sheep (fragment) C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep) C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep) C;Species: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000 C;Accession: C30554 R;Foley, R.C.; Beh, K.J. J. Immunol: 142, 708-711, 1989 A;Title: Isolation and sequence of sheep Ig H and L chain CDNA. A;Reference number: A30554; MUID:89083962; PMID:2492052	ology	Query Match Query Match Best Local Similarity 69.1%; Pred. No. 3.7e-73; Matches 215; Conservative 33; Matches 215; Conservative 33; Qy 27 LGCLVKDYFPEPVTVSMNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCN 86 Db 2 LGCLVSSYMPEPVTVTWNSGALTSGVHTFPAILQSSGLYSLSSVVTVPASTSGAQTFICN 61	ш—ш ш—ш 4 —	Db 178 FKCKTHNEALPAPIVRTISRIKGQAREPOYVLAPPGEELSKSTLSVTGLVTGFYPDYIA 237 Qy 261 VEWESNGOPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHY 318 Db 238 VEWQKNGQPESEDKYGTTTSQLDADGSYFLYSRLRVDKNSWQEGDTYACVVMHEALHNHY 297 Qy 319 TOKSLSLSLGK 329 Db 298 TQKSISKPPGK 308 RESULT 15 S63339 IG heavy chain V region precursor - human C.Species: Homo sapiens (man)
Qy 300 QEGNVFSCSVMHBALHNHYTQKSLSLSGK 329 ::	RESULT 13 G2GP IG gamma-2 chain C region - guinea pig IG gamma-2 chain C region - guinea pig) C;Species: Cavia porcellus (guinea pig) C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 16-Jul-1999 C;Accession: A94553; A90352; A90384; A90385; A02151 S;Tricochmann, T.M Submitted to the Atlas, April 1975	A; Reference number: A94553 A; Accession: A94553 A; Accession: A94553 A; Molecule type: protein A; Residues: 1-3 <tr1> B; Blrishtenin, B.K.; Hussain, Q.Z.; Cebra, J.J. B; Blrishtenistry 10, 18-25, 1971 A; Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am A; Reference number: A90352; MUID:71058471; PMID:5538606 A; Accession: A90352</tr1>	A, Molecule type: protein A, Residues: 4-68 < BIR> A, Residues: 4-68 < BIR> A, Turner, K.J.; Cebra, J.J. B, Turner, K.J.; Cebra, J.J. B, Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Ami A, Reference number: A90359, MUID: 71058486; PMID: 5538616 A, Accession: A90359 A, Molecule type: protein A, Residues: 69-13;312-329 < TUR>	NiTaceV, D.E.; Cabra, J. 1974 Blochemistry 13, 4796-4803, 1974 A;Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies. A;Reference numbber: A90384; MUID:75036072; PMID:4429665 A;Molecule type: protein A;Molecule type: protein A;Molecule type: 726 cTRA A;Molecule type: 7 M. Cabra	Ajrile: Primary 13, 4804-481, 1974 Ajrile: Primary structure of the C-H3 homology region from guinea pig 1gG2 antibodies. Ajrile: Primary structure of the C-H3 homology region from guinea pig 1gG2 antibodies. Ajreference number: A90385; MUID:75036073; PMID:4609467 Ajreference number: Ap0385 Ajmolecule type: protein Ajresidues: 227-311 cTR2> Rioliveira, B.; Lamm, M.E.	Biochemistry 10, 26-31, 1971 A;Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin. A;Reference number: A9034; MUID:71058474; PMID:4922544 A;Reference number: A90354; MUID:71058474; PMID:4922544 A;Contents: annotation; disulfide bonds A;Note: Cys-16 is involved in a heavy-light chain bond A;Note: Cys-16; Cys-107, and Cys-110 form inter-heavy chain bonds C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs. C;Complex: An immunoglobulin heerotetramer subunit consists of two identical light (kap chain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into I C;Superfamily: immunoglobulin C region; immunoglobulin homology	C; Reywords: duplication; glycoprotein; neterocetramer; immunoglobulin homology < IM12- F;11-81/Domain: immunoglobulin homology < IM2- F;13-204/Domain: immunoglobulin homology < IM3- F;28-79/Domain: immunoglobulin homology < IM3- F;28-79/Disulfide bonds: #status experimental F;28-79/Disulfide bonds: #status experimental F;178/Binding site: carbohydrate (Aan) (covalent) #status experimental F;248-308/Disulfide bonds: #status experimental F;248-308/Disulfide bonds: #status experimental Cuery Match 66.0%; Score 1158; DB 1; Length 329; Best Local Similarity 67.3%; Pred. No. 6.9e-74; Matches 224; Conservative 34; Mismatches 63; Indels 12; Gaps 4; Matches 224; Conservative 34; Mismatches 63; Indels 12; Gaps 60 Oy 3 ASTRGPSVFPLAPCSRSTSESTAALGCLVKDVFPEPVTVSWNSCALITSCVHTFPAVLQ-S 60 Dh 2 ARTTASSVFPLAASCSUTTGCLVKDVFPEPVTVSWNSCALITSCVHTFPAVLQ-S 60

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C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000 C;Accession: S69339; S72664
R;Khamilchi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Ehr. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 < KHA>
A;Residues: 1-374 < KHA>
A;Recence number: S72664
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A;Recession: S72664
A;Recession: S72664
A;Residues: 1-140, C',142-374 < KH2>
A;Residues: 1-140, C',142-374 < KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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1 EFASTKGPSVFPLAPCSRST......MHEALHNHYTQKSLSLSLGK 329
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Copyright (c) 1993 - 2004 Compugen Ltd.
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MEDLINE=8422592; PubMed=6329676;
Krawinkel U., Rabbitts T.H.;
"Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass genes.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=83001943; PubMed=6811139;
Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.,
"Structure of human immunoglobulin gamma genes: implications for evolution of a gene family.";
Cell 29:671-679(1982).
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Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982)
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
IG gamma-2 chain C region.
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100.0%; Pred. No. 100.0%; O; Mismatches
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MEDLINE=82197621; Pubmed=6804948;
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Matches 327, Conservative
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327 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-9525598, PubMed-7737190,
Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G., "Characterization of the two unique human anti-flavin monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Milstein C., Frangione B.; "Disulphide bridges of the heavy chain of human immunoglobulin G2."; Biochem. J. 121:217-225(1971).
                                                                                                                                                                                                                                                       MEDLINE=80001357; PubMed=113060;
Connell G.E., Parr D.M., Hofmann T.;
The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.";
Can. J. Biochem. 57:758-767(1979).
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MEDLINE=80114419; PubMed=118920;
Hofmann T., Parr D.M.;
Ha note of the amino acid sequence of residues 381-391 of human immunoglobulins gamma chains.";
Mol. Immunol. 16:923-925(1979).
                                                                                                    chain: genetic
                                                                                                                                                                                                                                 SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE)
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SMART; SW00407; ig; 3.
PROSITE; PSC0835; iG_LIKE; 3.
PROSITE; PSC0290; iG WHC; 2.
Immunoglobulin domain; Immunoglobulin C region.
                                                         Wang A.-C., Tung E., Fudenberg H.H.;
"The primary structure of a human IgG2 heavy evolutionary, and functional implications.";
J. Immunol. 125:1048-1054(1980).
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MEDLINE=6964124; PubMed=5782707;
Frangione B., Milstein C., Pink J.R.L.;
Structural studies of immunoglobulin G.";
Nature 221:145-148(1969).
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SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL). MEDLINE=81007873; PubMed=6774012;
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HINGE.
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HSSP, P01857, 1FC1.
Genew, HGNC:5526, IGHG2.
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PDB; 1FC1; 15
61 GLYSLGSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPP-VAGPSV 119
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REMOVED POST-TRANSLATIONALLY (PROBABLE)
S -> A (IN MYELOMA PROTEINS TIL & ZIE).
ATTGA-VAR. 003899.
C -> S (IN REF. 3).
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Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.
Waxdal M.J., Edelman G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Indels
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-> S (IN REF. 3).
8310878C6878CF9C CRC64;
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Ellison J.W., Berson B.J., Hood L.E.;
"The nucleotide sequence of a human immunoglobulin C
Nucleic Acids Res. 10:4071-4079(1982).
                                                                                                                                                                                                                                                                                                                                                                                                     Score 1605.5; DB 1
Pred. No. 2.4e-113;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SBP-2003 (Rel. 42, Last annotation update)
IG gamma-1 chain C region.
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Best Local Similarity 92.45
Matches 302, Conservative
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"Crystallographic refinement and atomic models of a human Fc fragment autit scamplex with fragment B of protein A from Staphylococcus aucids at 2.9- and 2.8-A resolution.";

Biochemistry 20:2361-2370(1981).

Biochemistry 20:2361-2370(1981).

MISCELLANBOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM (NON-1) MARKERS.

MISCELLANBOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF 35.116,198,269 & 272.

MISCELLANBOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 155, 166, 177, 198, 269, AND IN THE ORDER OF RESIDUES 268-272.
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MEDLINE-83289131; PubMed-6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
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MEDLINE=77070267; PubMed=1002129;
MEDLINE=77070267; PubMed=1002129;
Mile of antibody structure. The primary structure of a monoclonal 1gg1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
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"The covalent structure of a human gamma G-immunoglobulin. 8. Ami
acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
Biochemistry 9:3171-3181(1970).
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MEDLINE=77070269; PubMed=826475;
Ponsting1 H., Hilschmann N.;
"The rule of antibody structure. The primary structure of a monoclonal 1gG1 immunoglobulin (myeloma protein Nie). III. The chymcryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.",
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[3]
SEQUENCE OF 136-329 (EU).
MEDLINE=71064025; PubMed=5530842;
Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=71064027; PubMed=4923144;
Gall W.E., Edelman G.M.; dall W.E., Edelman G.M.; a human gamma G-immunoglobulin.
The covalent structure of a human gamma G-immunoglobulin.
Intrachain Gallfide bonds.";
Biochemistry 9:3188-3196(1970).
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MEDLINE=81208100; PubMed=7236608;
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PDB; 1FC2; 15-JUL-92.
PDB; 1AJ7; 12-NOV-97.
PDB; 1D5B; 09-FEB-00.
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300 DEGNVFSCSVMHEALHNHYTOKSLSLGK 329
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Best Local Similarity 90.9
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                                                                                    GO: GO:0005624; C:membrane fraction; NAS.
GO: GO:0005823; F:antigen binding activity; TAS.
GO: GO:0005923; F:antigen binding activity; TAS.
GO: GO:0006955; P:immune response; NAS.
InterPro: IPR003597; Ig.cl.
InterPro: IPR003597; Ig.cl.
InterPro: IPR003006; Ig.MC.
Pfam; PR00047; Ig.3.
SWART; SWC0407; IG.1.2.
PROSITE; PSSO835; IG.LIKE; 3.
PROSITE; PSSO835; IG.MHC; 2.
Immunoglobulin domain; Immunoglobulin C region; Glycopxotein;
                                                                                                                                                                                                                                           N-LINKED (GLCNAC. ..).
REMOVED POST-TRANSLATIONALLY.
K -> R (IN GIM(3) MARKER).
/PTIGA'VAR 003886.
D -> E (IN GIM(NON-1) MARKER).
/FTIGA'VAR 003887.
L -> M (IN GIM(NON-1) MARKER).
/FTIGA'VAR 003888.
                                                                                                                                                                                                           LIGHT CHAIN).
HEAVY CHAIN).
HEAVY CHAIN).
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HINGE.
CH2.
CH3.
PDB, 1D51, 09-FEB-00.
PDB, 1D6V, 04-CCT-00.
PDB, 1DKV, 06-CCT-00.
PDB, 1E4K, 06-UUN-01.
PDB, 1ECK, 12-UN-02.
PDB, 117Z, 08-MUG-01.
PDB, 117Z, 08-MUG-01.
PDB, 11X, 16-MAX-01.
PDB, 11K, 10-APR-02.
PDB, 11K, 10-APR-02.
PDB, 11K, 10-APR-03.
PDB, 12K, 10-APR-03.
PDB, 12K, 10-APR-04.
PDB, 12K, 10-APR-04.
PDB, 12K, 10-APR-04.
PDB, 12K, 10-APR-05.
PDB, 12K, 10-APR-06.
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MEDLINE=64030930; PubMed=6313520;
Bernstein K.E., Alexander C.B., Mage R.G.;
Bernstein K.E., Alexander C.B., Mage R.G.;
Inclocatide sequence of a rabbit igG heavy chain from the recombinant
F-I haplotype.";
Immunogenetics 18:387-397(1983).
SEQUENCE OF 1-128.
                                                                                                                                                                                                                                                                                                                                                                                                        61 GLYSLSSVVTVPBSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTPPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                63 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESK---YGPPCPSCPAPEFLGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 MTKNOVSLITCLVKGFYPSDIAVBWESNGOPENNYKTIPPVLDSDGSFFLYSRLIVDKSRW
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Pratt D.M.; Mole L.B.;
"Sequence studies on the constant region of the Fd sections of rabbit
immunoslobulin G of different allotype.";
Biochem. J. 151:337-349(1975)."
                                                                                                                                                                                                                                                  3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE
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MEDLINE-83299917; PubMed-6193512;
Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
"Heavy chain genes of rabbit 1gG: isolation of a cDNA encoding gamma heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                                                                                                 Gaps
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P01370;
21-UTU-1986 (Rel. 01, Created)
21-UTU-1986 (Rel. 04, Last sequence update)
15-SPP-2003 (Rel. 42, Last annotation update)
19 gamma chain C region.
Oryctolagus cuniculus (Rabbit).
Bukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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MEDLINE=70110015, PubMed=5461106;
Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
"Sequence studies of the Fd section of the heavy chain of rabbit
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ص
                                                                                                                                   90.7%; Score 1590.5; DB 1; Length 330; 90.9%; Pred. No. 3.2e-112; ive 12; Mismatches 15; Indels 3;
314
317
325
36106 MW, 3770EE106C2FA33D CRC64;
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244 QVSLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGN 303
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Submitted (APR-1975) to the PIR data bank.
                                                                                                                        298 VFTCSVMHEALHNHYTQKSISRSPGK 323
                                                                                              304 VFSCSVMHEALHNHYTQKSLSLSLGK 329
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Trischmann T.M., Cebra J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochemistry 13:4796-4803(1974).
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interPro; IPR007110; Ig-like.
interPro; IPR003597; Ig cl.
interPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                STANDARD;
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P01862;
                                                238
                                                                                                                                                                                                                    RESULT 5
GC2_CAVPO
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                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 SLSSVVSVTSSS---QPVTCNVAHPATNTKVDKTVAPS---TCSKPTCPPPELLGGPSVF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 VVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123
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                                                                                                                                                                                                D11 AND E15
                              SEQUENCE OF 129-131 AND 155-322.
Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
Stockholm (1967).
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                                                                                                                                                                      MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER. 104-THR. AND THE B14 MARKER, 185-THR. REF.3 HAS THE D11 ANI MARKERS AND REF.5 THE B15 MARKER. SIMILARITY: CONTAINS 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.4%; Score 1199; DB 1; Length 323; 69.0%; Pred. No. 7.1e-83; Live 35; Mismatches 58; Indels E
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N -> D (IN REF. 5).

Y -> W (IN REF. 5).

N -> S (IN REF. 5).

G9E8AA118D579A8B CRC64;
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(IN REF. 3 AND 4).
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| E15 MARKER).
| REF. 2).
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IG-LIKE 2.
IG-LIKE 3.
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InterPro; IRR07110, IG-like.
InterPro; IPR003597; IG_C1.
InterPro; IPR003597; IG_C1.
InterPro; IPR003006; IG_MHC.
Pfam; PF00047; ig; 2.
PR03TTE; PS09835; IG_LIKE;
PROSITE; PS06985; IG_LIKE;
PROSITE; PS06290; IG_MHC; 1.
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       J. 116:249-259(1970)
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PIR; A91749; GHRB.
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SEQUENCE
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-!- MISCELLANDOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN PIR, A94553; G2GP.
HSSP; P01842; 7FAB.
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MEDLINE-71058474;
MEDLINE-71058474;
MIDLINE-71058474;
MILLERCHAIN disulfide bridges of guinea pig gamma-2-immunoglobulin.";
Minterchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
Minterchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
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MEDIATE=71058486; PubMed=5538616;

MEDIATE=71058486; PubMed=5538616;

"Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal and hinge region cyanogen bromide fragments.";

Bjochemistry 10:9-17(1971).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 134-226.
MEDLINE-75036072; PubMed=4429665;
Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig 1gG2
                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2 chain C region.
Gavia porcellus (Guinea pig).
Gavia porcellus (Guinea pig).
Mammalia, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutharia, Rodentia, Hystricognathi, Caviidae, Cavia.
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SMART; SM00407; iGcl; 2.
PROSITE; PSS0885; IG_LIKB; 3.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 4-68.

MEDLINE=71058471; PubMed=5538606;

MISDLINE=71058471; PubMed=5538606;

MISTARCHIE D.K., Hussain Q.Z., Cebra J.J.;

"Structure of heavy chain from strain 13 guinea pig
"Structure of heavy chain from strain 13 guinea pig
immunoglobulin-0(2). 3. Amino acid sequence of the rainel-cystine joining heavy and light chains.";

Biochemistry 10:18-25(1971).
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Brueggemann M.;
Frolution of the rat immunoglobulin gamma heavy-chain gene family.";
Frolution of the rat immunoglobulin gamma heavy-chain gene family.";

Brueggemann M.;
Frolution of the rat immunoglobulin gamma heavy-chain gene family.";

Bruegemann M.;
Frologomann in gene 74:473-482(1988).

Richard Prologomann in gamma heavy-chain gene family.";

Richard Prologomann in gammann                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYG------PPCPSCPA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 GLYTLISSVT--SSTWPSQTVTCNVAHPASSTKVDKKVERRNGGIGHKCPTCPTCHKCPV 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 GPPTEQLTEQTVSLTCLTSGFLPNDIGVEWTSNGHIERNYKNIEPVMDSDGSFFWYSKLN 297
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Sciurognathi; Muridae; Murinae; Rattus
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  (WITH A LIGHT
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                                                  444
                                                  HTIW)
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MEDLINE=89232738; PubMed=3149946;
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Mammalia; Butheria; Rodentia;
NCBI_TaxID=10116;
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01-FEB-1991 (Rel. 17, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
16 gamma-2B chain C region.
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
111 TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family.";
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Brueggemann M.;

The Evolution of the rat immunoglobulin gamma heavy-chain gene family and the rat immunoglobulin gamma heavy-chain gene family selected the rat immunoglobulin-like domains.

Para 18 8 80018; P8 80018; P8 80018;

R PRS; P8 80018; P8 80018;

R InterPro; IPR0310; Ig-like.

R InterPro; IPR03507; Ig-d.

R Pfam; PF0047; Ig-d.

R PROSTE; P8 50835; IG LIKE; 3.

R PROSTE; P8 50835; IG LIKE; 3.

R PROSTE; P8 50835; IG LIKE; 3.
                                                                                                                                                                                                                                                                                                                                   63; Indels 12;
                                                                             CHAIN) CHAIN) CHAIN)
                                                                                                                                                                                                                                                                             66.0%; Score 1158; DB 1; Length 329; 67.3%; Pred. No. 8.7e-80; ive 34; Mismatches 63; Indels 1.
                                INTERCHAIN (WITH A LIGHT CHAIN)
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MEDLINE-89232738; PubMed=3149946;
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GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKR-VESKYGPPCPSCPAPEFLGG-- 119
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MEDLINE=81021548; PubMed=6774747;
Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
Frangione Structure of human gamma 3 immunoglobulin deletion mutant:
gamma 3 heavy-chain disease protein Wis.";
Biochemistry 19:4304-4308(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVISIONS TO 12-97 (PROTEIN WIS).
MEDLINE=77118561; PubMed=402363;
Michaelsen T.E., Frangione B., Franklin E.C.;
Michaelsen T.E., Frangione C., Franklin E.C.;
Michaelsen T.E., Frangione B., Franklin E.C.;
Michaelsen T.E., Frangione B., Franklin E.C.;
Juddruplication of a 15-amino acid residue basic unit.";
J. Biol. Chem. 252:883-889(1977).
                                                                                                                                                                                    7
                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL)
: 013BAB45EF49B9DA CRC64;
                                                                                                                                                  Query Match 63.8%; Score 1118.5; DB 1; Length 326; Best Local Similarity 63.3%; Pred. No. 7.9e-77; Matches 209; Conservative 49; Mismatches 65; Indels 7;
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MEDLINE=77021516; PubMed=823945;
Wolfenstein-Todel C., Frangione B., Frelli F., Franklin E.C.;
Who amino acid sequence acquerece acquerce of the FC fragment of immunoglobulin G3.";
Biochem. Biophys. Res. Commun. 71:907-914(1976).
 (WITH A HEAVY CHAIN).
(WITH A HEAVY CHAIN).
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21-UUL-1986 (Rel. 01, Last sequence update)
28-EEB-2003 (Rel. 41, Last annotation update)
1G gamma-3 chain C region (Heavy chain disease protein) (HDC)
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326 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its work non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                          DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
                                                                                                                                                                                                                                                                                                          MISCELLANBOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION AND ALL OF THE CHI REGION.
MISCELLANBOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL GAMMA-3 HEAVY CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 147120; --
GO; GO:0005621; C:membrane fraction; NAS.
GO; GO:0005623; F:antigen binding activity; TAS.
GO; GO:0005655; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-like.
InterPro; IPR003506; Ig-MHC.
FFAM; PF00047; Ig-2.
FRAM; PF00047; Ig-2.
FRAM; PS0025; IG-IKE; 2.
FROSITE; PS00290; IG-MHC; 1.
FROSITE; PS00290; IG-MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS: DISEASE PROTEIN OWM MAY REPRESENT AN ALLELIC FORM OR ANOTHER GAMMA CHAIN SUBCLASS.

MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE SEGMENT (12-28).
SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).

MEDLINE=82247835; PubMed=6808505;
Alexander A., Steinmetz M., Barritault D., Frangione B.,
Alexander A., Steinmetz M., Barritault D., Frangione B.,
Gamma Heavy chain disease in man: cDNA sequence supports partial
gene deletion model...;
Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1882).
INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
NORMALIY PRESENT IN THE HINGE REGION.
INSCELLANBOUS: THE HEAVY-CHAIN DISEASE PROTEIN WIS IS SHOWN.
INSCELLANBOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
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REMOVED POST-TRANSLATIONALLY
QV -> EB (IN ZUC).
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HSSP; P01857; 1FC1.
Genew; HGNC:5527; IGHG3.
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HGNC:5527; IGHG3.
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63 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVE---SKYGPPCPSCPAPEFLGG 119
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MEDLINE=80202559, PubMed=6769752,
Dabza M., Yamawaki-Kataoka Y., Takhashi N., Kataoka T., Shimizu A.,
Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.,
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SED-2003 (Rel. 42, Last annotation update)
15-SED-2003 (Rel. 42, Last annotation update)
1g gamma-1 chain C region secreted form.
1g gamma-1chain (Obrodata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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MEDLINES 80045036; PubMed=115593;

Horio T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,

Takahashi N., Mano Y.;

Takahashi N., Mano Y.;

Takahashi S., Mano M., Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                            CH1.
HINGE.
CH2.
CH3.
INTERCHAIN (WITH A LIGHT CHAIN)
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INTERCHAIN (WITH A HEAVY CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
63.2%; Score 1108; DB 1; Length 3
Best Local Similarity 62.7%; Pred. No. 4.9e-76;
Matches 207; Conservative 50; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36571 MW; 5FCD7B7933850773 CRC64;
                                                                                                    324 AA
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   Pfam, PF00047; ig; 2.
SMART; SM00407; IGG.; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS60230; IG_MAC; 1.
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222
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307
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143
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329 AA;
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P01868;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 TPPPCPRCPAPELLGGPSVFLFPPREXEXTIMISRTPSVTCVVVVVSYHEDPSVQFKWYVDG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 VQVHNAKTKPREQQFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKTKG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 SLSSVVTVPSSSLGTKTYTC--------NVDHKPSNTKVDKRVESK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 YGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPREPOVYTLPPSREEMIKNOVSLICLVKGFYPSDIAVEWESSGOPENNYNTTPPMLDSD 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUT-1999 (Rel. 38, Last annotation update)
16 gamma-2C chain C region.
Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
NGMMmalla, Butheria, Rodentia, Sciurognathi, Muridae, Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253
                                                                                                                                                                                                                                                                                                                                                                                                               63.5%; Score 1113.5; DB 1; Length 290; 73.8%; Pred. No. 1.6e-76; Indels 20; Mismatches 30; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 329
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                                                                                                                                                                                                         /FTId=VAR 003894.
MISSING (IN ZUC).
FTId=VAR 003895.
F -> Y (IN OMM).
/FTId=VAR 003896.
                                                                                        / FTId = VAR 003892,

T -> A (IN OMM).

/ FTId = VAR 003893.

S -> N (IN OMM).
                                  (IN OMM).
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      (IN
      P -> L (IN
/FTId=VAR
F -> Y (IN
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/FTId=VAR
MISSING (I)
/FTId=VAR
                                                                  F -> Y (IN
/FTId=VAR
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MEDLINE=88166903; Pubmed=3127222;
                                                                                                                                                                                                                                                                                                                                                         M.W.
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InterPro; IPR003597; Ig cl.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 73.8<sup>3</sup>
Matches 211, Conservative
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278 N -> D (IN REF. 3).
35704 MW; A338812F3D1F2C93 CRC64;
                                                 63.1%; Score 1106.5; DB 1; 62.0%; Pred. No. 6.2e-76; iive 55; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    330 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 EGNVFSCSVMHEALHNHYTQKSLSLGK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 AGNTFTCSVLHEGLHNHHTEKSLSHSPGK 324
                                               Query Match
Best Local Similarity 62.0%
Matches 204; Conservative
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                 324 AA;
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                                           SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
MEDLINE=80012837; PubMed=113776;
ROGETS J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; V00733; CAA24172.1; -...
REMBL; V00733; CAA24173.1; -...
REMBL; V00733; CAA24173.1; -...
REMBL; V00733; CAA24174.1; -...
REMBL; V00735; CAA24176.1; -...
REMBL; V00795; CAA24176.1; -...
REMPC; REMOSTOFILE 19-1ike.
REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMPC; REMP
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MEDILME-730088899; PubMed=5073237;

Svasti J., Milstein C.,

"The disulphide bridges of a mouse immunoglobulin G1 protein.";

Biochem J. 126:837-850(1972).

-i - SUBCELLIAR LOCATION: Secreted.
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CHAIN).
CHAIN).
CHAIN).
                                                                                                                                                           SEQUENCE (MYELOMA PROTEIN MOPC 21).
MEDLINE=78242288; PubMed=98524;
Adetugbo K.;
Mectugbo n.;
Menunoglobulin subclasses. Primary structure murine myeloma gammal chain.";
J. Biol. Chem. 253:6068-6075(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REMOVED POST-TRANSLATIONALLY.
N -> D (IN REF. 3).
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INTERCHAIN (WITH A HEAVY
INTERCHAIN (WITH A HEAVY
INTERCHAIN (WITH A HEAVY
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/FTId=CAR_000055.
                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Secreted,
Isotd=POL868-1; Sequence=Displayed,
Note=May be the major isoform,
Name=Membrane-bound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P01869-1; Sequence=External;
                                                                                                                               Nucleic Acids Res. 6:3305-3321(1979)
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HINGE.
CH2.
CH3.
cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
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400111
40097
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MOD_RES
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240
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                                                                                                                                                                                                                                                                                          63 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESK--YGPPCPSCPAPEFLGGP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 AKDKVSLICMIIDFFPEDIIVEWQWNGQPAENYKNIQPIMNINGSYFVYSKLNVQKSNWE 295
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                                                                                                                                                                                        1 AKTIPPSVYPLAPGSAAQINSMYTLGCLVKGYFPEPVIVTWNSGSLSSGVHIFPAVLQSD
                                                                                                                                             3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                          121 SVFLFPFKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 SVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 TFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQM
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MEDLINE=81223894; PubMed=6787604;
Ollo R., Auffray C., Morchamps C., Rougeon F.;
"Comparison of mouse immunoqlobulin gamma 2a and gamma 2b chain genes suggests that exons can be exchanged between genes in a multigenic
                                                                      Gaps
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Sikorav J.-L., Auffray C., Rougeon F.;
"Structure of the constant and 3' untranslated regions of the murine
Balb/C gamma 2a heavy chain messenger RNA.";
Nucleic Acids Res. 8:3143-3155(1980).
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21-UTU-1986 (Rel. 01, Created)
21-UTU-1986 (Rel. 01, Last sequence update)
15-SRP-2003 (Rel. 42, Last annotation update)
19 gamma-2A chain C region, A allele.
19 gamma-2A chain C region, A allele.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                  7.
DB 1; Length 324;
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1KC5;
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                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch)
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the evolution of immunoglobulin structure and function."; J. Biochem. 43:423-435(1974).
                                                de Preval C., Fougereau M.;
"Determination of the primary structure of a mouse gamma G2a immunoglobulin. Identification of the disulfide bridges.";
Bur. J. Blochem. 30:452-462(1972).
-!- SIMILARITY: Contains 3 immunoglobulin-like domains.
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IG-LIKE 2.
IG-LIKE 3.
INTERCHAIN (WITH A LIGHT CHAIN)
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                                        MEDLINE=73056887; PubMed=4565406;
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PDB; IBEAW, 12-UU1-01.
PDB; IBEAW, 12-UU1-01.
PDB; IMNU; 06-MAX-99.
InterPro; IPR0007110; Ig-like.
InterPro; IPR0003597; Ig-Cl.
InterPro; IPR0003597; Ig-MHC.
FRAM; PF000477; ig/2.
SWART; SMO0407; ig/2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00320; IG_MHC; 1.
Immunoglobulin domain; Immunoglo
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Best Local Similarity 63.0
Matches 209; Conservative
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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SEQUENCE OF 1-44 FROM N.A.

Yamawaki Kataoka Y., Nakai S., Miyata T., Honjo T.;

Yamawaki Kataoka Y., Nakai S., Miyata T., Honjo T.;

"Nuclectide sequences of gene segments encoding membrane domains ("minnoglobulin gamma chains.")

Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627 (1982)

-i - ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2] SEQUENCE OF 323-393 FROM N.A. MEDLINE=82197626; PubMed=6804950; S.D., Adams J.M., Bernard O. Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O. "mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=80045036; PubMed=115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami
Takahashi N., Mano Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 323-366 FROM N.A.
MEDLINE-82115295; Pubmed=6799207;
Rogers J., Calle B., Souza L., Carter C., Word C.J., Kuehl M.
Eisenberg D., Wall R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains.";
Cell 26:19-27(1981).
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GCIM_MOUSE STANDARD; PRT; 393 AA.
P01865;
P01867;
P01-10TL-1986 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 gamma-1 chain C region, membrane-bound form.
Mus musculus (Mouse)
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IsoId=P01868-1; Sequence=External;
Note=May be the major isoform;
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Cell 18:559-568(1979)
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1CL7; 12-JAN-00
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U.S.A. 79:2623-2627(1982)

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Event=Alternative splicing; Named isoforms=2;
immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. '-!- ALTERNATIVE PRODUCTS:
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SEQUENCE FROM N.A.
MEDLINE-82222190, PubMed-6283537,
Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains of
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Sciurognathi; Muridae; Murinae; Mus.
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P01865;
21-JUL-1966 (Rel. 01). Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 gamma-2A chain C region, membrane-bound form.
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
Mammalia; Eutheria; Rodentia; Sciurognathi; Muric
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   MGI:96446; Igh-4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 GGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGP---PCP--SCPAPEFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 ASTKGPSVPPLAPCSRSTSESTAALGCLVKDYPPEPVTVSWNSGALTSGVHTPPAVLQSS
                                                                                                                                                                                                                                                                                               POTENTIAL.
YOTOPILABRIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
4C38138BFAED3FF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 399;
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CHAIN).
CHAIN).
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62.8%; Pred. No. 1.9e-75;
ive 47; Mismatches 69; Indels
                                                              Note=Probably the major isoform; SIMILARITY: Contains 3 immunoglobulin-like domains
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IG-LIKE 2.
IG-LIKE 3.
INTERCHAIN (WITH A LIGHT
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IsoId=P01865-1; Sequence=Displayed;
Name=Secreted;
                                            IsoId=P01864-1; Sequence=External;
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179

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                      60 GLYTLSSSVTVTSNTWPSQTITCNVAHPASSTXVDKKIEPRVPITQNPCPPHQRVPPCAA 119
                                                                                                                                                                                                                                                                                                                                         234 PPSQEEMTKNQVSLITCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLT 293
                                                                                                                                                                                                                                                                                                                                                             240 PPPAREMIKKEFSLICMITGFLPAEIAVDWISNGRIEGNYKNTATVLDSDGSYFWYSKLR 299
                                                                                                                                  GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKY---GPPC-----PSCPA 113
                                                                                                                                                                                                    114 PEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 173
                                                                                     1 AKTTAPSVYPLVPVCGGTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPALLQ-S
                                                                                                                                                                                                                        120 PDLLGGPSVFIFPPKIKDVLMISLSPMVTCVVDVSEDDPDVQISWFVNNVEVHTAQTQT
                                                                                                                                                                                                                                                                                           180 HREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNRALPSPIEKTISKPRGPVRAPQVYVL
                                                                 3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                       174 REEQFINSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, J00451; -; NOT ANNOTATED_CDS.

R HSSP; B01857; 1FC1.

R HSSP; D01857; 1FC1.

R InterPro; IPR003597; 1g_c1.

R InterPro; IPR003597; 1g_c1.

R InterPro; IPR003597; 1g_c1.

R PEGM; PF00047; 1gg; 3.

R PROSITE; PS50835; 1G_LIKE; 3.

R PROSITE; PS00209; 1G_MHC.

R PROSITE; PS00209; 1G_MHC.

R Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; I Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE-89027161; PubMed-6092053; Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.M., Blatther P.R.; "Structural analysis of the murine IgG3 constant region gene."; EMBO J. 3:2041-2046(1984).
 Length 335;
                                69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  300 VQKSTWERGSLFACSVVHEVLHNHLTTKTISRSLGK 335
                                                                                                                                                                                                                                                                                                                                                                                                              294 VDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 329
62.7%; Score 1099; DB 1; 60.7%; Pred. No. 2.4e-75; ive 53; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  329 AA
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HINGE.
CH2.
                                    204; Conservative
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113
223
                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GC3_MOUSE
P22436;
                                                                                                                                      63
   Query Match
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Matches 20
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GC3_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDB; IHI6; 08-FEB-01.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
Pfam; PF00047; ig; 3.
SWART; SW00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS50835; IG_MIC.
Immunoglobulin domain; Immunoglobulin C region; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isold=P01865-1; Sequence=External;
--- MISCELLANBOORS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
FROM BALB/C MICE, AT 15% OF THE POSITIONS.
--- SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heavy
                                                                                                                                                                                                                                                                                                                            STRAIN=CS7BL/6;
MEDLINE=82037861; PubMed=6170065;
Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
"Multiple differences between the nucleic acid sequences of the IgG2aa and IgG2ab alleles of the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dognin M.J., Lauwereys M., Stroeberg A.D.;
"Multiple amino acid substitutions between murine gamma chain Fc regions of Igla and Iglb allotypic forms.";
Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
-!- SUBCELLUIAR LOCATION: Secreted (Potential).
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3-LIKE 3.
FA3382792CBB13C6 CRC64;
                                                                                                                                                      -JUL-1986 (Rel. 01, Created)
-JUL-1986 (Rel. 01, Last sequence update)
-SEP-2003 (Rel. 42, Last annotation update)
gamma-2A chain C region secreted form (B allele)
                       299 NWVERNSYSCSVVHEGLHNHHTTKSFSRTPG 329
   298 RWOEGNVFSCSVMHEALHNHYTOKSLSLSLG 328
                                                                                                                        335 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Secreted;
IsolaFol864-1, Sequence=Displayed;
Note=Probably the major isoform;
Name=Membrane-bound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IG-LIKE 1.
IG-LIKE 2.
IG-LIKE 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE.
MEDLINE=82037777; Pubmed=6794027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36596 MW;
                                                                                                                        STANDARD;
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330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1BOG; 23-MAR-99.
1HH6; 26-JAN-01.
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335 AA;
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                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                         21-JUL-1986
15-SEP-2003
                                                                                                                                                        21-JUL-1986
                                                                                                                        GCAB MOUSE
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PDB;
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64 LYSLSSUVTVPESSLGTKTYTCNVDHKPSNTKVDKRVESKY----GPPCPSCPAPEFLGG 119
                                                                                                                                                                                               60 FYSLSSLVIVESSTWPSQTVICHVAHPASKIELIRRIEPRIPKPSTPPGSSCPPGNILGG 119
                                                                                                                                                                                                                                          PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN 179
                                                                                                                                                                                                                                                             180 STYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGOPREPQVYTLPPSQEE 239
                                                                                                                                                                                                                                                                                                                            240 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW 299
                                                                                                                                                                                                                                                                                                                                                                                                240 MSKKKVSLTCLVINFFSEAISVEWERNGELEQDYKNTPPILDSDGTYFLYSKLTVDTDSM 299
                                                                                                                                  4 STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 63
                                                                                  5; Gaps
                                     Query Match 62.6%; Score 1098.5; DB 1; Length 329; Best Local Similarity 61.8%; Pred. No. 2.5e-75; Atches 204; Conservative 50; Mismatches 71; Indels 5;
224 327 CH3.
329 AA; 36228 MW; F45827174182BAD6 CRC64;
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Search completed: January 13, 2004, 12:39:29 Job time : 14.3668 secs Q8wux4 homo sapien Q8evox4 homo sapien Q96ga6 homo sapien Q96ga6 homo sapien Q96ga6 homo sapien Q9bert homo sapien Q9brt mus musculu Q9brt mus musculu Q9brt mus musculu Q8kr17 mus musculu Q9bre mus musculu Q8kr17 mus musculu Q9bre mus musculu

Q91WT1 Q91X92

091207 099KA4 09DCD9 090544

096BB9 08WDX4 096BY0 096GA6 096GA6 09VCX7 08VCX7 091DE0 090DE0 096KG8 096KG8 096KG8 096KG8

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January 13, 2004, 12:20:44 ; Search time 58.9039 Seconds (without alignments) 1441.318 Million cell updates/sec
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1754
1 EFASTKGPSVFPLAPCSRST......MHEALHNHYTQKSLSLGK 329
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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core greater than or equal to the score of the result being printed, nd is derived by analysis of the total score distribution.		Description	Q8tc63 homo sapien	Q8tc77 homo sapien	homo	Q8nf17 homo sapien	Q95m34 equus cabal	Q96pg8 homo sapien	Q8r3v9 mus musculu	Q991c4 mus musculu	Q9rla4 mus musculu	Q9d814 mus musculu	Q99131 mus musculu	Q99125 mus musculu	Q91z05 mus musculu	Q8r3h6 mus musculu	Q9bu10 homo sapien	homo
to the score of of the total so	SUMMARIES	םו	DBTC63	28TC77	28N4Y9	28NF17	Q95M34	096PQ8	Q8R3V9	Q99LC4	Q9R1A4	Q9D8L4	Q99L31	Q99L25	Q91205	Q8R3H6	Q9BU10	29BQB8
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reater than or equaderived by analysis		Query Match Length	473	471	521	509	337	701	469	463	437	473	468	473	473	474	597	597
ater tr rived b	oje	Query	99.4	90.7	0.06	89.5	69.4	65.0	64.0	63.8	63.6	63.4	62.6	62.6	60.2	60.2	25.7	25.7
core gre nd is de		Score	1743	1590.5	1578	1570	1217	1139.5	1122.5	1119.5	1115.5	1112	1097.5	1097.5	1055.5	1055.5	450	450

Result No.

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ALIGNMENTS		3 PRELIMINARY; PRT; 473 AA.	_	(TrEMBLrel. 21,	(TrEMBLrel. 23, Last			Chordata, Craniata, Vertebrata,	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9606;		SEQUENCE FROM N.A.	TISSUE=Kidney;		Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.	BC025985; AAH25	IPR000923;	IPR007110;	IPR003006;	33596;	F00047; ig; 4.	400406; IG	PS00196;	PS50835;	TE; PS00290; IG_MHC; 3.	ical prot	ה זייינאם הייים	99.48; S	Thomas O. Gans		3 ASTKGPSVPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 62	147 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 206	63 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
	RESULT 1 QBTC63	QBTC63	01-JUN-2002	01-JUN-2002	01-MAR-2003	Hypothet	Homo say	Eukaryo	Mammalia NCBI Tay	<u>-</u>	SEQUENC	TISSUE=1	Strauspe	Submitte	EMBL; B(InterPro;	InterPro;	InterPro;	InterPro;	Pfam; Pl	SMART; S	PROSITE;	PROSITE;	PROSTIE;	Hypothet	P P P P P P P P P P P P P P P P P P P	Query Match	Mest Local		,	147	9
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253 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHE 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 ASTRGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLOSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 IMISRIPEVICVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ODWINGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 -----AGPPCPSCPAPEFLGGPSVFLFPPKPKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Straubberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC033178; Ad3178-1; -
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR00306; Ig_WHC.
InterPro; IPR00306; Ig_WHC.
InterPro; IPR00306; Ig_W.
Ffam; PF00047; Igc1; 3.
SWART; SM00406; Igc1; 3.
SWART; PS00336; Ig_LKE; 4.
PROSITE; PS00239; Ig_LKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2AC7D22E72D6CAA2 CRC64;
                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.0%; Score 1578; DB 4; 179.8%; Pred. No. 3.8e-135; ive 11; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
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442 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Primary B-Cells from Tonsils;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 521 AA; 57156 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 ALHNHYTOKSLSLSLGK 329
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                                                                                                                                                                                                                          222,
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QBNF17;
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                               01-00T-2002 (TERMBLrel, 2:
01-00T-2002 (TERMBLrel, 2:
01-MAR-2003 (TERMBLrel, 2:
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 79.8
Matches 301; Conservative
                                                                                                                                                                      PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
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                                                                                                                                                                      Q8N4Y9
Q8N4Y9;
                                                                                                           RESULT 3
Q8N4Y9
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Q8NF17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 ITKNOVSLICLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRM 441
                                                                                          182
                                                                                                                                                                                                                                                     386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322 SIYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKOQPREDQVYTLPPSRDE 381
                                                                                                                                            FLFPPKPKDTLMISRTPEVICVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY 326
                                                                                                                                                                                                                                                                                                            NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
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     RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK
                                                                                                                                                                                                                                                  RVVSVLTVLHODWLNGKEYKCKVSNKGLPSSIEKTISKAKGOPREPQVYTLPPSQEEMTK
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Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Straueberg R.;
Submitted (FRE-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BC024289; AAH2489.1;
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003306; Ig-MHC.
InterPro; IPR003506; Ig-W.
Pfam; PF00047; Ig; 4.
PROSITE; PS00835; IG-IKE; 4.
PROSITE; PS00835; IG-IKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 protein.
471 AA; 51791 MW; 388F7F4CF588660E CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVFSCSVMHEALHNHYTOKSLSLSLGK 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
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01-UTN-2002 (TrEMBLrel. 21,
01-MAR-2003 (TrEMBLrel. 23,
Hypothetical protein.
Homo sapiens (Human).
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Best Local Similarity 90.99
Matches 300; Conservative
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SEQUENCE 4.
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324 192 252 444 504

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VX MEDLINE=98383416; PubMed=9717671;
VX MEDLINE=98383416; PubMed=9717671;
VX MEDLINE=98383416; PubMed=9717671;
VX MEDLINE=983838416; PubMed=9717671;
VX Leibold W. Radbruch A.;
VCganization of the equine immunoglobulin heavy chain constant region
VX Genes, III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
VX Genes, III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
VX Genes, III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
VX Genes, III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
VX InterPro; IPR001397; IG-11ke.

DR InterPro; IPR001397; IG-11ke.

PROMIT: SM0447; IG-12.

DR ROSITE; PS00239; IG-LIKE; 3.

PROSITE; PS00290; IG-MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GFYSLSSMYTVPASTWITSETYICHVVHAASNFKVDKRIEPIPDNHQKVCDMSK----CPK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 CPAPEFLGGESVELFPPKEKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ASTIAPKVFALAPGCGITSDSTVALGCLVSGYFPEPVKVSWNSGSLISGVHIFPSVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVE------SKYGPPCPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 TKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 YTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGOP--ENNYKTTPPVLDSDGSFFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                  Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 337 AA; 37438 MW; A60BF2B01DBFD1F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       096PQ8 PRELIMINARY; PRT; 701 AA. 096PQ8; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2003 (TrEMBLrel. 23, Last annotation update) Pactor VII active site mutant immunoconjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 YSRLTVDKSRWQEGNVFSCSVMHEALHNHYTOKSLSLGK
                                                                                                                                                                                                                                                                                                                                                                                69.4%; Score 1217; DB 6; 66.3%; Pred. No. 1.6e-102; attive 46; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=21477448; PubMed=11593034;
Hu Z., Garen A.;
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.3$
Matches 226; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LMISRTPEVICVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLH 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ODWINGKEYKCKVSNKGLPSSIEKTISKAKGOPREPQVYTLPPSQEEMTKNQVSLTCLVK 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ODMINGKEYKČKVSNIKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHE 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 GFYPSDIAVEWESSGQPENNYNTTPPMLDSDGSFPLYSKLTVDKSRWQQGNIFSCSVWHE 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 DIPPPCPRCPERSCOIPPPCPRCPERSCDIPPPCPRCPAPELLGGESVFLFPPRENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eguus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Eguidae; Eguus.
NCBI_TaxID=9796;
                                                                                                                                                                                Jiuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
"The nucleotide sequence of a long cDNA clone isolated from human
                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Immunogobulin gamma 1 heavy chain constant region (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
89.5%; Score 1570; DB 4; Length 509;
Best Local Similarity 79.9%; Pred. No. 2e-134;
Matches 299; Conservative 11; Mismatches 14; Indels 5
                                                                                                                                                                                                                                      Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases EMBL, AK090464; BAC034485.1; -
InterPro; IPR07110; Ig-like.
InterPro; IPR03597; Ig_c1.
InterPro; IPR03597; Ig_mARC.
Pfam; PF00047; Ig; 3.
SMART; SM00407; IGc1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                           509 AA; 56111 MW; 089498D8076E863C CRC64;
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
FLJ00385 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          337 AA
                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS00250; IG MHC; 2.
NON TER 1 1 1 1 SEQUENCE 509 AA; 56111 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALHNHYTOKSLSLS 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALHNRFTOKSLSLS 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                          NCBI_TaxiD=9606;
                                                                                                                                                                      TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
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                                                                                                                                                                                                                             spleen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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095M
10 095M
AC 095M
DT 01-D
DT 01-D
DT 01-D
DT 01-D
DT 01-M
DT 01-M
CO EMIXA
CO MAMM
CO MAMM
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146 AKTTPPSVYPLAPGSAAQINSMYTLGCLVKGYPPEPVTVTWNSGSLSSGVHTFPAVLQSD 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 TKONQVSLICLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 -LYTLSSSVIVPSSIMPSQTVICNVAHPASSTKVDKKIVPRDCGCKPC-ICTVPEV---S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 SVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 64.0%; Score 1122.5; DB 11; Lengt Best Local Similarity 62.9%; Pred. No. 1e-93; Matches 207; Conservative 53; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSB'; PULBAL; '.ch...
MGI:9646; IGH-4.
INTERPRO; IPRO07110; IG-11ke.
INTERPRO; IPRO03066; IG_MHC.
INTERPRO; SWORD; IG_14.
PRO047; IG 4.
PROSITE; PS00456; IG 11KE; 4.
PROSITE; PS00290; IG_MHC; 1.
PROSITE; PS00290; IG_MHC; 1.
SROUTHOUS 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
                                                      rausberg R.;
ubmitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.; Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC003435; AAH03435.1; -- HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ll protein.
469 AA; 51976 MW; 534793F155D05457 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) similar to RIKEN cDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           463 AA
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
                                                                                                                                            EWBL; BC024405; AAH24405.1; InterPro; IPR007110; Ig-like. InterPro; IPR007100; Ig-MHC. InterPro; IPR003596; Ig_V. PRan; PR0047; ig; 4. PR0711; ig; 4. PR081TE; P806839; IG_LIKE; 4. PROSITE; P806839; IG_MHC; 1. Hypochetical protein_BROTE; IR P806839; IG_MH; IR P806839; IR
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Q99LC4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 QEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 LPSSIEKTISKAKGOPREPOVYTLPPSQEEMTKNOVSLITCLVKGFYPSDIAVEWESNGOP 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 ENNYKITPPVIDSDGSFFLYSRLIVDKSRWQEGNVFSCSVMHEALHNHYTQKSISIGK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          642 ENNYKTTPPVLDSDGSFFLYSKLTVDKSR#QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 KPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               522 HEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDMLNGKEYKCKVSNKA 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 VSWNSGALTSG------VHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-UUN-2002 (TrEMBLrel. 21, Created)
01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae; Musi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.0%; Score 1139.5; DB 4; Length 701; 73.0%; Pred. No. 5.1e-95; ive 17; Mismatches 33; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGF-like domain, Hydrolase, Protease, Serine protease.
SEQUENCE 701 AA, 77826 MW, 94AC6CEB42CC992F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S00022; EGF 1, 501186; EGF 2; 1.

$501186; EGF 2; 1.

$5001187; EGF CA, 1.

$500011; EGF CA, 1.

$5000137; EGF CA, 1.

$5000240; TRYPSIN J.

$5000240; TRYPSIN J.

$5000134; TRY
                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR0013597; Ig_c1.
InterPro; IPR0013065; Ig_MGC.
InterPro; IPR001254; Ser protease_Try.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; Pr000084; RGF; 2.
Pfam; Pr00094; GGF; 2.
Pfam; Pr000494; GGF; 2.
Pfam; Pr000497; Ig; 2.
Pfam; Pr000497; Ig; 2.
Prm; Pr000497; Ig; 2.
Prm; Pr000497; IG; 2.
PRINTS; PR000102; GFFBLCOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SM00407; IGC1; 1.
SM00020; Tryp SPc; 1.
3; PS00010; ASX HYDROXYL;
5; PS00022; EGF 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PROUDU; EGFBLOOD.
PRINTS; PROUDU; GLABLOOD.
SMART; SM00179; EGF_CA; 1.
SMART; SM00069; GLA; 1.
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                                                                                                                                                                                                                                                                            InterPro; IP:
InterPro; IP:
InterPro; IP:
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SMART;
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Submara Shibata K., Yoshino M., Itoh M., Ishii Y., Radubne Shinadawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rahadawa A., Shibata K., Yomoo H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Komoo H., Adachi J., Fukuda S., Antawa T., Hara A., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kaukawa T., Saito R., Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Saito R., Okochiwa H., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda I., Naghio T., Radota M., Okido T., Puruo M., Aono H., Baldarelli R., Barsh G., Quadokenbush J., Sakai K., Okido T., Puruo M., Aono H., Baldarelli R., Barsh G., Baffello M.F., Blake J., Boffelli D., Bojunga N., Carninci D., Gariboldi M., Ash Brownstein M.J., Hull D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Antitaker C., Wilming L., Rymshaw-Booris A., Yoehida K., Hasegawa Y., Kawaji H., Kohtsuki S., Rhayashizaki Y., Wang K.H., Weitz C., Whittaker C., Wilming L., Rymshaw-Boris A., Yoehida K., Hasegawa Y., Kawaji H., Kohtsuki S., Rhuctional annotation of a full-length mouse cDNA collection.",
                                                                                                                                                                                                                                                         241 TKNQVSLTCLVKGFYPSDIAVBWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQ 300
                                                                                                                                                                                                                                                                                     229 SVFIFPPRPKDVLTITLTPRVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPRSEQFNS
                                                                                                                                                                                  181 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 ASTKGPSVPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001).

EMBL; AK007918; BAB25349.1; -. BMSP; PO1842; 7FAB.

MGD; MGI:9643; Igh-1.

InterPro; IPR007110; Ig-like.

InterPro; IPR003006; Ig MHC.

InterPro; IPR003006; Ig WHC.

InterPro; IPR00406; Ig WHC.

Pfam; PR00406; IGV; 1.

PROSITE; PS00293; IG LIKE; 4.

PROSITE; PS00293; IG LIKE; 4.

PROSITE; PS00293; IG LIKE; 4.

SEQUENCE 473 AA; $\overline{5}1699$ MW; 9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     473 AA
                                                                                                                                                                                                                                                                                                                                                            301 EGNVFSCSVMHEALHNHYTOKSLSLSKK 329
                                                                                                                                                                                                                                                                                                                                                                                              409 AGNTFTCSVLHEGLHNHHTEKNLSHSPGK 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.1-JUN-2001 (TrEMBLrel" 17, Cr
01-JUN-2001 (TrEMBLrel. 17, La
01-MAR-2003 (TrEMBLrel. 23, La
1810060009Rik protein.
IGH-1 OR 181006009RIK.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                            349
                                             121
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                                                                                                                                                                                                                                                                                                            180
                                                                                                                       GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVBSK--YGPPCPSCPAPEFLGGP 120
                                                                                                                                                                                                                                                                                                                                        255 SVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNS 314
                                                                                                                                                                                                                                                                                                                                                                                                                  181 TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 TKNOVSLITCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQ 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                               63 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESK--YGPPCPSCPAPEFLGGP 120
                                                                                             62
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                                                                                             3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                         SVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNS
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S., "Cloning of cDNAs encoding for anti-white pine blister rust monoclo antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFv).", Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases. EMBL, P01842, 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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63.6%; Score 1115.5; DB 11; Length 437;
Best Local Similarity 62.3%; Pred. No. 4.1e-93;
Matches 205; Conservative 55; Mismatches 62; Indels 7;
Pred. No. 1.9e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48142 MW; 5C3A7BB3EE7D697C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              435 AGNTFTCSVLHEGLHNHHTEKSLSHSPGK 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGNVFSCSVMHEALHNHYTQKSLSLGK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:96446; IGH-4.
InterPro; IPR007110; IG-like.
InterPro; IPR0033006; IG_MHC.
InterPro; IPR003596; IG_V.
Pfam; PF00047; ig; 4.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_LIKE; 4.
              Best Local Similarity 62.6
Matches 206; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   437 AA;
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SEQUENCE FROM N.A.
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SEQUENCE
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262 GGPSVFIFPPKIKDVLMISLSPMYTCVVVDVSEDDPDVQISWFVNNVEVLTAQIQIHRED 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GOPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 AKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPBPVTLTWNSGSLSSGVHTFPAVLQSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGP---PCP--SCPAPBFL
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01-DEC-2001 (TYEMBLrel. 19, Created)
01-DEC-2001 (TYEMBLrel. 19, Last sequence update)
01-MAR-2003 (TYEMBLrel. 23, Last annotation update)
Hypothetical 51.9 kDa protein.
Hypothetical 51.9 kDa protein.
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi,
                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003888, AM03888.1;
HSSP; PO1842; 7FAB.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; Lrkvocoso; Ig_v.
InterPro; Lrkvocoso; Ig_v.
Pfam; Pro0406; Icv; 1.
SMARI; SM00406; Icv; 1.
PROSITE; PS50835; Ig_LIKE; 4.
PROSITE; PS002209; Ig_MHC; 1.
PROSITE; PS002209; Ig_MHC; 1.
                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
similar to RIKEN CDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RWOEGNVFSCSVMHEALHNHYTOKSLSLSK 329
                                                  298 RWOEGNVFSCSVMHEALHNHYTOKSLSLGK 329
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                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 208; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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Q99L25;
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                                                                                                                                             RESULT 12
Q99L25
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ID O9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQ 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YNSTLRVVSALPIQHQDWASGKEFKCKVNNKALPAPIERTISKPKGSVRAPQVYVLPPPE 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297
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                                                                                                                                                                                                                                                     233
                                                                                                                                                                                                                                                                               318 HREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNRALPSPIEKTISKPRGPVRAPQVYVL 377
                                                                                                                                                                                                                                                                                                                                                                               PEFLGGPSVFLPPPKPENTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 173
                                                                                                                                                                                                                                                                                                                                                     PPSQBEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLT 293
AKTTAPSVYPLAPVCGGTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPALLQ-S 197
                                                  GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYG-----PP---CPSCPA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPR-GPTIKPCPPCKCPAPNLL
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                                                                             174 REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 11; Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
62.6%; Score 1097.5; DB 11; Lengt
Best Local Similarity 62.7%; Pred. No. 2e-91;
Matches 208; Conservative 47; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; FULS42; FEAD.
INTEXPRO; EDR007110; 1g-like.
INTEXPRO; IPR003506; 1g, MHC.
INTEXPRO; IPR003596; 1g_V.
INTEXPRO; IPR0040; 1g; 3.
SMART; SM00406; 1GV: 1.
PROSITE; PS00290; 1G_IXE; 4.
PROSITE; PS00290; 1G_IMC; 1.
SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
similar to RIKEN CDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VOKSTWERGSLFACSVVHEGLHNHLTTKTISRSLGK 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                     VDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI TaxID=10090;
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Gaps

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139 AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQ-S 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 PAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 TLPPSQEEMTKNOVSLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 STKGPSVFPLAPCSRSTSE-STAALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQ 60
                                                                                                                                                                                                                                                                                                                                                      172 KPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVY
                                                                                                                                                                                                                                                                                                                           63 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGP----PCP----SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYPPEPVTVSWNSGALTSGVHTFPAVLQSS
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                         60.2%; Score 1055.5; DB 11; Length 474; 59.5%; Pred. No. 1.3e-87; Indels 13; ive 51; Mismatches 73; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antch 25.7%; Score 450; DB 4; Length 597; Local Similarity 26.9%; Pred. No. 2.6e-32; Loservative 71; Mismatches 132; Indels 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SSGLYSLSSVVTVPSSSL--GTKTY-TCNVDHKPSNTKVDKRV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65274 MW; 2DAFA8FB7E055851 CRC64;
     PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
HYDOThetical protein.
SEQUENCE 474 AA, 51748 MW; 8608B57C6CD2874A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hypothetical (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292 LIVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437 LDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ
BEBL; BC002963; AAH02963.1; --
HSSP; P01825; 7PAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    597 AA
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InterPro; IPR00306; Ig_MHC.
InterPro; IPR003596; Ig_W.
Ffam, PP00047; Ig; S.
SWART; SM00406; IGV; 1.
PROSITE; PS00835; IG_MHC; 3.
PROSITE; PS00290; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 597 AA; 65274 MW;
                                                                                                                                                   Best Local Similarity 59.59
Matches 201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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TISSUE=Lymph;
                                                                                                                              Query Match
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Q9BU10;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 PAPNLEGGPSVFIFPPNIKDVLMISLIPKVTCVVVDVSEDDFDVQISWFVNNVEVHTAQT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              376 ILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSK 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 PAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 KPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 TLPPSQEEMTKNQVSLTÇLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Gaps
       Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.2%; Score 1055.5; DB 11; Length 473; 59.5%; Pred. No. 1.3e-87; Artive 51; Mismatches 73; Indels 13;
                                                                                                                                                                                          InterPro; IPR001345; Cytc heme_bind.
InterPro; IPR00110; Ig-11ke.
InterPro; IPR003106; Ig_MRC.
InterPro; IPR003596; Ig_WRC.
InterPro; IPR003596; Ig_WRC.
InterPro; IPR00406; Ig_WRC.
InterPro; IPR00406; Ig_WRC.
INTERPOSITE; PS00409; CytCHROME C; I.
PROSITE; PS00290; IG_MRC; 1.
INTERPOSITE; PS00290; IG_MRC; 1.
INTERPOSITE; PS00290; IG_MRC; 1.
INTERPOSITE; PS00290; IG_MRC; 1.
INTERPOSITE; PS00290; IG_MRC; 1.
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InterPro; IPRO00345; CytC heme_bind.
InterPro; IPRO03105; Ig_MC.
InterPro; IPRO03596; Ig_MC.
InterPro; IPRO03596; Ig_V.
PROMIT: SMO4047; ig_f: 3.
PROSITE; PS00190; CYTOCHROME_C; 1.
                                                                                                      Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010327; AAH10327.1; -.
MGD; MGI:2144967; AU044919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 LTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TYEMBLrel. 21, Created)
01-JUN-2002 (TYEMBLrel. 21, Last sequence update)
01-JUNA-2003 (TYEMBLrel. 23, Last annotation update)
Hypothetical 51.7 kba protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 59.59
Matches 201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                         SEQUENCE FROM N.A.
Mammalia; Eutheria
NCBI_TaxID=10090;
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101	ESKYGPPCPSCPAPEFL121	
263	PRDGFFGNPRKSKLICQAIGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAKESGPTTYKV 322	
122	136	
323	TSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPDQDTAIRVFAIPPS-FASIFLT 381	
137	RIPEVICVY	
382	KSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISESHPNATFSAVGEASICEDDWN 440	
197	NGKEYKCKVSNKGLPSSIEKTISKAKGQP-REPQVYTLPPSQEEMT-KNC	
441	SGERFICTVTHIDLPSPLKQTISREKGVALHRPDVYLLPPAREQLNURESATITCLVTGF 500	
255	YPSDIAVEWESNGOPENNYKT	
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311	HEALHNHYT	
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Search completed: January 13, 2004, 12:43:11 Job time : 59:9039 secs

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Immunoglobulin C-9
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1 EFASTKGPSVFPLAPCSRST......MHEALHNHYTQKSLSLSLGK 329
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1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*

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4: /SIDS1/gcgdata/geneseqf/geneseqp-embl/AA1983.DAT:*

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/SIDS1/gcgdata/genesed/genesedp-embl/AA21010.DAT:
/SIDS1/gcgdata/genesed/genesedp-embl/AA2101.DAT:
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/SIDS1/gcgdata/genesed/genesedp-embl/AA2101.DAT:
/SIDS1/gcgdata/genesed/genesedp-embl/AA2103.DAT:
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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ALIGNMENTS

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This protein comprises an immunoglobulin (Ig) C-gamma-4 region.

The invention provides a method for the production of tumour-
specific Ig derived from a B-cell lymphoma patient. In the novel
method, expression plasmids containing the patient's VH region(8)
joined to either a C-gamma-3 (see AAT97188) or C-gamma-4 (see AAT97189)
cequence and expression plasmids containing the patient's VL
region(8) joined to either a C-kappa (see AAT97190) or C-lambda-2
(see AAT97191) sequence are cotransfected along with a selectable and
amplifiable marker into a cell line (e.g. BW5147.61.4), and
camplifiable marker into a cell line (e.g. BW5147.61.4), and
transfected cells are then subjected to selection and amplification.
The method permits the production of a multivalent vaccine which
reflects the degree of sometic variation found within the patient's
tumour. These novel multivalent vaccines provide superior vaccines
for the treatment of B-cell lymphoma.
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              comprises at least 2 different recombinant variable regions of immunoglobulin molecules derived from B cell lymphoma cells
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 327;
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to treat B cell lymphoma or leukaemia different recombinant variable region
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100.0%; Pred. No. 2.1e-126;
iive 0; Mismatches 0;
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                                                                          Example 10; Page 126-127; 177pp; English
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Best Local Similarity 100.0
Matches 327; Conservative
  Multivalent vaccine to
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The invention relates to an immunoadhesin comprising:

(a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising a chinovirus receptor protein linked to at least a portion of an immunoglobulin heavy chain, and

(b) optionally a J chain and secretory component associated with the chimeric ICAM-1 molecule. The immunoadhesin has plant-specific glycosylation and virucide activity. The immunoadhesin is useful for reducing infection by human rhinovirus (HRV) and hence the initiation or spread of the common cold by HRV. The immunoadhesin hinds to HRV and reduces its infectivity, competing with cell surface ICAM-1 for binding sites, interfering with virus entry or uncoating and directing premature of viral RNA and formation of empty capside. Expression of the immunoadhesin having multiple binding sites have a higher effective immunoadhesin having multiple binding sites have a higher effective of fining the virus, thereby increasing the effectiveness of the immunoadhesin association of secretory component and immunoadhelin J chain increases the stability of the immunoadhesin in the mucosal chain increases the stability of the immunoadhesin in the mucosal chain increases the stability of the immunoadhesin in the mucosal chain increases the stability of the immunoadhesin in the mucosal chain increases the stability of the immunoadhesin in the plants than in animal cell culture and production in plants is safer for human use, since plants are not known to harbor any animal viruses. The present sequence is that of a human immunoglobulin protein sequence, useful to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK
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                                                                                                                                                                                                                                   Immunoadhesin for treating human rhinovirus infection comprises chimeric intercellular adhesion molecule-1, and optionally a J chain and secretory component in association
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                        and secretory component in association
                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 7; 138pp; English.
                                                               (PLAN-) PLANET BIOTECHNOLOGY INC.
               28-APR-2000; 2000US-200298P.
                                                                                                                    Wycoff KL
                                                                                                                                                                 WPI; 2002-041481/05
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Matches 327; Conser
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                                                                                                                                                                                         N-PSDB; ABA05268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the invention.
                                                                                                                    Larrick JW,
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AAE32630 standard; Protein; 327

RESULT 3 AAE32630 ID AAE3

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                                                                                                                                                                                                                                                                                                                                    181 RVVSVITVIHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK 240
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                                                                                                                              9
                                                                                                                                                                                          GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVBSKYGPPCPSCPAPEFLGGPSV
                                                                                                                                                                                                                                       FLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY
                                                                                                 3 ASTKGPSVPPLAPCSRSTSESTAALGCLVKDYPPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                    GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV
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                              Length 327;
                                                                 Indels
                              99.4%; Score 1743; DB 24;
100.0%; Pred. No. 2.1e-126;
iive 0; Mismatches 0;
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                                               Local Similarity 100.
327 AA;
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NOVSLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG

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122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for reducing the immunogenicity of a fusion protein which involves identifying a candidate T-cell epitope within a junction spanning a fusion junction of a fusion protein, and changing an amino acid within the junction region to reduce the ability of the candidate T-cell epitope to interact with a T-cell receptor. The method is useful for reducing the immunogenicity of a fusion protein. It is useful for analysing, changing or modifying one or more amino acids in the junction region of a fusion protein to identify a T-cell epitope and reduce its ability to interact with a T-cell receptor. The epitope and reduce its ability to interact with a T-cell receptor. The less immunogenic fusion proteins are useful in providing therapeutic treatment. The present sequence is human immunoglobulin G4 (1964) heavy chain Fc region used to illustrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reducing the immunogenicity of a fusion protein comprises changing a amino acid within the junction region to reduce the ability of the candidate T-cell epitope identified within the junction spanning to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                    r-cell; immunogenic; therapy; human; immunoglobulin G4; IgG4
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                                                                                                                                                                                                                       Human immunoglobulin G4 (IgG4) heavy chain Fc region.
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Pred, No. 2.1e-126;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 53-54; 68pp; English.
                     standard; Protein; 327 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.4%; Scc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interact with T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001US-280625P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2002; 2002WO-US09815
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                                                                                                                                                                                                                                                                                                                                                                                                                               WO200279232-A2
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gillies SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S:
Matches 327,
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                     AAE32918
                                                                                         AAE32918;
4AE32918
                                                         SYSTEM STATEM ST
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63 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-SEP-1998;
19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-SEP-1999;
                                                                                                                                                                                                                                                                                                                                               01-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
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Peptide
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                                                                                                                                                                                         ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents the amino acid sequence of C-gamma-4. The protein is used in the course of the invention. The specification describes cytokine antagonists comprising only the extracellular domain of the specificity-determining component of the cytokine receptor. The cytokine receptor and the extracellular domain of a signal-transducing component of the cytokine receptor. The cytokine is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15), gamma-interferon or transforming growth factor (GM-CSF), gamma-interferon or transforming growth factor-beta (TGF-beta). The complex. The compounds have therapeutic activity as gytokine antagonists and can also be used in assays for identifying novel agonists and antagonists of cytokines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytokine antagonists - comprising extracellular domains of specificity-determining and signal-transducing components of
                                                                                                                                                                                                                      gpl30; cytokine antagonist; interleukin; gamma-interferon;
granulocyte macrophage colony-stimulating factor; J peptide;
transforming growth factor-beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
99.4%; Score 1743; DB 20;
Best Local Similarity 100.0%; Pred. No. 2.1e-126;
Matches 327; Conservative 0; Mismatches 0;
                    NVFSCSVMHEALHNHYTQKSLSLGK 329
                                           301 NVFSCSVMHEALHNHYTOKSLSLGK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yancopoulos GD;
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
2..329
/note= "C-gamma-4"
                                                                                                                                                                                              Amino acid sequence of C-gamma-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Fig 12; 46pp; English.
                                                                                                                AAW70801 standard, protein, 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REGE-) REGENERON PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0563105.
                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0563105,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           93US-0140222.
                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stahl N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-044669/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytokine receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                     27-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                             27-NOV-1995;
20-OCT-1993;
                                                                                                                                                                    03-FEB-1999
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                                                                                                                                                                                                                                                                             Synthetic
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                    303
                                                                                                                                          AAW70801;
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182
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                                                                                                                                           302
                                                                                                                                                                243 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention concerns production of antagonists to any cytokine that utilizes an alpha specificity determining component, which when combined which the cytokine, binds to a first beta signal transducing component to form a non-functional intermediate which then binds to a second beta signal transducing component causing beta-receptor dimerization, the soluble alpha specificity determining component of the receptor (SR-alpha) and the extracellular domain of the first beta signal transducing component of the cytokine receptor (beta-1) are combined to them heterodimers (sR-alpha:beta-1) that act as antagonist to the cytokine by binding the cytokine to form a non-functional complex. The receptor components are shared by cytokines such as the CNTF (ciliary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecule for treating cytokine-related diseases or disorders encodes a fusion polypeptide capable of binding a cytokine to form a nonfunctional complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gpl30-C-gamma-1; cytokine; antagonist; CNTF; -receptor; fusion protein;
cytostatic; immunomodulator; osteopathic.
                                                                                              RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK
                                                                                                                                           NOVSLITCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG
FLFPPKPKDTLMISRTPEVTCVVVDVSQEDPBVQFNWYVDGVEVHNAKTKPREEQFNSTY
                       123 FLFPPKFKDTLMISKTPEVTCVVVDVSQBDPEVQFNWYVDGVEVHNAKTKFREEQFNSTY
                                                                     RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK
                                                                                                                                                                                                                   NVFSCSVMHEALHNHYTQKSLSLSLGK 329
                                                                                                                                                                                                                                              NVFSCSVMHEALHNHYTQKSLSLGK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Ser-Gly bridge"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 AAY92190 standard; protein; 329 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4, Fig 12; 152pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3..329
/label= C-gamma-4
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99US-0313942.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human 1gG1 C-gamma-4 domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122

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(PROT-) PROTEIN DESIGN LABS INC

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neurotrophic factor) family of cytokines. The invention provides the basis for the development of IL-6 antagonists, as they show that if, in the presence of a ligand, is anon-functional intermediate complex, consisting of the ligand, its alpha receptr and its beta-I receptor component, can be formed, it will effectively block the action of the ligand. Effective antagonists of IL-6 or CWTF consist of heterodimers of the extracellular domains of the alpha specificity determining components of their receptors and the extracellular domain of gpl30. The resultant heterodimers, function as high-affinity traps, rendering the cytokine inaccessbile to form a slighal transducing complex with the native membrane-bound forms of their receptor. The nucleic acids and picypeptides are useful for treating cytokine-related diseases or disorders such as osceoporosis and primary and secondary effects of cancer including multiple myeloma or cachexia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.4%; Score 1743; DB 21; Length 329; 100.0%; Pred. No. 2.1e-126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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95EP-0112895.
95EP-0114696.
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Best Local Similarity 100.
Matches 327; Conservative
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Chimeric Homo sapiens
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19-SEP-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                       Humanised anti-L-selectin antibody Hubreg 55 comprises 2 heavy chains each having the sequence given in AAM13564 and 2 light chains each having the sequence given in AAM13563. These are encoded by the cDNA clones given in AAT61280. Hubreg 55 can be used to prevent multiple organ failure associated with polytrauma and for the prevention of acute organ damage associated with extracorporeal blood circulation. The antibody inhibits interaction between the carbohydrate-recognising domain of the selectin and the corresponding cell surface receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 FLFPFKPKDTLMISRIPEVICVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 RVVSVLTVIHQDWINGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGGFFLYSRLTVDKSRWQEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 FLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IgG4; C-gamma-4; antibody; fusion protein; circulating half-life; human; drug delivery.
                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                          Using anti-selectin antibody to prevent acute organ damage and multiple organ failure - during extracorporeal circulation or following polytrauma, e.g. haemorrhagic-traumatic shock
                                                                                                                                                                                                                                                                                                                                                                                                              Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.117
/note= "the identity of these residues is specified"
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                           99.4%; Score 1743; DB 18;
100.0%; Pred. No. 3.1e-126;
iive 0; Mismatches 0;
                             Ü
                             Schumacher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NVFSCSVMHEALHNHYTQKSLSLSLGK 329
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                                                                                                                                                                             Disclosure; Page 34-36; 52pp; English
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                             Martin U,
                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 327; Conservative
                             Haselbeck A,
                                                             WPI; 1997-165036/15.
N-PSDB; AAT61281.
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Misc-difference
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                                                                                                                                                                                                                                                                            The present sequence represents the constant region of human IgG isotype 4 (IgG4, C-gamma-4). C-gamma-1 (see AAY31669) and C-gamma-3 (see AAY31671) bind For receptors with high affility, whereas C-gamma-4 has 10-fold lower binding affinity and C-gamma-2 (see AAY31670) does not bind to For receptor gamma-1. The invention provides methods for the genetic construction and expression of antibody-based fusion proteins with enhanced circulating half-lives. The fusion proteins with enhanced circulating half-lives. The fusion proteins with enhanced circulating half-lives. The receptors, either as a consequence of the antibody isotype used for corresponding to the gamma-1.

To gamma-4 For receptor, or through directed mutagenesis of antibody isotypes that normally bind For receptors, i.e. C-gamma-1.

Or C-gamma-3. The methods can be used for to increase the circulating half-life of a non-immunoglobulin (Ig) protein such as a cytokine, e.g. tumour necrosis factor (IMFP), an interleukin or a lymphotoxin or a colony stimulating factor, a ligand-binding protein, e.g. CD4, CTLA-4, TNF receptor or an interleukin receptor, or a protein toxin (claimed). The fusion protein ser used to deliver selectively the second non-Ig protein can expect cell in vivo so that the second non-Ig protein can exert a localised biological effect.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVBSKYGPPCPSCPAPEFLGGFSV
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                                                                                                                                                                                                   New antibody-based fusion proteins, used for the delivery of e.g. a cytokine, ligand-binding protein or protein toxin to target cells in
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larity 100.0%; Pred. No. 3.1e-126;
Conservative 0; Mismatches 0;
                                                                                                                                                 Wesolowski J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NVFSCSVMHEALHNHYTQKSLSLGK 329
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                                                                                                                                                                                                                                                        Disclosure; Page 35-36; 41pp; English
                                                                 99WO-US03966
                                                                                         98US-0075887
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자
                                                                                                                     (LEXI -) LEXIGEN PHARM CORP.
                                                                                                                                                 Lan Y,
                                                                                                                                                                         WPI; 1999-527594/44.
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Matches 327; Conserv
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           WO9943713-A1
                                                                 24-FEB-1999;
                                                                                           25-FEB-1998;
                                                                                                                                                 SD,
                                       02-SEP-1999
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257 FLEPPKPKDTLMISRTPEVICVVVDVSQEDPEVQENWYVDGVEVHNAKIKEREEQENSTY 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 ASTKGPSVFPLAPCSRSTSBSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              correspond to murine anti-porcine soluble vascular cell adhesion molecule (VCAM) monoclonal antibody 2A2 (see also AAN14931-32). The are encoded by a 2A2 human 1954 expression plasmid insert (see also AAT62933). A chimeric antibody specific for porcine VCAM can k produced in transfected host cells. It is useful for diagnosing human rejection of porcine xenotransplants and for improving xenotransplantation of porcine cells, tissues and organs into human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human cell interaction
for rejection of xenografted
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                                                                                                                                                    2A2 Human IgG4 expression plasmid insert product (heavy chain)
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                                                                                                                                                                                                  Xenotransplantation, graft rejection, cell interaction, pig, vascular cell adhesion molecule, VCAM; monoclonal antibody; chimeric antibody; diagnosis.
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100.0%; Pred. No. 3.2e-126;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mueller EE, Mueller JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Page 48-50; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibodies binding to porcine but not proteins - useful to treat and assay porcine organs, tissues or cells
AA.
AAW14935 standard; Protein; 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0004489.
95US-0004489.
                                                                                                   (first entry)
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Best Local Similarity
Matches 327; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-212855/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAT62933
                                                                                                                                                                                                                                                                                                                                                                       WO9711971-A1
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28-SEP-1995;
                                                                                                   16-JUN-1997
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Rother RP;
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                                                   AAW14935;
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Length 463;

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Heavy chain (AAW14932) and light chain (AAW14931) sequences are provided for the murine anti-porcine soluble vascular cell adhesion molecule (VCAW) monoclonal antibody (MAD) 2A2. Hybridoma 2A2 was produced by standard techniques using recombinant, soluble porcine VCAW as immunogen. Chimeric antibodies can be produced by cloning vCAW as immunogen. Chimeric antibodies can be produced by cloning expression plasmid pAPEX.3P modified to contain the human gamma4 constant region in place of the human gamma1 C1 region. Sequences are provided for 2A2 chimeric) human G2/G4 cDNA (AAW14933), and 2A2 human G2/G4 expression plasmid insert product (AAW14935.36). The chimen ingG4 expression plasmid insert products (AAW14935.36). The chimen cantibodies are specific for porcine VCAM. They are useful for diagnosing human rejection of porcine vcancransplants and for improving xenotransplantation of porcine cells, tissues and organs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibodies binding to porcine but not human cell interaction proteins - useful to treat and assay for rejection of xenografted porcine organs, tissues or cells
                                                                                                                                                                                                                            splantation, graft rejection, cell interaction, pig,
cell adhesion molecule; VCAM; monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mueller JP, Rollins S;
                                                                                                                                                                                                     Murine anti-porcine VCAM 2A2 heavy chain.
                                     NVFSCSVMHEALHNHYTQKSLSLSLGK 329
                                                    NVFSCSVWHEALHNHYTQKSLSLGK 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 40-42; 105pp; English.
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                          AAW14932 standard; Protein; 463 AA
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                                                                                                                                                                                                                                                     chimeric antibody; diagnosis.
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/label= CDR2
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/label= CDR1
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/label= CDR3
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                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matis LA,
                                                                                                                                                                                                                             Xenotransplantation;
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28-SEP-1995;
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Rother RP;
                                                                                                                                                    AAW14932;
                                    303
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Region
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improving xenotransplation human recipients.

463 AA;

Sequence

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                                                                                                                                                                                                                                                                                                                                      302
                                                                           62
                                                                                                                                                                                                                                                                                                                                                                 377 NOVSLICLVKGFYPSDIAVEWESNGQPENNYKTIPPVLDSDGSFFLYSRLTVDKSRWQEG 436
                                                                                                                                                                   197 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV
                                                                                                                                                                                                                                                                        RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK
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                                                                                                       137 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                         FLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY
                                                                                                                                                                                                                                       257 FLFPPKPKDTLMISRTPEVTCVVVDVSQBDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY
                                                                                                                                                                                                                                                                                                                                      NOVSLICLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG
                                                                           3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                           Gaps
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            ; DB 18;
3.2e-126;
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                             Pred. No. 3.2
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                     437 NVFSCSVMHEALHNHYTOKSLSLSLGK 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 62-64; 105pp; English.
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99.4%; SCC...
100.0%; Pre
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                             Best Local Similarity 100. Matches 327; Conservative
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28-SEP-1995;
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Rother RP;
                                                                                                                                          63
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Heavy chain (AAW14938) and light chain (AAW14937) sequences are provided for the murine anti-porcine soluble vascular cell adhesion molecule (VCAM) monoclonal antibody (WAAD) 3F4. Hybridoma 3F4 was produced by standard techniques using recombinant, soluble porcine VCAM as immunogen. Chimeric antibodies can be produced by cloning constant region in place of the human gammal craspion in place of the human gammal Cl region. Sequences are provided for 3F4 (Chimeric) human G2/64 contain the human gammal cl region in place of the human gammal Cl region. Sequences care provided for 3F4 (Chimeric) human G2/64 contain the standard insert product (AAW14949), and 3F4 human IGG4 expression plasmid insert products (AAW14940), and 3F4 chuman insert antibodies are specific for porcine VCAM. They are useful for diagnosing human rejection of porcine xenotransplants and for improving xenotransplants and organs into human recipients.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  318 RVVSVLTVLHQDMLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEMTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 FLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 FLFPPKPKDTLMISRIPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY
                                                                               Antibodies binding to porcine but not human cell interaction proteins - useful to treat and assay for rejection of xenografted porcine organs, tissues or cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-human interleukin-4; IL-4; humanised; purification;
traatment; IL-4 diseases; immunoassay; heavy chain; h25D2-9;
antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-human IL-4 humanised MAb h25D2-9 mature heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.4%; Score 1743; DB 18;
100.0%; Pred. No. 3.2e-126;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 NVFSCSVMHEALHNHYTOKSLSLGK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              438 NVFSCSVMHEALHNHYTQKSLSLGK 464
                                                                                                                                                  Disclosure; Page 53-55; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR80617 standard; Protein; 467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
                                WPI; 1997-212855/19.
N-PSDB; AAT62935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR80617;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG 437
                                                                                                                                                                                                                                                                                             GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV
                                                                                                                                                                                                                                                                                                                                                                FLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY
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                                                                                                                                                                                                      3 ASTKGPSVFPLAPCSRSTSBSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
produced in transfected host cells. It is useful for diagnosing human rejection of porcine xenotransplants and for improving xenotransplantation of porcine cells, tissues and organs into human recipients.
                                                                                                                                                                    ö
                                                                                                                                  Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenotransplantation; graft rejection; cell interaction; pig; vascular cell adhesion molecule; VCAM; monoclonal antibody; chimeric antibody; diagnosis.
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                                                                                                                                                                    Indels
                                                                                                                                   99.4%; Score 1743; DB 18;
.larity 100.0%; Pred. No. 3.2e-126;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mueller JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine anti-porcine VCAM 3F4 heavy chain.
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50..54
/label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW14938 standard; Protein; 464 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69..85
/label= CDR2
118..126
/label= CDR3
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                                                                                                                                   Query Match
Best Local Similarity
Matches 327; Conserv
                                                                                                     464 AA;
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28-SEP-1995;
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Rother RP;
                                                                                                     Sequence
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Region
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Gaps

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Length 464;

197 122

62

317 242 377 302 437

us-09-990-586-100.rag

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NOVSLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOVSLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 Polypeptides (AAW14925-27) respectively comprise the heavy chain regions of human gamma-4, gamma-4E carrying an L236E mutation in the hinge region, and gamma-4PE carrying L236E and 8229P mutations. They can be incorporated into novel monoclonal and chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4FE and CE9 gamma-4PE, in which the human Ig46 FC binding domain framework is combined with the antigen binding domains framework is combined with human CD4 monoclonal antibody E9:1. These antibodies show high affinity to human CD4, have little or no immunogenitity in humans and show reduced or absence of effector function. They can be used to treat autoimmune diseases such as rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
                            CD4; monoclonal antibody; chimaeric antibody; recombinant an cynomolgus monkey; autofimmune disease; rheumatolid arthritis; leukaemia; lymphoma; graft-versus-host disease; asthma; transplant rejection; HIV; therapy; CE9 gamma 4.
                                                                                                                                                                                                                                                                                                                                                                              Chimeric antibody comprising monkey variable domains and hum constant domains - affects CD4-mediated immune functions, euseful for treatment of autoimmune disease, e.g. rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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100.0%; Pred. No. 3.3e-126;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 82-84; 155pp; English
                                                                                                                                                                                                                                                                                                  Reff ME;
                                                                                                                                                                                                       96WO-US14324
Human gamma-4 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327; Conservative
                                                                                                                                                                                                                                                                    (IDEC-) IDEC PHARM CORP
                                                                                                                                                                                                                                                                                                  Hanna N, Newman RA,
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                                                                                                                                                                                                                                                                                                                                WPI; 1997-201913/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    467 AA;
                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT62868
                                                                                                             Homo sapiens.
                                                                                                                                         WO9709351-A1
                                                                                                                                                                                                       05-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 ASTKGPSVPPLAPCSRSTSESTAALGCLVKDYFPBPVTVSWNSGALTSGVHTPPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              AAR80617 is the anti-human IL-4 humanised monoclonal antibody (MAE) AB5D2-9, mature heavy chain. It can be used for the prepp., purifcn. and immunosesay of the humanised Abs. Pharmaceutical compsns. and anti-idiotypic Abs (against the MAD) can also be prepd. for the treatment of IL-4 related diseases by respectively suppressing, or imitating the binding activity of IL-4. The humanised MAD is derived from the rodent. MAD 25D2.
                                                                                                                                                                                                                                                                                                                Humanised monoclonal antibody against human interleukin (IL)-4 has increased binding affinity and expression, and hence greater therapeutic value in the treatment of IL-4 related diseases
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                  1..19
/label= leader_sequence
20..467
/label= mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Pages 109-110; 116pp; English
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 Location/Qualifiers
                                                               mat_peptide
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                                                                                                                                                                                                                                                     Murgolo N,
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                                                                                                                                                                                                                                                      Miller K,
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Hindili fragment of pMDR1001 (see AAG30905); he 7913 bp Not1 linearised pSAB122 (see AAG30906) and a 2109 bp Not1/Hindili fragment of pBAG101 (see AAG30909). These fragments were ligated together and the ligation mixture was used to transform B. coli JA221(fg) to ampicillin esistance. This sequence represents the immunoglobulin signal sequence, amino acids (AA) 1-122 of the humanised SAB heavy chain, variable region (HV) and AA114-AA478 of the humanised SAB heavy chain, i. the constant region (HC). This polypeptide is an antibody homolog which was shown to bind to CD4 but did not block the binding of gp120 to CD4. CD4 is a cell surface glycoprotein of CD4+ lymphocytes (helper/inducer cells). The homolog blocked HIV-induced syncytia formation. This homolog can be used in the detection, prophylaxis and treatment of diseases caused by infective agents whose primary
                                                                                                                                                          Vector; pWDR1002; Not1; HindIII; pWDR1001; pSAB132; pBAG101; E. coli; JA221(Iq); ampicillin; resistance; immunoglobulin; signal sequence; humanised; 588; heavy chali, variable; region; HV; 1gG4; constant; HC; antibody; homelog; CD4; gp120; cell surface glycoprotein; CD4+; lymphocytes; helper; inducer; HIV; syncytia; formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New anti-CD4 antibody homolognes - which bind CD4, do not block binding of HIV gp120 to CD4 but block HIV-induced syncytia formation between CD4+ cells
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'note= "Immunoglobulin signal peptide"
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/note= "Humanised 5A8 HV"
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/note= "Human IgG4 HC"
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                AAR28808 standard; Protein; 468 AA.
                                                                                                                               pre-5A8 humanised heavy chain.
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N-PSDB; AAQ30910.
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3 ASTKGPSVFPLAPCSRSTSBSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                     GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV
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                                                          142 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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Sequence 8, Appli
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                                                                                                                  January 13, 2004, 12:43:20 ; Search time 52.5825 Seconds (without alignments) 1260.812 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB.pep:*

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ALIGNMENTS

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BLOOD COAGULATION AND METHODS		EPVTVS	CNVDHKPSNTKVDKRVESKYGPPCPSCPAPEF	FNWYVE	SVFLFPPKFKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNS
	4; DB 11 1.7e-140 hes 0;	VXDYFP VXDYFP	PSNTKV	EDPEV	EDPEVC
10 NHIBITING 190,586	Score 1754; Pred. No. 1. 0; Mismatches	AALGCL AALGCL	CNVDHK	OSVOVS OVOVS 	WDVSC
9905E FOR ERECE 709/3		STSEST STSEST	GTKTYT	PEVIC	PEVICA
ULT 1 192-990-586-100 UDJication No. US20030109680A1 ENERAL INCORMATION: APPLICANT: JIAO, JUN-AN APPLICANT: JIAO, JIN-AN APPLICANT: WONG, HING C. TITLE OF INVENTION: ANTIBODIES FOR I TITLE OF INVENTION: ANTIBODIES FOR I TITLE OF INVENTION: QUEST THEREOF FILE REPERENCE: 71758/46943-CIP2 CURRENT APPLICATION NUMBER: US/09/99 CURRENT FILING DATE: 2001-11-21 PRIOR APPLICATION NUMBER: 09/293,854 PRIOR PEDITOR DATE: 1999-04-16 NUMBER OF SEQ ID NOS: 102 LENGTH: 209 LENGTH: 209 LENGTH: 209 TYPE: PRT ORCANISM: Home sapiens 09-990-586-100	100.0%; 100.0%; ive	BEASTKGPSVFPLAPCSRSTSBSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLO 	SSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKKVESKYGPPCPSCPAPEFLGGP	SWELFSESSY, VYSSS LEIKI I I CONUDAKTONIKY EDANGED I GFFFF SCEPTE EFFESSY. SVELFPPRRRKOTIMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQPNS	LMISRT
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RESULT 1 US-09-990-586-100 US-09-990-586-100 Sequence 100, Application US/09 Publication No. US20030109680A1 GENERAL INCOMATION: APPLICANT: UTAO, JIN-AN APPLICANT: WONG, HING C. TITLE OF INVENTION: ANTENDIES CURRENT APPLICATION NUMBER: U9/12 CURRENT FILING DATE: 1999-04-16 NUMBER OF SEQ ID NOS: 102 SOFTWARE: PATENTING DATE: 201 SEQ ID NO 100 LENGTH: 329 TYPE: PRT TYPE: PRT GRGANISM: Homo sapiens	Query Match Best Local Similarity Matches 329, Conser				
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                                          241 TKNOVSLICLVKGFYPSDIAVEWESNGOPENNYKTIPPVLDSDGSFFLYSRLIVDKSRWQ 300
                                                                241 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFLYSRLTVDKSRRQ 300
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FUBLICATION NO. US20030176664A1
GENERAL INFORMATION:
APPLICANT: JIAC, JIN-AN
APPLICANT: MICUES, ESPERANZA LILIANA
APPLICANT: NIEUES, ESPERANZA LILIANA
APPLICANT: NIEUES, ESPERANZA LILIANA
APPLICANT: NIEUENA, LUIS A.
TITLE OF INVENTION: THROMBOSES
TITLE OF INVENTION: THROMBOSES
FILE REPRENCE: $8122(1758)
CURRENT APPLICATION NUMBER: 09/990,586
FRICA FILING DATE: 2001-11-21
PRICA PAPLICATION NUMBER: 60/343,306
FRICA FILING DATE: 2001-10-29
FRICA PAPLICATION NUMBER: 09/293,854
FRICA FILING DATE: 1999-04-16
FRICA FILING DATE: 1997-03-10
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181 TYRVVSVITVLHODWLNGKEYKCKVSNKGLPSSIEKTISKAKGOPREPQVYTLPPSQEEM
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1.7e-140;
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Best Local Similarity 100.0%; Pred. No. 1.7
Matches 329; Conservative 0; Mismatches
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                                                                                                                                                             301 EGNVFSCSVMHEALHNHYTQKSLSLGK 329
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US-10-310-113-169
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241 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQ 300
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Sequence 100, Application US/10230880

Publication No. US20030190705A1

GENERAL INFORMATION:
APPLICANT: WONG.
APPLICANT: WONG.
APPLICANT: WONG.
APPLICANT: WOSQUERA, UUIS A.
ITLE OF INVENTION: WETHER A.
ITLE OF INVENTION: WETHER 0.05/10/230, 880

CURRENT FILING DATE: 2002-12-23

PRIOR APPLICATION NUMBER: 09/990, 586

PRIOR PILING DATE: 2001-11-21

PRIOR PILING DATE: 2001-10-29

PRIOR PILING DATE: 2001-02-29

PRIOR PILING DATE: 2001-02-29

PRIOR FILING DATE: 2001-02-29

PRIOR PILING DATE: 201-10-29

SOFTWARE OF SEQ ID NOS: 174

SOFTWARE PEERLING DATE: 201-10-29

SEQ ID NO 100

SEQ ID NO 100

TENGRAL DATE: 201-10-29

PRIOR PILING DATE: 201-10-29

SOFTWARE PEERLING DATE: 201-10-29

SOFTWARE PEERLING DATE: 201-10-29

SOFTWARE PEERLING DATE: 201-10-29

SEQ ID NO 100

TENGRAL DATE: 201-10-29

PRIOR PILING DATE: 201-10-29

PRIOR PILING DATE: 201-10-29

SOFTWARE PEERLING DATE: 201-10-29
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Fatent No. US2002016000641
General No. US2002016000641
General No. US2002016000641
General No. US2002016000641
General No. US2002016000641
General No. US2002016000649
FILE REFERENCE: CENITOPE-06459
FURRENT APPLICATION NUMBER: US/09/925,664
CURRENT FILING DATE: 2001-08-09
FRIOR PLING DATE: 1999-08-09
FRIOR FILING DATE: 1996-06-09
FRIOR FILING DATE: 1996-05-01
FRIOR PLING DATE: 1996-12-06
FRIOR PLING DATE: 1996-12-06
SOFTWARE: Patentin Version 3.1
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100.0%; Score 1754; DB 12; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.7e-140;
Matches 329; Conservative 0; Mismatches 0; Indels 0;
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us-09-990-586-100.rapb

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  242
                                                                                                                          241 NQVSLTCLVKGFYPSDIAVEWBSNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQEG 300
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  183 RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK
                                    181 RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK
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; Sequence 7, Application US/10310719
; Publication No. US2000166163A1
; GENERAL INFORMATION:
    APPLICAT: Gillies, Stephen
; TITLE OF INVENTION: Immuncytokines With Modulated Selectivity
    FILE REFERENCE: LEX.-020
    CURRENT APPLICATION NUMBER: US/10/310,719
    CURRENT FILING DATE: 2002-12-04
    PRIOR APPLICATION NUMBER: 60/337,113
    PRIOR APPLICATION NUMBER: 60/337,113
    PRIOR PILING DATE: 2001-12-04
    PRIOR APPLICATION NUMBER: 60/337,13
    RIOR FILING DATE: 2002-04-12
    NUMBER OF SEQ ID NOS: 37
    SOFTWARE: Patentin Version 3.1
    SEQ ID NO
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; LOCATION: (1)...(327)

; CTHER INFRWATION: Human gamma 4 constant region

US-10-319-7
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                                                                                                                 Length 327;
                                                                                                                                                             Indels
                                                                                                                 Query Match 99.4%; Score 1743; DB 10; Best Local Similarity 100.0%; Pred. No. 1.4e-139; Matches 327; Conservative 0; Mismatches 0;
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; OTHER INFORWATION: Ig gamma-4 chain C region
US-10-112-582-4
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; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-664-47
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Best Local Similarity
Matches 327; Conserv
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US-10-112-582-4
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US-10-282-162-12

US-10-282-162-12

| Sequence 12, Application US/10282162
| Publication No. US20030143697A1
| GENERAL INFORMATION:
| TILL OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
| TILLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
| TILLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
| TILLE NETRIENCE: REG 20.3-B-US
| CURRENT APPLICATION NUMBER: US/10/282,162
| CURRENT APPLICATION NUMBER: 09/787,835
| PRIOR FILING DATE: 1999-09-22
| PRIOR FILING DATE: 1999-09-22
| RIOR FILING DATE: 1999-09-22
| NUMBER OF SEQ ID NOS: 56
| SEQ ID NO 12
| LENGTH: 329
                                                                                                                                                                                     123 FLEPPKPKDTLMISRIPEVICVVJDVSQEDPEVQFNWYVDGVEVHNAKIKPREEQFNSTY
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3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPSPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                    GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV
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CORGANISM: Homo sapiens
US-10-282-162-12
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US-09-935-868-12

US-09-935-868-12

Sequence 12, Application US/09935868

Patent No. US20020164690A1

Patent No. US20020164690A1

Patent No. US20020164690A1

Patent No. US20020164690A1

PAPLICANTON:

APPLICANTON:

REGENERAL REG 203D

CURRENT PILING DATE: 2002-04-11

PRIOR PAPLICATION NUMBER: PCT/US99/22045

PRIOR PERIOR PLING DATE: 1999-09-22

NUMBER OF SEQ ID NOS: 52

SOFTWARE PATENTIN OF SEQ ID NOS: 52

SOFTWARE PATENTIN OF SEQ ID NOS: 52

SOFTWARE PATENTIN OF SEQ ID NOS: 52

SEQ ID NO 12

LENGTH: 329
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       APPLICANT: LARRICK, JAMES W.
APPLICANT: WYCOFF, KEITH L.
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: AND BACTERIAL DISEASES
FILE REFERENCE: 030905.0004.CIP1
CURRENT APPLICATION NUMBER: US/10/047,542
CURRENT FILING DATE: 2001-10-26
PRIOR PAPLICATION NUMBER: PCT/US01/13932
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR PILING DATE: 2001-04-28
PRIOR PILING DATE: 2001-04-28
NUMBER OF SEQ ID NOS: 101
SEQ ID NOS: 101
SEQ ID NOS: 201
LENGTH: 327
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99.4%; Score 1743; DB 10; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.4e-139;
Matches 327; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

99.4%; Score 1743; DB 14; Length 327;
Best Local Similarity 100.0%; Pred. No. 1.4e-139;
Matches 327; Conservative 0; Mismatches 0; Indels 0
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Sequence 4, Application US/09256156A Publication No. US20030105294A1 GENERAL INFORMATION: Stephen D APPLICANT: GILLIES, Stephen D
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                               CITY: New York
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                                                                                                                                                                                                                                                 GAPPLICANT: Neil Stahl and George D. Yancopoulos
TILLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TILLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF WAKING
FILE REFERENCE: REG 203DA
CURRENT APPLICATION NUMBER: U$/10/287,035
CURRENT FILING DATE: 2002-11-01
PRIOR FILING DATE: 2001-08-23
PRIOR FILING DATE: 2001-08-23
PRIOR FILING DATE: 2001-03-22
PRIOR FILING DATE: 2001-03-22
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1998-05-19
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Patent No. US20020098183A1
GENERAL INFORMATION:
APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;
CO, Man S
TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF PREVENTION OF PREVENTION OF PREVENTION OF PREVENTION OF PREVENTION OF PREVENTION OF PREVENTION EXTRACORPOREAL BLOOD CIRCULATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n 99.4%; Score 1743; DB 15; Similarity 100.0%; Pred. No. 1.4e-139; 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 NVFSCSVMHEALHNHYTOKSLSLGK 329
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                                                                                                                                                               ; Sequence 12, Application US/10287035; Publication No. US20030104567A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 327; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: FRT
; ORGANISM: Homo sapiens
US-10-287-035-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-09-917-410-4
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297 RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 FLEPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY
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STATE: New York
CINTINEW YORK
ZIT: 100.2.A.
ZIP: 100.2.A.
ZIP: 100.2.A.
ZIP: 100.2.A.
COMPUTER: BADABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC Compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII, WordPerfect 5.1
CURRENT APPLICATION NUMBER: US/09/917,410
FILING DATE: 26-Jul-2001
CLASSIFICATION NUMBER: 08/578,953
FILING DATE: CURMOWN>
APPLICATION NUMBER: 08/578,953
FILING DATE: CURMOWN>
APPLICATION NUMBER: B 95 114 969.9
FILING DATE: 19-Sep-95
ATORNEY/AGENT INFORMATION:
NAME: Hanson, No. US/20020098183Alman D.
RECTSTRATION NUMBER: 30,946
RECTSTRATION NUMBER: 30,946
REFERENCE/DOCKET WUMBER: BOER 1059-PFF/NDH/SLH
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

99.4%; Score 1743; DB 9; I

Best Local Similarity 100.0%; Pred. No. 2.1e-139;

Matches 327; Conservative 0; Mismatches 0;
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DOPOLOGY: LINear
;
MOLECTLE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-917-410-4
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122 236

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CONFUTER REALMELE FOKEN

WEDDING TYPE: 35 " Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM. PC-DOS/MS-DOS
SOFFWARE: ASCII, WORDERfect 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION: -UNknown>
PRIOR APPLICATION: -UNknown>
APPLICATION NUMBER: 08/578,953
FILING DATE: -UNKnown>
APPLICATION NUMBER: 08/578,953
FILING DATE: -UNKnown>
APPLICATION NUMBER: 89 55 114 969.9
FILING DATE: 10-Sep-95
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US2002009183Alman D.
REFERENCE/DOCKET NUMBER: 30,946
TELECOMMUNICATION NUMBER: 30,946
TELECOMMUNICATION NUMBER: 30,946
TELECOMMUNICATION NUMBER: 30,946
TELECOMMUNICATION NUMBER: 30,946
TELECOMMUNICATION NUMBER: 30,946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 448 amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-917-410-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 838-3
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-401-344-2
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                                             APPLICANT: MESOLOWSKI, John
TITLE OF INVENTION: Enhancing the Circulating Half-life of Antibody-based
TITLE OF INVENTION: Enhancing the Circulating Half-life of Antibody-based
FITLE OF INVENTION: Pusion Proteins
FITLE OF INVENTION: NUMBER: US/09/256,156A
CURRENT APPLICATION NUMBER: US/09/256,156A
EARLIER APPLICATION NUMBER: US 60/075,887
EARLIER PILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTION OF: 2.0
SEQ ID NO 4
LENGTH: 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:

NAME/KEY: VARIANT

LOCATION: (1.17)

OTHER INFORMATION: The Xaa at positions 1 to 117 are non-conserved

COTHER INFORMATION: amino acids

US-09-256-156-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 99.4%; Score 1743; DB 11;
Best Local Similarity 100.0%; Pred. No. 2.1e-139;
Matches 327; Conservative 0; Mismatches 0;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09917410 Patent No. US20020098183A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
  Kin-Ming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-917-410-6
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Sequence 2, Application US/10401344

Sequence 2, Application NO. US2030194404A1

Publication NO. US2030194404A1

Publication NO. US2030194404A1

APPLICANT: Schering Corporation and Abgenix, Inc.

APPLICANT: Greenfeder, Scott

APPLICANT: Correlan, Jose

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO INTERLEUKIN-5 AND METHODS AND COMITITLE OF INVENTION: COMPRISING SAME

TITLE OF INVENTION: COMPRISING SAME

TITLE OF INVENTION: COMPRISING SAME

CURRENT APPLICATION NUMBER: US/10/401,344

CURRENT FILING DATE: 2003-03-27

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn version 3.1
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                                                                                                                                            3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPRPVTVSWNSGALTSGVHTFPAVLQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                     123 FLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY
                                                                           Gaps
                                                                           ö
Query Match
99.4%; Score 1743; DB 9; Length 448;
Best Local Similarity 100.0%; Pred. No. 2.2e-139;
Matches 327; Conservative 0; Mismatches 0; Indels
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COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNABR: US/10/211,357
FILING DATE: 05-Mq-2002
CLASSIFICATION: <unbr/>
VUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.4%; Score 1743; DB 15; 100.0%; Pred. No. 2.3e-139;
                                                                                                                                                                                                                         PRIOR APPLICATION DATA

APPLICATION NUMBER: US/09/612,914A
FILING DATE: 10-041-2000
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-SEP-195
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 912712-165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
99.4%; Score 1743; E
Best Local Similarity 100.0%; Pred. No. 2.3
Matches 327; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 NVFSCSVMHEALHNHYTQKSLSLGK 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECTLE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 8: US-10-211-357-8
                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 467 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
           ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
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Therapy
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ADDRESSES: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
99.4%; Score 1743; DB 12;
Best Local Similarity 100.0%; Pred. No. 2.3e-139;
Matches 327; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVFSCSVMHEALHNHYTQKSLSLSLGK 329
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Publication No. US20030077275A1
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Newman, Roland A.
Reff, Mitchell E.
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                                                                                                                         FEATURE: Variable Region LOCATION: (20)..(138) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                     NAME/KEY: Hinge Region
LOCATION: (237)..(248)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CH2 Region
LOCATION: (249)..(358)
OTHER INFORMATION:
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                  NAME/KEY: CH1 Region
LOCATION: (139)..(236)
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CH3 Region
LOCATION: (359)..(465)
OTHER INFORMATION:
                                                         NAME/KEY: SIGNAL
LOCATION: (1)..(19)
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG
                                                                                                                                             3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
Length 467;
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ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: PLOSDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,277A
FILING DATE: 06-DEC-1996
CLASSIFICATION DATE: 08-D64,664
PRIOR APPLICATION DATE: NO-BAY-1996
TILING DATE: 01-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: MACKAIGHT, KARMIN T.
REGISTRATION NUMBER: 38,230
REGISTRATION NUMBER: 38,230
REFERENCE/POCKET NUMBER: GENITOPE-02406
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 100.0%; Pred. No. 7.8e-158;
Matches 327; Conservative 0; Mismatches 0;
US-09-054-255-2
US-09-26-005-14
US-09-296-005-16
US-09-296-005-18
US-09-282-846-2
US-09-02-144-71
US-09-02-449-71
US-09-02-449-71
US-09-02-449-71
US-09-02-443-71
US-09-214-340A-71
US-09-214-340A-71
US-09-214-340A-71
US-09-214-340A-71
US-09-214-340A-71
US-09-214-340A-71
US-09-214-340A-71
US-09-09-07-22
US-08-146-2066-22
US-08-146-206-22
US-08-08-148-22
US-09-672A-8
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                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 47, Application US/08761277A, Patent No. 597234
GENERAL INFORMATION:
APPLICANT: Denney Jr., Dan W.
TITLE OF INVENTION: Vaccines For Trea TITLE OF INVENTION: Leukemia NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSES: Medlen & Carroll, LLP STREET: 220 Montgomery Street, Suite CITY: San Francisco STATE: California COUNTRY: United States Of America ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 47:
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amino acid
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     MOLECULE TYPE: protein
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Sequence 12, Appl
Sequence 4, Appli
                                                                                                                          ; Search time 28.4463 Seconds (without alignments) 489.353 Million cell updates/sec
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1754
1 EFASTKGPSVFPLAPCSRST......MHEALHNHYTQKSLSLGK 329
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/cgn2_e/ptodata1/iaa/5A_COMB.pep:*
/cgn2_e/ptodata1/iaa/5B_COMB.pep:*
/cgn2_e/ptodata1/iaa/6A_COMB.pep:*
/cgn2_e/ptodata1/iaa/6B_COMB.pep:*
/cgn2_e/ptodata1/iaa/BECOMB.pep:*
/cgn2_e/ptodata1/iaa/PCTUS_COMB.pep:*
/cgn2_e/ptodata1/iaa/Packfiles1.pep:*
                      5.1.6
Compugen Ltd.
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US-08-523-894-8

US-08-523-894-10

US-08-523-894-10

US-08-523-894-10

US-08-523-894-10

US-08-379-516-4

US-08-379-516-4

US-08-379-516-4

US-08-379-516-4

US-08-495-378-4

US-09-409-006A-4

US-09-408-378-67

US-09-408-378-90

US-09-408-378-10

US-09-807-3528-14

US-08-897-3528-16

US-08-109-207C-16
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                      GenCore version (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
                                                                                          protein search, using sw model
                                                                                                                            January 13, 2004, 12:33:50
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Maximum DB seq length: 200000000
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                                       Copyright
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Match
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                                                                                          OM protein
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TYPE: amino acid
STRANDEDNESS: dou
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              PCT-US96-13152-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK 242
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                                                                                                                                                                                RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK 240
                                                                                                                                                                                                                                                         241 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQEG 300
                                GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 120
                                                                       FLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY 182
                                                                                                              PLFPPKPKDTLMISRIPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY 180
                                                                                                                                                 RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK 242
                                                                                                                                                                                                                             NOVSLICLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG 302
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APPLICANT: REGENERON PHARMACEUTICALS, INC.
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: AND USING
FILE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
CURRENT FILING DATE: 1999-05-19
CURRENT FILING DATE: 1999-05-19
PRIOR PELICATION NUMBER: 00/101,858
PRIOR PELICATION NUMBER: 00/101,858
PRIOR FILING DATE: 1999-05-15
PRIOR FILING DATE: 1999-05-5
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV
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Best Local Similarity 100.0%; Pred. No. 7.8e-158;
Matches 327; Conservative 0; Mismatches 0;
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Sequence 12, Application US/09313942
Patent No. 6472179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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APPLICANT: Martin, Ulrich, et al.
APPLICANT: Martin, Ulrich, et al.
TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai
TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: 4
CORRESPONDENCES: Attn: Norman D. Hanson
STREET: 805 Third Avenue
CITY: New York
CUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SUSTWARE: ASCIII.
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99.4%; Score 1743; DB 5; Length 443;
Best Local Similarity 100.0%; Pred. No. 1.2e-157;
Matches 327; Conservative 0; Mismatches 0; Indels
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SOFRARING SISLAM.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13152
FILING DATE:
CLASSIFICATION NUMBER: PCT/US96/13152
FILING DATE:
APPLICATION NUMBER: BP 95.12 895.8
FILING DATE: 17-AUG-95
APPLICATION NUMBER: EP 95.14 969.9
FILING DATE: 19-Sep-95
APPLICATION NUMBER: BP 95.16
FILING DATE: 19-Sep-95
APPLICATION NUMBER: BP 95.16
FILING DATE: 19-Sep-95
APPLICATION NUMBER: BP 95.16
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APPLICATION NUMBER: BP 95.16
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APPLICATION NUMBER: BP 95.16
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APPLICATION NUMBER: BP 95.17
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APPLICATION NUMBER: BP 95.17
FILING DATE: 19-Sep-95
APPLICATION NUMBER: BP 95.17
FILING DATE: 19-SEP-95
APPLICATION NUMBER: BP 95.17
FILING DATE: 19-SEP-95
APPLICATION NUMBER: BP 95.17
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Sequence 4, Application PC/TUS9613152 GENERAL INFORMATION:
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MOLECULE TYPE: protein
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321 KVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSGEEMTK 380
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381 NQVSLTCLVKGFYPSDIAVEWBSNGOPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG 440
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APPLICANT: Hanna, Nabil
APPLICANT: Hanna, Nabil
APPLICANT: Hanna, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
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99.4%; Score 1743; DB 3; I
Best Local Similarity 100.0%; Pred. No. 1.3e-157;
Matches 327; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: BURNS, DOANE, SWECKER & MATHIS 699 Prince Street
                                                                                                                                                                   441 NVFSCSVMHBALHNHYTQKSLSLSLGK 467
                                                                                                                    303 NVFSCSVMHEALHWHYTOKSLSLGK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONTINUE TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOT
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ATTORNEY FLACTION: 424
NAME: Teskin, Robin L.
REGISTATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01271
TELECOMMUNICATION INFORMATION:
TELEFAX: 703-836-620
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                    RESULT 5
US-08-523-894-8
Sequence 8, Application US/08523894
; Patent No. 6136310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-523-894-8
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                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Daile, Barbara
APPLICANT: Daile, Kenneth
APPLICANT: Muller, Kenneth
APPLICANT: Musgolo, Nicholas
APPLICANT: Tindall, Stephen
TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 ASTKGPSVFPLAPCSRSTSBSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Schering-Plough Corporation STREET: 2000 Galloping Hill Road CITY: Kenilworth
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COMPUTER READABLE FORM:

MADIUM TYPE: FORPY disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.5.3

SOFTWARE: Microsoft Word 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/704,744

FILING DATE: US 08/20886

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US/95/02400

FILING DATE: 10-MAR-1994

APPLICATION NUMBER: PCT/US/95/02400

FILING DATE: 10-MAR-1995

ATTORNEY AGENT INFORMATION:

NAME: FOLIKE, CYNICHIA L.

NAME: FOLIKE, CYNICHIA L.

NAME: FOLIKE, CYNICHIA L.

REGISTRATION WUMBER: 32,364

PETENDENCE CYNICHIA L.

NAME: FOLIKE, CYNICHIA L.

REGISTRATION WUMBER: 32,364
           NVFSCSVMHEALHNHYTQKSLSLSLGK 443
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TBLECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2987
                                                                                                                                                                                                                                 Sequence 81, Application US/08704744
Patent No. 5705154
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321 KVVSVLTVLHQDWINGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK 380
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                                                                                                                                                                                                                                                                 PARTENT NO. 6115410:

APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Newman, Roland A.
APPLICANT: Newman, Roland A.
APPLICANT: Newman, Roland A.
APPLICANT: Newman, Recombinant Anti-CD4 Antibodies for Human TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STRRET: 699 Frince Street
STREET: 699 Frince Street
STREET: USA
COUNTRY: USA
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
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98.7%; Score 1731; DB 3;
Best Local Similarity 99.4%; Pred. No. 1.8e-156;
Matches 325; Conservative 0; Mismatches 2;
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441 NVFSCSVMHEALHNHYTQKSLSLSLGK 467
                                                                                                                                                                                                    Sequence 12, Application US/08523894
Patent No. 6136310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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Sequence 10, Application US/08523894

Patent No. 6136310

GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human TITLE OF INVENTION: STREES.

CONDESSEE: BURNES.

COUNTRY: USA

COUNTRY: USA

CONPUTER: NAM COMPATIBLE FORM:
MEDIUM TYPE: RIOPDY disk

COMPUTER: NAM COMPATIBLE FORM:
MEDIUM TYPE: PIOPDY disk

COMPUTER: NAM COMPATIBLE FORM:
MEDIUM TYPE: PATENTIN Release #1.0, Version #1.30

CURRART APPLICATION NUMBER: US/08/523,894

FILING DATE: 06-SEP-1995

CURRARIA APPLICATION NUMBER: US/08/523,894

FILING DATE: USFORM: TYRPORM: TY
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99.0%; Score 1736; DB 3;
Best Local Similarity 99.7%; Pred. No. 6.2e-157;
Matches 326; Conservative 0; Mismatches 1;
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                                                                                                      441 NVFSCSVMHEALHNHYTQKSLSLGK 467
                                                 303 NVFSCSVMHEALHNHYTQKSLSLGK 329
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US-08-523-894-10
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Sequence 4 Application US/08477460B

Patent No. 6034223

GENERAL INFORMATION:
PALED INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
UMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE:
CORRESPONDENCE ADDRESS:
ADDRESSEE:
COOPER & DULDam
243 NOVSLICLVKGFYPSDIAVEWESNGOPENNYKTIPPVLDSDGSFFLYSRLIVDKSRWQEG 302
                                                                                       381 NOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG 440
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COUNTRY:

COUNTRY:

COMPUTER READABLE FORM:

MEDIUM TYPE: IDPDPY disk

CONDUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Batentin Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,460B

FILING DATE: 0 - JUN-1995

CLASSIFICATION NUMBER: US/08/477,460B

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/927,931

FILING DATE: 07-40G-1992

ATTORNEY/AGENT INFORMATION:

NAME: WHITE, JOHN P.

REGERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM

TELEFONMUNICATION INFORMATION:

TELEFONMUNICATION INFORMUNICATION:

TELEFONMUNICATION INFORMUNICATION:

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                                                                                                                                                                                                                   303 NVFSCSVMHEALHNHYTOKSLSLGK 329
                                                                                                                                                                                                                                                                                                                      441 NVFSCSVMHEALHNHYTQKSLSLSLGK 467
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30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 530 amino acide TYPE: amino acide STRANDEDNES: unknown TOPOLOGY: unknown MOLECULE TYPE: CDNA
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US-08-477-460B-4
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STATE: New York
COUNTRY: USA
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                                                                                                                                                              Patent No. 581732
GENERAL INFORMATION:
APPLICANT: GHISHOLM, PATRICIA L.
APPLICANT: GHISHOLM, PATRICIA L.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, WARGARET D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 GLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 FLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWTVDGVEVHNAKTKPREEQFNSTY 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          322 RVVSVLTVLHODWLNGKEYKCKVSNKGLPSSIEKTISKAK-OPREPOVYTLPPSOESMTK 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPRPVTVSWNSGALTSGVHTFPAVLQSS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 GLYSLSSVVIVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FURM:
MEDIUM TYPE Floppy disk
COMBUTER: IBM PC compatible
COMBUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: WARD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,098A
FILING DATE: UNJY 24, 1992
CLASSIFICATION: 424
PRIOR APPLICATION WINDER: PCT/US91/08843
FILING DATE: NO. 5871732ember 27, 1991
CLASSIFICATION WINDER: PCT/US91/08843
APPLICATION WINDER: PCT/US91/08843
APPLICATION WINDER: 26,949
REFERENCE/DOCKET WINDER: 26,949
REGISTRATION NUMBER: 26,949
REGISTRATION STATEMENT NUMBER: 26,949
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MEDIUM TYPE: Floppy
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NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 KNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE 301
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Pred, No. 5.4e-145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 91.9%; Score 1611.5;
Best Local Similarity 92.4%; Pred. No. 5.4e-
Matches 303; Conservative 10; Mismatches
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                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DUS/MS-LOSS
SOCTHARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/329,916
FILING DATE:
CLASSIFICATION:
RECORD APPLICATION DATA:
APPLICATION NUMBER: US/07/927,931
FILING DATE: 07-AUN-1995
APPLICATION NUMBER: 28,678
FILING DATE: 07-AUN-1995
APPLICATION NUMBER: 28,678
REFERENCE DOCKET NUMBER: 41215-A-PCT
TELEPHONE: (212) 977-950
TELEAX: (212) 977-950
TELEX: 422223 COOP UI
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                   ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.2
TITLE OF INVENTION: NON-PEPTIDYL
TITLE OF INVENTION: CD4-GAMMA2 AN UNBER OF SEQUENCES:
SORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham STREET: 30 Rockefeller Plaza CITY: New York STATE: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: homo sapien
;
CELL TYPE: lymphocyte
US-09-329-916-4
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MOLECULE TYPE: c
ORIGINAL SOURCE:
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Patent No. 6083478

Patent No. 6083478

GENERAL INFORMATION:

APPLICANT: Allaway, Graham P.

APPLICANT: Maddon, Paul J.

TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2

TITLE OF INVENTION: No. 8083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2

TITLE OF INVENTION: Immunoconjugates and Uses Thereof

FILE REFERENCE: 41215-A-PCT-US

CURRENT PELING DATE: 1996-06-10

EARLIER APPLICATION NUMBER: PCT/US93/07422

EARLIER APPLICATION NUMBER: 07/927,931

EARLIER APPLICATION NUMBER: 07/927,931

SARIATER APPLICATION NUMBER: 07/927,931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323 VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNST 382
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                                                                                                                                                     241
                                                                                                                           242 KNOVSLICLVKGPYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMT
                                    YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMT
                                                                383 FRVVSVLTVVHQDMLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
91.9%; Score 1611.5; DB 3; Length 530;
Best Local Similarity 92.4%; Pred. No. 5.4e-145;
Matches 303; Conservative 10; Mismatches 14; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09329916
Patent No. 6177549
GENERAL INFORMATION:
APPLICANT: Progenice Pharmaceuticals, Inc.
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ORGANISM: Homo sapiens
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US-09-329-916-4
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US-08-379-516-4
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GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 INMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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91.9%; Score 1611.5; DB 4; Length 530;
Best Local Similarity 92.4%; Pred. No. 5.4e-145;
Matches 303; Conservative 10; Mismatches 14; Indels 1;
503 GNVFSCSVMHEALHNHYTQKSLSLSPGK 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: ENORPY disk
COMPUTER: DATE OF COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT NO DATA:
APPLICATION NUMBER: US/09/409,006A
FILING DATE: 29-SEP-1999
CLASSIFCATION: 424
PRIGR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,931
FILING DATE: 07-AUG-1992
ATTORNEY, ACENT THORNAMION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REPRERENGE/DOCKER NUMBER: 41215-A-PCT,
TELECHONE: (212) 977-9809
TELECK: 42253 COOP UI
TELECK: 42253 COOP UI
SEQUENCE CHARACTERISTICS:
LINGTH: 530 amino acids
LENGTH: 530 amino acids
                                                                                                      RESULT 13
12-09-409-006A-4
: Sequence 4, Application US/09409006A
; Patent No. 6342586
                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Cooper & Dunham STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: homo sapien
CELL TYPE: lymphocyte
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STATE: New York
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MOLECULE TYPE: C
ORIGINAL SOURCE:
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                                                                                                                      APPLICANT: Beaddry, Gary A.
APPLICANT: Maddon, Paul J.
ITILE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMBRAS NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSES: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,227
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P. REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 37690-II-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,372A
                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                Sequence 4, Application US/08485372A
Patent No. 6187748
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amino acid
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SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acid
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                                                                                                                                                                                                                                                                                                                                 STATE: New York COUNTRY: USA
                                                                                                 GENERAL INFORMATION:
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APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDERSS:
ADDRESSEE: Cooper & Dunham
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242 KNOVSLICLVKGFYPSDIAVEWESNGOPENNYKTIPPVLDSDGSFFLYSRLTVDKSRWQE 301
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                                                               443 KNOVSLICLVKGFYPSDIAVEWESNGOPENNYKTIPPMLDSDGSFFLYSKLTVDKSRWOO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41215-A-PCT/JPW/AJM
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                                                                                                                                     302 GNVFSCSVMHEALHNHYTOKSLSLGK 329
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SOFTWARE:
SOFTWARE:
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SOFTWARE:
APPLICATION NUMBER:
FILING DATE:
PRIOR APPLICATION:
FILING DATE:
PRIOR APPLICATION:
APPLICATION NUMBER:
TICKNEY/AGENT INFORMATION:
RAME:
RAME DATE:
ATTORNEY/AGENT INFORMATION:
RAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Cooper & Dunham STREET: 30 Rockefeller Plaza CITY: New York STATE: New York COUNTRY: USA ZIP: 1011
                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application PC/TUS9307422 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPRONE: (212) 977-9809
TELER: (212) 977-9809
TELER: 422523 COP UI
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               530 amino acide
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Best Local Similarity 92.43
Matches 303; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nomo sapien
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TYPE: amino acid
STRANDEDNESS: un)
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MOLECULE TYPE: c
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 VFLPPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST 181
       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPS
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                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
91.9%; Score 1611.5; DB 4
Best Local Similarity 92.4%; Pred. No. 5.4e-145;
Matches 303; Conservative 10; Mismatches 14;
                                                                                                                                                                           503 GNVFSCSVMHEALHNHYTQKSLSLSPGK 530
                                                                                                            GNVFSCSVMHEALHNHYTOKSLSLGK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,681
FILING DATE: 07-07N-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFTWARE: PATENTIN Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37690-II-B
                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08484681
Patent No. 6451313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 530 emino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 278-04 TELEFAX: (212) 391-0525
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unknown
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;
CELL TYPE: lymphocyte
US-08-484-681-4
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                                                                                                                                                                                                                                                                                                                US-08-484-681-4
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383 FRVVSVLTVVQDMLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVTLFPSREEMT 442
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	301	502
	DGSFFLYSRLTVDKSRWQE	443 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQ 502
	PENNYKTTPPVLDS	DPENNYKTTPPMLDS
1	GFYPSDIAVEWESNG	GFYPSDIAVEWESNG
	KNOVSLTCLVK	KNOVSLTCLVK
	242 K	443

³⁰² GNVFSCSVMHEALHNHYTQKSLGLSLGK 329

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Search completed: January 13, 2004, 12:46:36 Job time : 29.4463 secs QQ

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Ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain pre ig heavy chain pre ig heavy chain pre ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r ig heavy chain v r
                                                          / Search time 1.23231 Seconds
(without alignments)
1326.664 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                     283308 segs, 96168682 residues
                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                         Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       - protein search, using sw model
                                                           January 13, 2004, 12:22:35
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$26320
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S52445
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137262
PH1493
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$28572
$26312
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Gapop 10.0 , Gapext 0.5
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1 YIDPYNGITIYDQNLKG 17
                                                                                                                                                                                                              seq length: 0
seq length: 200000000
                                                                                                  US-09-990-586-101
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Match Length
          Copyright
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1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*
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                                                                                                            Perfect score:
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Maximum DB
                                        OM protein
                                                                                                                       Sequence:
                                                                                                                                                                       Searched:
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30 50 52.6 109 2 PH1094 Ig heavy chain V r
31 50 52.6 109 2 PH1096 Ig heavy chain V r
32 50 52.6 109 2 PH0989 Ig heavy chain V r
33 50 52.6 110 2 PH0989 Ig heavy chain V r
34 50 52.6 111 2 PH0999 Ig heavy chain V r
35 50 52.6 111 2 PH0999 Ig heavy chain V r
36 50 52.6 111 2 PH0999 Ig heavy chain V r
37 50 52.6 111 2 PH0999 Ig heavy chain V r
38 50 52.6 112 2 A30502 Ig heavy chain V r
40 50 52.6 114 2 PH1522 Ig heavy chain V r
41 50 52.6 114 2 PH1523 Ig heavy chain V r
42 50 52.6 119 2 PH1523 Ig heavy chain V r
43 50 52.6 119 2 PH1517 Ig heavy chain V r
44 50 52.6 119 2 PH1521 Ig heavy chain V r
45 50 52.6 119 2 PH1521 Ig heavy chain V r
46 50 52.6 119 2 PH1521 Ig heavy chain V r
47 50 52.6 119 2 PH1521 Ig heavy chain V r
48 50 52.6 119 2 PH1521 Ig heavy chain V r
48 50 52.6 119 2 PH1521 Ig heavy chain V r
48 50 52.6 119 2 PH1521 Ig heavy chain V r
48 50 52.6 119 2 PH1521 Ig heavy chain V r
48 50 52.6 119 2 PH1521

ALIGNMENTS

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RESULT 2
A49982
Igheavy chain V region (BA7.1) - mouse (fragment)
Igheavy chain V region (BA7.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Keptus preliminary
A;Reference number: A49982; MUID:94132051; PMID:8300613
A;Residues: 1-120 < LIN>
A;Residues: 1-120 < LIN>
A;Residues: 1-120 < LIN>
A;Residues: 1-120 < LIN>
A;Residues: 1-120 < LIN>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology < INM>
F;15-98/Domain: immunoglobulin homology < INM>
anti-digoxin transfectoma antibody light chain V region precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: PHO105
R;Near, R.I.; Ng, S.C.; Mudgett-Hunter, M.; Hudson, N.W.; Margolies, M.N.; Seidman, J.G.
R;Near, R.I.; Ng, S.C.; Mudgett-Hunter, M.; Hudson, N.W.; Margolies, M.N.; Seidman, J.G.
A;Title: Heavy and light chain contributions to antigen binding in an anti-digoxin chain A;Reference number: PHO105; MUID:91015092; PMID:2120577
                                                                                                                                                                                                                                                                                                                                                                                                                                  A)Cross_references: GB:X56622, GB:S44836; NID:g49875; PIDN:CAA39960.1, PID:g49876
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>
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Pred. No. 0.025;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 60; DB 2;
Pred. No. 0.02;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YIDPYNGITIYDQNLKG 17
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Best Local Similarity 62.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 58.8%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                        A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-138 <NEA>
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1 YIDPYNGITIYDONEK 16 : | | | | | | | | |

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Gaps

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;Accession: PS0057
;Yaoita, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, T.
;Yaoicem. 104, 37-343, 1988
;Title: Biased expression of variable region gene families of the immunoglobulin heavy
;Reference number: PS0057; MUID:89197817; PMID:2467902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and after H chain swi
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A Molecule type: DNA

A) Residues: 1-13 c XAO.

A) Residues: 1-13 c XAO.

A) Residues: 1-13 c XAO.

A) Cross-references: GB:D00307; NID:g220448; PIDN:BAA00213.1; PID:g220449

A) Note: the authors translated the codon AAG for residue 32 as Asn and GAC for 92.

C) Comment: The gene encoding this protein was isolated from a hybridoma that product C; Superfamily: immunoglobulin V region; immunoglobulin homology

C) Keywords: heterotetramer; immunoglobulin munoglobulin homology

C) Regionaln: signal sequence #status predicted <SIG>

F; 1-13/Domain: signal sequence #status predicted <AMAI>

F; 34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                             ) heavy chain precursor V region (PAR) - mouse
Species: Mus musculus (house mouse)
Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jacobs that the precursor V region (I29) - mouse Ig heavy chain precursor V region (I29) - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Species: Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999 C;Accession: A27609 #s.frlain, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.
R;Klain, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.
A;Title: I.29 lymphoma cells express a nonmutated V-H gene before and after A;Reference number: A27609; MUID:88154467; PMID:3126234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A)Accession: A27609
A;Molecule type: DNA
A;Residues: 1-139 «KLE»
A;Cross-references: EMBL:M19401; NID:g195441; PIDN:AAA38303.1; PID:g553992
A;Antrons: 16/1
C;Genetics: A;Antrons: L6/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramery chain V region 129 #status predicted «SIG»
F;20-139/Product: Ig heavy chain V region 129 #status predicted «VAR»
F;34-117/Domain: immunoglobulin homology <IMM>
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                                                                                                                                              4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
0.061;
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Pred. No. 0.063;
2; Mismatches
                                                                                        DB 2;
                                                                                                                    0.05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.0%; Score 57; DB 62.5%; Pred. No. 0.06 iive 2; Mismatches
                                                                                                                                                 Mismatches
C; Keywords: heterotetramer; immunoglobulin F;11-94/Domain: immunoglobulin homology <IMM>
                                                                                        Score 57;
Pred. No.
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58.8%;
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                                                                                     60.0%;
ilarity 62.5%;
Conservative
                                                                                                                                                                                                             2 IDPYNGITIYDQNLKG 17
                                                                                                                                                                                                                                                                  47 INPÝNGDÍFÝNOKFKG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YIDPYNGITIYDONLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 YINPYNDYTSYNOKFKG
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Best Local Similarity 58.8°
Matches 10, Conservative
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Best Local Similarity 62.5
Matches 10; Conservative
                                                                                        Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: PS0057
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S26320
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
R;Stark, S.E.; Caton, A.J.
A;Tite: Antibodies that are specific for a single amino acid interchange in a protein e A;Reference number: S26309; MUD:91341421; PMID:1908510
A;Reference number: S26309; MUD:91341421; PMID:1908510
A;Residues: 1-107 <STA>
A;Residues: BMBL:X59206
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;3-86/Domain: immunoglobulin homology <IMM>
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C; Species: Max musculus (house mouse)
C; Species: Max musculus (house mouse)
C; Accession: S26319
S; Stark, S.E., Caton, A.J.
D.Exp. Med. 174, 613-624, 1991
A,71tle: Antibodies that are specific for a single amino acid interchange in a protein A, Recession: S26319
A,Accession: S26319
A,Molecule type: mRNA
A,Residues: 1-114 <S73.
A,Crose-references: STRA.
A,Crose-references: STRA.
C,Crose-references: STRA.
C,Crose-references: STRA.
C,Crose-references: STRA.
C,Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                        RESULT 3
517604
19 heavy chain V region - mouse
C) Species: Mus musculus (house mouse)
C) Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000.
C) Accession: S17604
R) Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
R) Title: Making antibody fragments using phage display libraries.
A) Reference number: S17230; MuID:91326098; PMID:1907718
A) Accession: S17604
A) Residues: 1-98 <CLAA
A) Residues: 1-98 <CLAA
C) Superfamily: immunoglobulin V region; immunoglobulin homology
C) Keywords: heterotetramer; immunoglobulin
F;8-91/Domain: immunoglobulin homology <INM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 60.0%; Score 57; DB 2; Length 98; Best Local Similarity 62.5%; Pred. No. 0.043; Matches 10; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
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0.047;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 IDPYNGITIYDQNLKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INPYNGDTFYNOKFKG 59
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Best Local Similarity 66.7
Matches 10, Conservative
               50 HISPYNGATTYNONFK
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Gaps

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Ig heavy chain V region (1G3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C;Accession: B37263
R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
BAOL. Chem. 26.4, 2144-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same antigen: A;Reference number: A38601; MUID:91115823; PMID:1703527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain V region (7D4) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C;Accession: 637263
B;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A;Pitle: Common structural features among monoclonal antibodies binding the same antigen A;Reference number: A38601; MUID:91115823; PMID:1703527
A;Accession: 637263
A;Status; preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain V region precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S5445
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; not compared with conceptual translation A;Status: preliminary; not compared with conceptual translation A;Molacule type: mRNA A;Residuse: 1-102 <GOS> A;Residuse: 1-102 <GOS> A;Residuse: 1-101 <GOS> CSOS <A;Cross-references: GB:MS7997; NID:g195426; PIDN:AAA63335.1; PID:g195427 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;7-90/Domain: immunoglobulin homology <INM>
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Pred. No. 0.2;
                                                                                                Length 120;
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                                                                                                    DB 2;
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C; Keywords: glycoprotein
F;15-99/Domain: immunoglobulin homology <IMM>
                                                                                                    Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 53;
Pred. No.
                                                             56.8%; Scc.
62.5%; Pred
2; J
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Local Similarity 62.5%;
Les 10; Conservative 1
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                                                                                                                                                                                                                                                                                                                   67
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52 INPYNGGTSYNQKFKG
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Best Local Similarity 62.5%
....hes 10; Conservative
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                                                                                                    Query Match
Best Local Similarity 62.5
Matches 10; Conservative
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A; Residues: 1-72 <GOS>
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Matches
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C; Species: Mus musculus (house mouse)
C; Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C; Accession: E4572
R; Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu A; Virol, 67, 4894-496, 1993
A; Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu A; Reference number: A45722; MUID: 93100833; PMID: 7677958
                                                                                                Ig heavy chain precursor V region (Mab 1G3) - mouse (fragment)

C) Species: Was musculus (house mouse)

C) Species: Was musculus (house mouse)

C) Accession: 845249, 841429

C) Accession: 845249, 841429

C) Accession: 845249, 841429

Nucleic Acids Res. 22, 1768-1769, 1994

A) Title: PCR amplification of antibody variable regions using primers that anneal to compare service ammber: 845249, MUID: 94261453; PMID: 8202386

A) Reference number: 845249, MUID: 94261453; PMID: 8202386

A) Accession: 845249

A) Residues: 1-138 < SAS>

A) Residues: 1-138 < SAS>

A) Residues: Lila & SAS>

A) (C) Superfamily: immunoglobulin v region; immunoglobulin homology

C) Superfamily: immunoglobulin homology < INM>

F) 34-117/Domain: immunoglobulin homology < INM>
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$17608
Igheavy chain V region - mouse
Igheavy chain V region - mouse
Igheavy chain V region - mouse
Igheavy chain V region - mouse
Igheavy chain V region - mouse
Igheavy chain V region - mouse
Igheavy region 10-Nov-1995 #text_change 21-Jan-2000
Igheave 122-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
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A, Status: preliminary; not compared with conceptual translation A, Status: preliminary; not compared with conceptual translation A, Molecule type: nucleic acid A, Regiues: 1-20 <51M > A, Note: sequence extracted from NCBI backbone (NCBIP:120593) C, Superfamily: immunoglobulin V region; immunoglobulin homology
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;8-91/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 138;
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60.0%; Pred. No. 0.091;
tive 3; Mismatches
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Pred. No. 0.088;
2; Mismatches
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Matches 10; Conservative
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Actes: 30-Aug-1931 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C;Actession: 137262
R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
B;Goshorn, Chem. 256, 2134-2142, 1991
A;Title: Chem. 256, 2134-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same antigen A;Reference number: A38601; MUD:91115823; PMID:1703527
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C. Species: Mus musculus (house mouse)

C. Species: Mus musculus (house mouse)

C. Date: 30-Aug-1991 #sequence_revision 03-Apr-1992 #text_change 16-Aug-1996

C. Chacession: A37-263

R. Gocshorn, S. C.; Retzel, E.; Jemmerson, R.

J. Biol. Chem. 266 2134-2142, 1991

A. Aitle: Common structural features among monoclonal antibodies binding the same antigen A. Reference number: A38601; MUID: 91115823; PMID: 1703527

A. Accession: A37-263

A. Status: preliminary

A. Residues: 1-93 < GOS.

A. Accession: Brandland A. Residues: 1-93 < GOS.

A. Accession: A37-263

A. A. Cross-references: GB: MS7-96

A. A. Cross-references: GB: MS7-96

A. Mote: the authors translated the codon CAA for residue 38 as His, AGA for residue 39 a C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: heterotetramer; immunoglobulin
R;Berdoz, J.; Kraehenbuhl, J.P.
submitted to the EMBi. Data Library, November 1994
A;Description: Specific amplification by the polymerase chain reaction of rearranged gen
A;Reference number: S52445
A;Accession: S52445
A;Accession: S52445
A;Accession: S52445
A;Accession: S52445
A;Accession: S52445
A;Corosr-references: DNA
A;Residues: 1-137 <BRS
A;Cross-references: EMBL:X82690; NID:g673439; PIDN:CAA58011.1; PID:g673440
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-115/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 52.9%; Pred. No. 0.28;
Matches 9; Conservative 3; Mismatches 5; Indels
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Search completed: January 13, 2004, 12:44:44 Job time: 2.23231 secs

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Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,

Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,

Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,

A Marshak-Rochstein A.;

"The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";

If "The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.";

If "Interprose the strain A mouse.";

Burn Genetic Dasis Strain A mouse.";

Interprose Train A mouse
P35580 homo sapien
O9jlt0 rattus norv
P02555 mus musculu
P37930 pseudomonas
008691 mus musculu
008701 rattus norv
P47516 mycoplasma
P51487 calliphora
P93841 lycopersico
083401 treponema p
P03100 human papil
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
(CPI_TaxID=10090;
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                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
By heavy chain V region 36-65.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                            120 AA
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    MYHA HAT
MYHA RAT
CRBA MOUSE
HRPR PSESY
ARGZ MOUSE
ARGZ MAUGE
ODPA WYCGE
ARRB CALVI
ISPE IYCES
MYETTREPA
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Pfam, PF00047; ig; 1.
PROSITE; PSS0835; IG LIKE; 1.
Immunoglobulin V region; Hybridoma.
111 IG-LIKE.
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       STANDARD;
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        HV03 MOUSE
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                      GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                 127863 seqs, 47026705 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
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RP04_MOUSE
RP04_MOUSE
HV15_MOUSE
HV12_MOUSE
HV13_MOUSE
HV13_MOUSE
HV13_MOUSE
HV13_MOUSE
HV02_MOUSE
VUL HPV13
WUL HPV13
VUL FCPV1
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ATIN HSVBP

ATTA MYCGE

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Gapop 10.0 , Gapext 0.5
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95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-8222222; PubMed-6806821;
KRAPP M.K., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S., Blattner F.R.;
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Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
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ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, I BETA CHAIN, AND
                                                          -!- SIMILARITY: Belongs to the RNA polymerase beta chain family.
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PIR; T43230; T43230.

RISSP; OSKWUT; 1HQM.

RISSP; OSKWUT; 1HQM.

PEam; PP04563; RNA_pol_Rpb2_1; 1.

Pfam; PP04565; RNA_pol_Rpb2_2; 2.

Pfam; PP06565; RNA_pol_Rpb2_3; 1.

Pfam; PP06562; RNA_pol_Rpb2_6; 1.

Pfam; PP04560; RNA_pol_Rpb2_6; 1.

PROSTE; PS01166; RNA_pol_Rpb2_7; 1.

PROSTE; PS01166; RNA_pol_Rpb2_7; 1.

RICHARGERASE; Transcription; DNA_directed RNA polymerase.

SEQUENCE 1302 AA; 146533 MM, 6D971C23EB9FBB2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 47; DB 1; Length 1302;
Pred. No. 15;
4; Mismatches 3; Indels
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21-UUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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HSSP, P01772, 2FB4.
InterPro; IPR00710; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR03596; Ig_V.
Pfam; PF00047; ig; 1.
SWART; SM00406; IGV; 1.
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Best Local Similarity 50.0
Matches 7; Conservative
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HV15_MOUSE
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                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its web by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.

MEDILINE=65257200; PubMed=8675039;

Laigret F., Gaurivaud P., Bove J.;

The unique organization of the rpoB region of Spiroplasma citri: a restriction and modification system gene.is adjacent to rpoB.";

Gene 171:95-98(1996).
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01-FEB-1996 (Rel. 33, Last sequence update)
11-DEC-1998 (Rel. 37, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RA polymerase beta subunit).
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          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
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Givol D., Zakut R., Effron K., Rechavi G., Ram D., Cohen J.B.;
"Diversity of germ-line immunoglobulin VH genes.";
Nature 292:425-430(1981).
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51.6%; Score 49; DB 1; Length 117;
Best Local Similarity 62.5%; Pred. No. 0.51;
Matches 10; Conservative 1; Mismatches 5; Indels
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IG-LIKE.
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117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;
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Spiroplasmataceae; Spiroplasma.
NCBI TaxID=2133;
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SMART; PR00406; IGv.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL
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AC P47767;
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HV12 MOUSE
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Kunst F., Ogasawara N., Moszer I., Bototin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S.,
RA Derriss R., Bourschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Broullet S., Bruschi C., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Ghoi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Britz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron D.,
RA Ghim S.Y., Claser P., Goffeau A., Gollghily B.J., Grandi G.,
Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hibbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Krodh S., Kumano M.,
RA Kunita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kobayashi Y., Koetter P., Mizuno M., Mosell D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Report R., Scanlan E., Schleich S., Schroeter R., Sadaie Y.,
Rateger M., Rivolta C., Rocha B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Resecon B., Takagi T., Takahashi H., Takahashi H., Takahashi H., Takahashi H., Takahashi H., Takahashi H., Takahashi H., Takahashi H., Takahashi H., Takahashi H., Takahashi H., Takahashi H., Takahashi H., Takahashi H., Takahashi H., Takahashi H., Takahashi H., Takahashi H., Takahashi H., Vanisasarotti A.,
Rakeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Teppera
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STRAIN=168 (7 HB2058).
MEDLINE=168 (7 HB2058).
Chen L., Helmann J.D.;
"The Bacillus subtilis sigma D-dependent operon encoding the flagellar proteins FilD, Fils, and Filt.";
J. Bacteriol. 176:3093-3101(1994).
                                                                                               IG HEAVY CHAIN V REGION BCL1. IG-LIKE.
                                                                                                                                                                                                                                                              Score 46; DB 1; Length 136; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                               20 136 IG HEAVY CHAIN V REGION BG
20 135 IG-LIKE.
136 136 W, 6827CFBC6DB3F35E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Flagellar protein flir.
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MEDLINE=98044033; PubMed=9384377;
       PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region; Signal.
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                                                                                                                                                                                                                                                                                                                                 9; Conservative
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Best Local Similarity
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FILT BAGSU  
AC P39740,  
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AC P39740,  
BACTINES PREB-1995 (Re. DT 0.1-FEB-1995 (Re. DE FIGURE FROM NC NCEL FROM NC STRAIN=168 / HB MEDLINE=9425297 RA CHen L. Helman RT TABLINE=9425297 RA CHEN L. HELMAN REPUBLINE=9425297 RA CHEN L. HELMAN REPUBLINE=9404401 RA STRAIN=168; BEN SEQUENCE FROM NC STRAIN=168; BEN SEQUENCE FROM NC STRAIN=168; BEN SEQUENCE FROM NC STRAIN=168; BEN SEQUENCE FROM NC STRAIN=168; BEN SEQUENCE FROM NC STRAIN=168; BEN SEQUENCE FROM NC STRAIN=168; BEN SEQUENCE STRAIN RA CONSER RA CONSER RA CONSER RA CONSER RA CONSER RA CONSER RA RESEQUENT NC NC NC RA STACKIN RA SACTOUND NC THE RA SACTOUND NC THE RA SACTOUND NC THE RA SACTOUND NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE RA TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC THE TAKEUCH NC TH
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=83075344; PubMed=6816276;
Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
Hood L.E.;
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BY SIMILARITY.
N-LINKED (GLCNAC. . .) (COMPLEX).
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EMBL; U56901; AAC44555.1; -.
EMBL; U56912; CAB15549.1; -.
FIR; I40399; I40399.
Subtilist; BG10939; flift.
Flagella; Complete protecome.
SEQUENCE 113 AA; 13536 MW; 5AA78802EBDBABBE CRC64;
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Pred. No. 2.2;
3; Mismatches
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, Last annotation update)
                                                                                                                                               -i- FUNCTION: NOT KNOWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence
15-SEP-2003 (Rel. 42, Last annotati
15 heavy chain V region MOPC 104E.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12983 MW;
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95 YLNPYNNITIDGTYYDK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YIDPYNGITI----YDO 13
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InterPro; IPR003006; IG MHC.
InterPro; IPR003596; IG_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.4%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 52...
Best Local Similarity -- Yr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                 Nature 390:249-256(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 1
117 AA;
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P01756;
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440 DPYDGINFWNVNLK 453
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Best Local Similarity 56.21
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Major capsid protein L1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Papillomavirus.
NCBI_TaxID=10602;
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NON TER
SEQUENCE
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Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
"A V region determinant (idiotope) expressed at high frequency in B
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-03N-1988 (Rel. 06, Created)
01-03N-1988 (Rel. 06, Last sequence update)
15-0UL-1999 (Rel. 38, Last annotation update)
15-busy chain V region AC38 205.12.
Mus musculus (Mouse).
Mus musculus (Mouse).
Mus musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
Musculus (Mouse).
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Musculus (Musculus).
Musculus (Musculus).
                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
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Best Local Similarity 56.2%; Pred. No. 2.3;
Matches 9; Conservative 2; Mismatches 5; Indels
    DB 1; Length 117;
                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;
                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
heavy chain V region J558.
Mus musculus (Mouse).
  Query Match
47.4%; Score 45; DB 1
Best Local Similarity 56.2%; Pred. No. 2.3;
Matches 9; Conservative 2; Mismatches
                                                                                                                                                                                                        117 AA
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INPNNGGISYNOKFKG 66
                                                                            2 IDPYNGITIYDONLKG 17
                                                                                                  |:| |:| |:| |:| 51 INPNNGGTSYNQKFKG 66
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                                                                                                                                                                                                          STANDARD;
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P06330;
                                                                                                                                                                                                        MOUSE
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SEQUENCE
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                                                                                                                                                                    RESULT 7
HV13 MOUSE
ID HV13 MOUS
AC P01757;
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lymphocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523(1984).
EMBO J. 3:517-523(1984).
EIR, A002040; MEMES B.
HSEP: PO17089; 1MCP.
INTERPRO; IPRO03106; Ig_MHC.
INTERPRO; IPRO03066; Ig_MHC.
INTERPRO; IPRO03066; Ig_V.
Pfam; PF00047; ig; 1.
PROSITE; PSSO835; IG_LIRE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDIINE=91374616; PubMed=1716694;
Reuter S., Delius H., Kahn T., Hofmann B., Zur Hausen H., Schwarz E.;
Reuter S., Delius H., Kahn T., Hofmann B., Zur Hausen H., Schwarz E.;
"Characterization of a novel human papillomavirus DNA in the cervical carcinoma cell line ME180.";
J. Virol. 65:5564-5568(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.4%; Score 45; DB 1; Length 118; 56.2%; Pred. No. 2.3; ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human papillomavirus type ME180.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; B40509; PIWLPR.
InterPro; IRR002210; PV_capsid_L1.
InterPro; IRR002210; PV_capsid_L1.
PRIMTS; PR00865; HPVCAPSIDLI.
PRINTS; PR00865; HPVCAPSIDLI.
Prodom; PD00644; PV_capsid_L1; 1.
Cact protein; Late protein L1; 1.
SEQUENCE 505 AA; 56805 MW; 595DE493B708207B CRC64;
                                                                                                                                                                                                                                                                                                                                                           1 98 V SEGMENT.

99 104 D SEGMENT.

105 118 J SEGMENT.

2 96 BY SIMILARITY.

118 118 118 11934 MW; 94F7BEE4C762A018 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VII HPVME STANDARD; PRT; 505 AA. P27564; 01-AUG-1992 (Rel. 23, Created) L4UG-1992 (Rel. 23, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M73258; AAF14010.1; -.
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Gaps

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us-09-990-586-101.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rodriguez-Sainz M.C., Hernandez-Chico C., Moreno F.; "Molecular characterization of pmbA, an Bscherichia coli chromosomal gene required for the production of the antibiotic peptide MccB17."; Mol. Microbiol. 4:1921-1932(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND CHARACTERIZATION.
STRAIN=K12;
MURDLINES-8617756; PubMed=8604133;
Murayama N., Shimizu K., Miki T.,
Horiuchi T., Sekimizu K., Miki T.,
Faiddence for involvement of Escherichia coli genes pmbA, csrA and previously unrecognized gene tidb, in the control of DNA gyrase by letb (ccdB) of sex factor F.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
NCBI_TaxID=562, 83334,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Analysis of the Bacherichia coli genome VI: DNA sequence of region from 92.8 through 100 minutes."; Nucleic Acids Res, 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 1; Length 335;
Pred. No. 10;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEĞUENCE FROM N.A.
STRALN=XL2 / MG1655,
MEDLINE-95334562; Pubmed=7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
               Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                             40139 MW; 9DE51B219062E8E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
PmbA protein (TidE protein)
PMBA OR TIDE OR B4235 OR Z5845 OR ECS5212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91186828; PubMed=2082149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Biol. 256:483-502(1996).
                                                                                                                                                                                                                                         EMBL; U10401; AAA19057.1; -.. PIR; T16904; T16904. Wormhep; T20812.4; CE01410. Hypothetical protein. SEQUENCE 335 AA; 40139 MM;
                                                                                                                                                                                                                                                                                                                                                                   46.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli, and Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 IDPYESITIY 307
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Best Local Similarity
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P24231;
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-aib.ch/announce/or send an email to license@isb-sib.ch).
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                             MEDLINE-82152818; PubMed-6801765;
Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
                                                                                                                                                                                                                                                                                                                                                                                         "Somatic mutation in genes for the variable portion of the finanuoglobulin heavy chain."; science 216:309-311(1982).
-i- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 1; Length 140;
Pred. No. 4;
3; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Hypothetical 40.1 kDa protein T20B12.4 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;
                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region 93G7 precursor.
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PROSITE; PSS0835; IG LIKE; 1.
Immunoglobulin V region; Hybridoma; Signal.
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7 47,1%; Pred
3; N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YIDPYNGITIYDQNLKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 YINPGNGYINYNEKFKG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 47.1
es 8; Conservative
                                                           STANDARD;
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                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=A/J:
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SEQUENCE FROM N.A.
STRAIN=Bristol N2;
                                   HV02 MOUSE
ID HV02 MOUSE
AC P01746;
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SEQUENCE
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P41844;
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CHAIN SIGNAL

YO94_CAEEL
AC AC P4184_C
AC P41844_C
AC P4184_C
AC D1.NOV
DT 01.NOV
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RESULT 11

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VL1 PCPV1
Q02274;
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VL1_PCPV1
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SEQUENCE FIRSTON PubMed=11258796;

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MEDLINE=21156231; PubMed=11258796;

MEDLINE=21156231; PubMed=11258796;

MID T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

A. Inda T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

M. Complete genome sequence of enterohemorrhagic Escherichia coli

O157:H7 and genomic comparison with a laboratory strain K-12.";

O157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).

PUNCIION: MAY FACILITATE THE SECRETION OF THE PEPTIDE ANTIBIOTIC

NICROCIN B17 (MCGB17) BY COMPLETING ITS MATURATION. SUPPRESSES THE

INHIBITORY ACTIVITY OF THE CHEON STORAGE REGULATOR (CSRA).

C. I. SIMILARITY: BELONGS TO THE TLDD/FWBA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-92391075; PubMed-1325697;
van Ranst M., Fuse A., Fiten P., Beuken E., Pfister H., Burk R.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; Lin G., Yen G., Schwartz D.C., "Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.", Nature 409:529-533 (2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.3%; Score 44; DB 1; Length 450; 72.7%; Pred. No. 14; ive 1; Mismatches 2; Indels
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Major capsid protein L1.
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InterPro; IPR002510; PmbA_TldD.
Pfam; PF01523; PmbA_TldD; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X54152; CAA38091.1; -.
EMBL; D44452; BAA07915.1; -.
EMBL; U14003; AAA97132.1; -.
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67 GITVYHQNRKG 77
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EMBL; AE00565; AAG59
EMBL; AP002668; BAB38
PIR; D86121; D86121.
PIR; D81280; D91280.
PIR; S13730; S13730.
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Best Local Similarity
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NCBI_TaxID=10573;
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SEQUENCE 450 AA
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Q02273;
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VL1_HPV13
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type 1: comparison of the genome organizations.";
Virology 190:587-596(1992).
Opdenakker G., "Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: comparison of the genome organizations.",
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van Ranst M., Fuse A., Fiten P., Beuken E., Pfister H., Burk R.D.
Opdenakker G.;
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Pred. No. 16;
4; Mismatches 3; Indels
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Pfam; PF00500; late_protein_L1; 1.

PRINTS; PR00665; HPVCAPRIDI1.

ProDom; PD000544; PV capsid_L1; 1.

Coat protein; Late protein.

SEQUENCE 502 AA; 55718 MW; A22D1980EEA94BA3 CRC64;
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InterPro; IPRO210; PV_capsid_L1.
PFfam, PF005050; late_protein_L1; 1.
PRINTS; PR00865; HPVCAPSIDL1.
Probom; PD000444; PV_capsid_L1; 1.
Crobom; PD000444; PV_capsid_L1; 1.
SEQUENCE 499 AA; 55773 WW; AA6D5F7FFFD24759 CRC64;
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01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Major capsid protein L1.
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7; Conservative
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                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=99128221; PubMed=9929332;
Douglas S.E., Penny S.L.;
"The plastid genome of the cryptophyte alga, Guillardia theta:
complete sequence and conserved synteny groups confirm its common ancestry with red algae.";
J. Mol. Evol. 48:236-244(1999),
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF64483; RNA pol Rpbl 3; 1.
Pfam; PF64089; RNA pol Rpbl 4; 1.
Pfam; PF65000; RNA pol Rpbl 4; 1.
Pfam; PF64089; RNA pol Rpbl 5; 2.
SEQUENCE 1286 AA; 145044 MW; BEFF46FEF552C73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  {RNA}(N).
-!- SUBUNIT: In chloroplasts, the RNA polymerase is composed of four subunits: alpha, beta, beta', and beta''
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBSTRATES.
CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                    Guillardia theta (Cryptomonas phi).
Chloroplast.
Eukaryota, Cryptophyta, Cryptomonadaceae, Guillardia.
NCBI_TaxID=55529;
                                                                                                                                                                               15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase beta" chain (EC 2.7.7.6).
                                                                                                                        PRT; 1286 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF041468; AAC35674.1; -.
HSSP; Q9KWU6; 1HQM.
INCEPPO; IPR007052; RNA pol A.
InterPor; IPR007066; RNA pol Rpbl 3
InterPro; IPR007081; RNA pol Rpbl 3
InterPro; IPR007081; RNA pol Rpbl 3
                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
                   | | | | | :: :: | | | | 437 DPYAGLSFWEVNLK 450
3 DPYNGITIYDQNLK 16
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078483,
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RPOD_GUITH
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Gaps ô Score 44; DB 1; Length 1286; Pred. No. 44; 2; Mismatches 3; Indels Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative ò

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4 PYNGITIYDONLK 16

363 PFNGIIRYPKNLK 375

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Search completed: January 13, 2004, 12:39:32 Job time : 3.74236 secs

us-09-990-586-101.rspt

£3.

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Hypothetical protein.
SEQUENCE 481 AA; 5
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Q92Vari mus musculu
Q92008 mus musculu
O11401 reindeer pa
O11401 reindeer pa
O28486 archaeoglob
Q81c07 plasmodium
Q94c07 plasmodium
Q9yqe9 anabaena sp
Q9qe9 anabaena sp
Q9qe9 anabaena sp
Q9qe9 anabaena sp
Q9qe9 musculu
Q9ywy3 arabidopsis
Q9wy3 arabidopsis
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Q81070 1
Q9wiv1 1
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                 830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                  Listing first 45 summaries
                                                 OM protein - protein search, using sw model
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Q9PQS6
Q9FNMS
Q8RWP3
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Q920E8
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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sp_invertebrate:*
sp_mammal:*
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sp_bacteriap:*
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sp_organelle:*
sp_phage:*
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sp_bacteria:*
sp_fungi:*
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Maximum DB seg length: 200000000
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Perfect score:
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0 0 5	Q8ub53 agrobacteri Q8xgj7 salmonella Q8faf2 escherichia		QBidaB plasmodium QBdZw4 wiggleswort QBazr7 pseudomonas QBiows neeudomonas	Q911h9 white spot Q8vb97 white spot Q8cy30 white spot Q8cy30 brucella su Q8cxnf7 clostridium	Q81b35 plasmodium Q9122 schistcsoma Q9422 chistcsoma Q8427 human papil Q93qw3 bacteroides Q93qw3 bacteroides Q91hd9 bowine herp Q99fw7 human papil
Q17518 Q8BDQ8 Q8HTL4 Q96XK1 Q50398	Q8UB53 Q8XGJ7 Q8FAF2	09FXA5 09C7W9 08FPZ7	Q8IDA8 Q8D2W4 Q93SR7	Q91045 Q91LH9 Q8CVB97 Q8CY30 Q8XNT7	Q81835 Q9GYZZ Q84227 Q93QW3 Q97XC8 Q91HD9
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ALIGNMENTS

Gaps 01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hyporhetical 52.3 kDa protein.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae; Murinae;
WCEI_TaxID=10090; ö 65.3%; Score 62; DB 11; Length 481; 64.7%; Pred. No. 0.18; 1; Mismatches 4; Indels SEQUENCE FROM N.A.
TISSUB-Breast tumor;
Strauberg R.;
Submitted (DRC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC018455, AAH18455.1; InterPro; IPR007110; Ig-like.
InterPro; IPR003066; Ig-MHC.
InterPro; IPR003596; Ig-V.
Ffam; PP00047; 49; 4. 481 AA; 52326 MW; 52B44C5826807143 CRC64; 481 AA PRT; SMART; SM00406; ĪGV; 1. PROSITE; PSS0835; IG_LIKE; 4. PROSITE; PS00290; IG_MHC; 2. 11; Conservative PRELIMINARY;

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51 IDPYYGGISYNQKFKG 66

PRELIMINARY;

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% STRAIN=BALB/C;

X MEDLINE=BALB/C;

XA Malkiel S., Liao. Lunningham M.H., Diamond B.;

A Malkiel S., Liao. Lunningham M.H., Diamond B.;

A Malkiel S., Liao. Lunningham M.H., Diamond B.;

RT "T-Cell-dependent antibody response to the dominant epitope of reprococcal polyaaccharide, N-acetyl-glucosamine, is cross-reactive RT with cardiac mycosin."; Aacetyl-glucosamine, is cross-reactive RT with cardiac mycosin."; AAE693-50001.

RE WHIST POROGOLI, AAE69329-1; -.

DR RESP: PO1810: ZFBJ.

B InterPro; IPR003506; Ig.MC.

DR InterPro; IPR003506; Ig.V.

DR Ffam; PP00047; ig; 1.

DR SMART; SM0406; IGV; 1.
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                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINES973322; PubMed=9188556;
Chan S.Y., Bernard H.U., Ratterree M., Birkebak T.A., Faras A.J.,
Ostrow R.S.;
                                                                                                                                                                                                                                                                                                                                                                        "Genomic diversity and evolution of papillomaviruses in rhesus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.7%; Score 51; DB 12; Length 148; 53.3%; Pred. No. 2.8; tive 4; Mismatches 3; Indels
                                                                                                                                                                               LI.
Reindeer papillomavirus (RPV).
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 AA; 16623 MW; 56C5A7C98A785928 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBirel. 15, Created)
01-OCT-2000 (TrEMBirel. 15, Last sequence update)
01-OCT-2000 (TrEMBirel. 23, Last sentotation update)
Auti-myosin immunoglobulin heavy chain variable region
                                                                                                   01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Reindeer papillomavirus il (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 AA.
                                                                                                                                                                                                                                                                                                                                                                                       monkeys.";
J. Virol. 71:4938-4943(1997).
EMBL. 189670; ARE3856.1;
InterPro; IPR002210; PV capsid L1.
Pfam; PF00500; late_profein_L1;
PRINTS; PR00865; HPVCAPSIDL1.
ProDom; PD000544; PV_capsid_L1:
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                                                                 PRELIMINARY;
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Mus musculus (Mouse).
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es 8; Conserva
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                          RESULT 4
011401
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H., "Definition of the Idiotope of Pterin-Mimicking Antibodies Expr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.8%; Score 54; DB 11; Length 488; 62.5%; Pred. No. 3.3; tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0920E8 PRELIMINARY, PRT, 120 AA.
0920E8;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 23, Last annotation update)
Pterin-mimicking anti-idiotope heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 53.7%; Score 51; DB 11; Length 120; Best Local Similarity 62.5%; Pred. No. 2.3; Matches 10; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                              Strausberg R.;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013539, AAH13539.1;
MGI: 96466; Igh-VJ558.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR03306; Ig_W.
Ffam; Pr0047; Ig; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF307936; AAL09420.1; ...
InterPro; IPR007110; Ig-like.
InterPro; IPR003066; Ig-MFC.
InterPro; IPR003596; Ig-V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;
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01-DEC-2001 (TYENBLrel. 19, Created)
01-DEC-2001 (TYENBLrel. 19, Last sequence update)
01-MAX-2003 (TYENBLrel. 23, Last annotation update)
Hypothetical 53.0 kDa protein.
IGH-VJ558 OR AI893585.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                     SMART; SMO0406, IGv; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 IDPYNGITIYDONLKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 INPYNGGTSYNOKFKG 85
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Best Local Similarity 62.59
Matches 10; Conservative
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                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                               ISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Fragment)
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RESULT 6 028486

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Mus musculus (Mouse),
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
          Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N., Quall M., Barrell B.; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, A1844506, CAD50834.1; -.
Hypothetical protein.
SEQUENCE 954 AA; 115329 MW; 25417952D67DD6C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBYQE9 PRELIMINARY; PRT; 595 AA.
QBYQE9;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Periplasmic oligopeptide-binding protein of oligopeptide ABC
                                                                                                                                                DB 5; Length 954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11; Length 481; 42;
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MEDLINE=21595285; PubMed=11759840;
Kaneko T., Nakamura Y.; Wolk C.P., Kuritz T., Sasamoto S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anabaena sp. (strain PCC 7120).
Bacteria: Cyanobacteria; Nostocales; Nostocaceae; Nostoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Colon;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013488; AAH13488 1; -.
MGD; MGI:96486; Igh-VJ558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ll protein:
481 AA; 52022 MW; 4EEB5C253038B718 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
1-DEC-2001 (TrEMBLrel. 23, Last annotation update)
Hypotherical 52.0 kDa protein.
1GH-VJSS8 OR AI893585.
                                                                                                                                                                                                                                                                                                                                                             481 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.5%; Score 47; DB 50.0%; Pred. No. 42; artive 3; Mismatches
                                                                                                                                            Query Match
Best Local Similarity 52.6%; Pred. No. 72;
Matches 10; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                 462 YIQPHNGIIHITNYKQNIR 480
                                                                                                                                                                                                                           1 YIDPYNG---ITIYDONLK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 IDPFDSYTSYNOKFKG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 IDPYNGITIYDQNLKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Cyanobac
NCBI_TaxID=103690;
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical
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MEDILINE-80649343; PLUDMed-3889475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Craham D.E., Kyrpides N.C.,
Richardson D.L., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Retreson S., Reich C.I., Weidman J.F., McDonald L., Utterback T.,
Cotton M.D., Sprigge T., Artland P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
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Plasmodium falciparum (isolate 3D7).
Bukaryota, Alveolata; Apicomplexa; Haemosporida, Plasmodium.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.5%; Score 48; DB 17; Length 243; 53.3%; Pred. No. 14;
                                                      52.6%; Score 50; DB 11; Length 109; 52.9%; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                Archaeoglobus fulgidus.
Archaea, Euryarchaeota, Archaeoglobi, Archaeoglobales;
Archaeoglobaceae, Archaeoglobus.
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Pfam; PF00896; Mtap_PNP; I.
Hypothetical protein; Complete protecme.
SEQUENCE 243 AA; 27201 MW; C8FCFE74DAC89DCC CRC64;
                    12118 MW; FF65E441BBF936A6 CRC64;
                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        954 AA
                                                                                                                                                                                                                                                                   243 AA.
                                                                                            3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                             Methylthioadenosine phosphorylase (MTAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSM 4304 / ATCC 49558;
                                                                                                                                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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HSSP, Q13126; 1CB0.
TIGR; AF1788; -.
                                                                                                                                  1 YIDPYNGITIYDQNLKG 17
                                                                                                                                                                    41 YINPYNDGTKYNEKFKG 57
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                                          Query Match
Best Local Similarity 52.9%
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-WAR-2003 (TrEMBLrel.
Hypothetical protein.
PRO7_0028.
  109 1
109 AA;
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wes 8; Conserv
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  NON TER
SEQUENCE
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Gaps

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Indels

QBIC07

RESULT 7 Q8IC07

Matches

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SKARFFERRES

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SEQUENCE FROM N.A.

Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,

Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,

Chalm C.J., Boweer L., Jones T., Bahn J., Carninci P., Chen H.,

Chenk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,

Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,

Sakurai T., Satou M., Seki M., Pham P., Yamada K., Shinozaki K.,

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AY029558, AAM12957.1;

InterPro; IPR000640; EFG_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Southwick R.O. N.A.
Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
Palm C.J., Bones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL TaxID=3702;
                                                                                                                                                                                                       "Structural analysis of Arabidopsis thaliana chromosome 5. II. Sequence features of the regions of 1,044,062 bp covered by thirteen physically assigned PI clones.",
DNA Res. 4:291-300(1997).
EMBL; AB006697; BAB10014.1; -.
                                                                                                                         STRAIN=Columbia;
MEDLINE=88069011; PubMed=9405937;
Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.4%; Score 46; DB 10; Length 675; 41.2%; Pred. No. 87; tive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               824A3D0B093497E5 CRC64;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
[11]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
GTP-binding protein LepA-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00679; EFG C; II.—
Pfam; PF00009; GTP_BFTU; I.
Pfam; PF03144; GTP_BFTU; I.
PRINTS; PR00315; ELONGATNET.
TIGREPAMS; TIGR01393; lepA; I.
TIGREPAMS; TIGR0231; small GTP; I.
PROSITE; P800301; EFACTOR GTP; I.
GTP-binding; Protein blosynthesis:
SEQUENCE 675 AA; 74874 MW; 824A;
                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000640; BPG_C.
InterPro; IPR004161; BFTU D2.
InterPro; IPR0004095; BF_GTPbind.
InterPro; IPR006297; LopA.
InterPro; IPR006297; LopA.
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                HSSP; P13551; 1DAR
                                                                                                   SEQUENCE FROM N.A.
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QBRWP3
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 15, Last annotation update)
GTP-binding protein LepA homolog.
Arabidopsis thaliama (Mouse-ear crea), Embryophyta; Tracheophyta; Spermatophyta; Wiridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Serovar 3;
MEDLINE=20500219; PubMed=11048724;
Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
Cassell G.H.;
                          Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.", DNA Res. 8.205-213(201).

EMBL, AP003394, BAB7583.1, -.
InterPro; IPR009914; SBP_bac_5.
Pfam; PP00496; SBP_bac_5.
Complete proteome.
SEQUENCE 595 AA; 67165 MW; D7070EBAB85F0D17 CRC64;
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma
NCB1_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 52.9%; Pred. No. 48;
Matches 9; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                              49.5%; Score 47; DB 16; Length 595;
43.8%; Pred. No. 53;
tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The complete sequence of the mucosal pathogen Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prodom; PD000001; Prot_Kinase; 1.
PROSITE; PS0111; PROTEIN KINASE DOM; 1.
PROSITE; PS01016; PROTEIN KINASE_ST; 1.
ATP-binding; Transferase; Complete proteome.
SEQUENCE 386 AA; 45241 MW; 789374CC15D1CAD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
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InterPro; IPR000719; Prot Kinase.
InterPro; IPR002290; Ser Ehr pkinase.
Pfam; PF00069; Dkinase: I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9PQS6;
01-OCT-2000 (TrEMBLrel. 15, C.
01-OCT-2000 (TrEMBLrel. 15, L.
01-MAR-2003 (TrEMBLrel. 23, L.
Serine/threonine Kinase.
PKN OR UU216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   379 YLSPEEGLKVYDYNLE 394
                                                                                                                                                                                                                                                                                                                                                                                                                     1 YIDPYNGITIYDQNLK 16
                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         urealyticum.";
Nature 407:757-762(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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ProDom; PD000001; Prot_k
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Best Local Similarity
Matches 7; Conserva
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RESULT 10

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O9FNMS
AC C95FNM
DT 01-MA-DT 01-MA-DT 01-MA-DT 01-MA-DT 00-MA-DT
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Gaps

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STRAIN=IS362;
MEDLINE=56186743; PubMed=8627792;
MEDLINE=56186743; PubMed=8627792;
MEDLINE=56186743; PubMed=8627792;
Perewart A.C., Eriksson A.M., Manos M.M., Munoz N., Bosch F.X.,
Peto J., Wheeler C.M.;
"Intratype variation in 12 human papillomavirus types: a worldwide
                                                                                                                                                                                                                              Query Match

47.4%; Score 45; DB 11; Length 117;
Best Local Similarity 56.2%; Pred. No. 20;
Matches 9; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 45; DB 12; Length 152;
Pred. No. 26;
4; Mismatches 3; Indels
Clemens A., Rademaekers A., Specht C., Koelsch E.; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases. EMBL, AJ225.17; CAB65236.1; -. HSSP; PO1789; IMCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus type 68.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=45240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                      117 117
117 AA; 13060 MW; D816AD0858A47E4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 AA; 17331 MW; CCF76574491F7D2D CRC64;
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17, Last annotation update)
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InterPro; IPR002210; PV capsid_L1.
Pfam; PF00500; late_profein_L1; 1.
PRINTS; PR00865; HPVCAPSIDLI.
ProDom; PD000544; PV capsid_L1; 1.
NON_TER 152 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last seq 01-UTM-2001 (TrEMBLrel. 17, Last ann Major capsid protein L1 (Fragment).
                                                               Interpro; IPR007110; Ig-like.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_v.
Pfam; PF00047; Ig; I.
SMART; SM00406; IGv; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            perspective.";
J. Virol. 70:3127-3136(1996).
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                                                                                                                                                                                                                                                                                                   2 IDPYNGITIYDQNLKG 17
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168 7; Conservative
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
(VGH_TaxID=10090;
                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                  'Match 48.4%; Score 46; DB 10; Length 681; Local Similarity 41.2%; Pred. No. 97; conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 56.2%; Pred. No. 20;
Matches 9; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clemens A., Rademaekers A., Specht C., Koelsch E.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ225174; CAB65237.1; -.
HSSP; P01810; ZEBJ.
                                   117 AA; 13000 MW; CDDE2AF84D499734 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        1.WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
11-MAR-2003 (TrEMBLrel. 23, Last annotation update)
1mmunoglobulin heavy chain V-D-J region (Fragment).
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                   IPRO00795; EF GTPbind
IPRO06297; LepA.
IPRO05225; Small_GTP.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; I.
SWART; SM00406; IGV; I.
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Q9QXF0
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Q9QXE9
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Gaps

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January 13, 2004, 12:18:44; Search time 3.96419 Seconds (without alignments) 680.681 Million cell updates/sec
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| SIDS1/gcddata/geneseq/geneseqp.embl/AA1984.DAT:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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95
1 YIDDYNGITIYDQNLKG 17
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Sequence:
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Maximum DB 8
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		Description		Human anti-tissue	Human anti-tissue	Anti-tissue factor	Anti-tissue factor	Vitronectin alpha-	Murine vitronectin	Humanised anti-alp	Reshaped human AUK	puc-RVh-1220b. Sy
		ΠD		AAW71859	AAW71288	AAY52755	AAY52756	AAW84099	AAW84093	AAW84097	AAW22418	AAR29016
		DB	1	13	19	20	20	20	50	50	18	13
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pUC-RVN-1220d. Sy p12-h2. Synthetic TSH receptor antib TSH receptor antib VH FV fragment of Antidigoxin monocl Muxine monoclonal Heavy chain variab	Murine monoclonal TSH receptor antib TSH receptor antib TSH sceptor antib Binding site. Hom Schools of the AA	Connerio de superi Multifunctional pr 26-10 anti-digoxin 26-10 anti-digoxin Anti-digoxin scPv' Anti-digoxin scPv'	Anti-digoxin singl Chimeric Ig superf Chimeric Ig superf Anti-digoxin shapl 26-10 sFv. Synthe Chimeric Ig superf Multifunctional pr Multifunctional pr	Single chain antib Sequence encoded b Murine 66425 heavy Humanised 66425 F(Humanised murine 6 Murine 66425 heavy Humanised 6642 heavy Humanised 6645 F(
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## ALIGNMENTS

Human, anti-tissue factor light chain variable region, H36.D2.B7, anti-tissue factor heavy chain variable region, inhibition; antibody; blood coagulation, thrombosis, restenosis, thromboembolic condition, cardiovascular, infection, neoplastic disease, clot, diagnosis. Human anti-tissue factor antibody hypervariable region #5. Wong HC; Nieves EL, AAW71859 standard; peptide; 17 AA. (SUNO-) SUNOL MOLECULAR CORP 98WO-US04644. 97US-0814B06. (first entry) Jiao J, Luepschen L, WPI; 1998-520804/44. N-PSDB; AAV61138. 10-MAR-1998; WO9840408-A1. 10-MAR-1997; 10-DEC-1998 Homo sapiens 17-SEP-1998. AAW71859; RESULT 1 

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The present sequence represents a hypervariable region from the human and does not bind non-native TP. The antibody capable of specifically and does not bind non-native TP. The antibody capable of specifically binding native TP may be used for inhibiting blood coagulation and also for reducing TP levels in a mammal. The antibodies can be used, e.g. treat thromboses particularly to prevent or inhibit restenosis, or other thromboses following an unvasive medical procedure such a arterial or cardiac surgery (e.g. angioplasty, endarterectomy, deployment of a stert, use of catheter, graft implantation or use of anteriovenous shunt). The antibodies can also be used as a carrier for arteriovenous shunt). The antibodies can also be used as a carrier for arteriovenous shunt) when antibodies can also be used as a carrier for arteriovenous shunt) when antibodies can also be used as a carrier for arteriose, or a cytotoxic agent by conjugating a suitable toxin to the antibody. Further the antibodies can be used for treating a tromboembolic condition associated with cardiovascular disease, and the antibody and associated with cardiovascular disease, and the antibody.
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New antibody to human tissue factor - used for, e.g. treating thrombosis or restenosis or thromboembolic conditions associated with cardiovascular, infectious or neoplastic disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 95.8%; Score 91; DB 19; Length 17; I Similarity 94.1%; Pred. No. 3.5e-08; 16; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                          infectious disease, a neoplastic disease or as a
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                                                                                   Claim 13; Page 31; 53pp; English.
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N-PSDB; AAV54962.
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Matches 16; Conserv
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The present sequence represents the human anti-tissue factor heavy chain variable region from an antibody that binds native human tissue factor (TF) and does not bind non-native TF. The antibody capable of specifically binding native TF may be used for inhibiting blood coagulation and also for reducing TF levels in a mammal. The antibodies can be used, e.g. to treat thromboses particularly to prevent or inhibit restencis, or other thromboses following an invasive medical procedure such as arterial or cardiac surgery (e.g. angigplasty.) condatrescency, deployment of a stent, use of catheter, graft implantation or use of an arteriovenous shunt). The antibodies can also be used as a carrier for drugs, particularly pharmaceuticals targeted for interaction with a blood clot such as streptokinase, tissue plasminogen activator (t-pA) or unokinase, or a cytocoxic agent by conjugating a suitable toxin to the antibody. Further the antibodies or as arthromboshly condition associated with cardiovascular disease, an infection disease, a neoplastic disease or a simple of the antibodies can also be used for detection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody; ATR-2; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC; disseminated intravascular coagulation; immunogenicity; chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes chimeric antibody (Ab) heavy (H) chains containing the variable region of the H chain of a mouse monoclonal Ab recognising human tissue factor (hTF) and the constant region of the H chain of a human Ab. The variable region is one of six specified sequences (which are the H chain variable regions from mouse monoclonal Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L)
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Best Local Similarity 94.1%; Pred. No. 3.5e-07;
Matches 16; Conservative 0; Mismatches 1; Indels
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N-PSDB; AAZ33006.
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and diagnosis.
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The present invention describes chimeric antibody (Ab) heavy (H) chains containing the variable region of the H chain of a mouse monoclonal Ab recognising human tissue factor (hrr) and the constant region of the H chain of a human ab. The variable region is one of six specified sequences (which are the H chain variable regions from mouse monoclonal Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L) and answer or ariable region of the L chain of a mouse monoclonal Ab recognising human tissue factor (hrr) and the constant region of the L chain of a human Ab, the variable region being one of six specified sequences (which are the L chain variable regions from mouse monoclonal Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for the treatment and prevention of thrombotic disease, especially of disseminated intravascular coagulation (DIC). The humanised antibody has
chains containing the variable region of the L chain of a mouse monoclonal Ab recognising human tissue factor (hTF) and the constant region of the L chain of a human Ab, the variable region being one of six specified sequences (which are the L chain variable regions from mouse monoclonal Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for the treatment and prevention of thrombotic disease, especially of disseminated intravascular coagulation (DIC). The humanised antibody has the high hift binding activity of the mouse monoclonal antibody but greatly reduced immunogenicity, AAZ33001 to AAZ33031 and YS27007 to AAY52767 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
ATR-2, ATR-3; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
disseminated intravascular coagulation; immunogenicity; chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.8%; Score 72; DB 20; Length 118; 76.5%; Pred. No. 0.00048;
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N-PSDB; AAZ33007.
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Matches 13; Conserv
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the high hTF binding activity of the mouse monoclonal antibody but greatly reduced immunogenicity. AAZ33001 to AAZ33091 and Y527007 to AAX52767 represent sequences used in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                              Humanised antibody; monoclonal antibody; MAb; antibody engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the amino acid sequence of the region of the murine monoclonal antibody (WAD) D12 heavy chain variable region (VH) that is altered in humanised D12 VH (see also AMM4097). A synthetic gene (see AAV81901) encoding the protein was prepared from synthetic oligonucleotides and used to prepare an expression vector for humanised D12 VH. D12 is an anti-human alpha-v beta-3 vitronectin receptor MAD. Humanised D12 MADs can be used for passive immunotherapy of disorders mediated by the alpha-v beta-3 vitronectin receptor, e.g. restenosis and anglogenic associated
                                                                                                                                                                                                                                                                                                                                                                                                             mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis; cancer; metastasis; rheumatoid arthritis; atherosclerosis; anglogenesis; diabetic retinopathy; inflammation; macular degeneration; osteoporosis; Paget's disease; hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New anti alpha v beta 3 vitronectin receptor antibodies - used immunotherapeuTic treatment of e.g. diabetic retinopathy, inflammatory disorders, atherosclerosis, restenosis, cancers or
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                                                                                                       Length 118,
                                                                                                         Score 72; DB 20; Length 11
Pred. No. 0.00048;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                              AAW84099 standard; Protein; 110 AA
                                                                                                                                                                                                                                                                                                                                                                        Vitronectin alpha-v beta-3 MAb VH.
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                                                                                                            75.8%;
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                                                                                                                                                                       1 YIDPYNGITIYDQNLKG
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Best Local Similarity 70.6
Matches 12; Conservative
                                                                                              Query Match
Best Local Similarity 76.5-
Best Local 3, Conservative
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N-PSDB; AAV71801.
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                                                                                 118 AA;
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us-09-990-586-101.rag

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This is the amino acid sequence of the heavy chain variable region (VH) of the anti-human alpha-v beta-3 vitronectin receptor murine monoclonal antibody D12, as deduced from isolated DNA (see ANV1797). D12 VH and VL (see AAM84094) show sequence similarity to Kabat VH subgroup I (see AAM84095) and Kabat VK subgroup III (see AAM84099) were constructed by combining the framework regions of the human V region consensus sequences with complementarity determining regions of D12 (keeping some preferred murine framework regidues). The human vegion some preferred murine framework residues). The human vegion some preferred murine framework residues. The human vegion some preferred murine framework residues. The human vegion some preferred murine framework residues. The human vegion some preferred murine framework residues. The human vegion receptor and capable of neutralising the receptor. They can be used for passive immunotherapy of a disorder ceptor. They can be used for passive immunotherapy of a disorder sesociated by the alpha-v beta-3 receptor, e.g. cardiovascular cisorders or angiogenic-related disorders, such as angiogenesis associated with diabetic retinopathy, atherosclerosis and cancer especial architis and cancer, e.g. solid tumour metastasis, and cisoasses where bone resorption is associated with pathology such as osteoporosis, hypercalcamia
                                                                                                                                                                                                                                                                Humanised antibody; monoclonal antibody; MAD; antibody engineering; mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis; cancer; metastasis; rheumatoid archritis; atherosclerosis; anglogenesis; diabetic retinopathy; inflammation; macular degeneration; osteoporosis; paget's disease; hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New anti alpha v beta 3 vitronectin receptor antibodies - used for immunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory disorders, atherosclerosis, restenosis, cancers or
                                                                                                                                                                                                                                     Murine vitronectin alpha-v beta-3 receptor MAb VH region.
                                                                                                                                                                                                                                                                                                                                                                                                                                          location/Qualifiers
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                                                                                                                          AAW84093 standard; Protein; 117 AA
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/label= CDR2
99..106
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                   YIDPYNGDIFYNOKFKG 64
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/label= CDR1
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1 YIDPYNGITIYDQNLKG
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of malignancy, osteolytic lesions produced by bone metastasis, bone loss due to immobilisation or sex hormone deficiency. They can also be used for targeted drug therapy, and for detection and diagnosis.
                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New anti alpha v beta 3 vitronectin receptor antibodies - used for immunotherapeutic treatment of e.g. diabetic retinopathy, inflammatory disorders, atherosclerosis, restenosis, cancers or osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the amino acid sequence of the heavy chain variable region (VH) of humanised anti-alpha-v beta-3 vitronectin receptor monoclonal antibody D12RIZHC 1-0. It is based on the VH sequence determining regions (CDRs) from the murine anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody D12 (see AAW84093). 7 Murine framework residues (24, 48, 67, 68, 70, 72 and 74)
                                                                                                              0
                                                                                 72.6%; Score 69; DB 20; Length 117; 70.6%; Pred. No. 0.0015; ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                     Humanised anti-alpha-v beta-3 MAb D12HZHC 1-0 VH.
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                                                                                                                                          1 YIDPYNGITIYDQNLKG 17
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/label= CDR2
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/label= CDR1
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                                                                                                 Local Similarity
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/label= (
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N-PSDB; AAV71799.
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                                                                                                                                                                                                              RESULT 7
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are retained. The humanised heavy chain can be expressed in host
cells using nucleic acid molecules (see AAV71799) of the invention.
Humanised D12 VL is also provided (see AAV84098)). The humanised
antibodies can be used for passive immunotherapy of disorders
mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or
angiogenic-related disorders, such as angiogenesis associated
with diabetic retinopathy, atherosclerosis and restenosis, chronic
inflammatory disorders, macular degeneration, rheumatorid arthritis
and cancer, e.g. solid tumour metastasis, and diseases where bone
resorption is associated with pathology such as osteoprosis,
hyperparathyroidism, Paget's disease, hypercalcemia of malignancy,
csteolytic lesions produced by home metastasis, bone loss due to
immobilisation or sex hormone deficiency. They can also be used for
targeted drug therapy, and for detection and diagnosis.
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117 AA; Sequence

This polypeptide comprises version 'b', of a reshaped human antibody AUK12-20 VH region. A DNA fragment encoding the polypeptide was subcloned into vector pucins as a template for PCR amplification and production of version 'a' of a reshaped human 21.6 VH region (see AAW22413) that can be used in the construction of novel humanised anti-alpha-4 integrin antibodies. Claimed humanised antibodies are useful in the treatment of asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory bowel disease, theumatoid arthritis, transplant rejection, graft versus host disease, tumour metastasis, nephritis, atopic dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte

mediated lung injury

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Gaps

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Uses of humanised alpha-4 integrin antibody - for treatment of asthma, atherosclerosis, AIDS, dementia, etc.

WPI; 1997-297879/27.

Example 6; Page 44; 107pp; English.

Score 69; DB 20; Length 117; Pred. No. 0.0015; 1; Mismatches 4; Indels 99 1 YIDPYNGITIYDQNLKG 17 72.6%; 50 YIDPYNGDTFYNOKFKG Query Match
Best Local Similarity 70.6'
Matches 12; Conservative g ò

AAW22418 standard; Protein; 116 AA.

(first entry) 08-DEC-1997 AAW22418;

Reshaped human AUK12-20 VH.

Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis; transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy; AUK12-20.

Chimeric Homo sapiens; Chimeric synthetic.

Location/Qualifiers 31..35 /label= CDR1 36..49 /label= FR2 l..30 /label= FR1 Region Region Region

50..66 /label= CDR2 99..105 /label= CDR3 7..98 |abel= FR3 106..116 /label= FR4 Region Region Region

69..85 /label= CDR2 86..117 /label= FR3

0..54 label= CDR1

0..49 label= FR1

Region Region Region Region Region Region Region

FR2

55..68 /label= E

118..124 /label= CDR3 125..135

/label= FR4

W09219759-A1 12-NOV-1992. 92WO-JP00544

24-APR-1992;

96WO-US18807

95US-0561521

(ATHE-) ATHENA NEUROSCIENCES INC

Jones ST, Leger OJ, Saldanha J, Yednock TA; WO9718838-A1, 21-NOV-1996; 21-NOV-1995; Bendig MM, Region RESULT 8
AAW22418
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                                                                                                                                                                                                                                                                Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;
complementarity determining region; monoclonal; hybridoma; PCR;
plasmid; polymerase chain reaction; amplify.
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0
                                                                                                                                       65.3%; Score 62; DB 18; Length 116; 64.7%; Pred. No. 0.021;
                                                                                                                                                     4; Indels
                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                              ...19
'note= "Leader peptide"
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                           AAR29016 standard; Protein; 135 AA.
                                                                                                                                                                 1 YIDPYNGITIYDQNLKG 17
                                                                                                                                                                             50 YIDPFNGGISYNÓKFKG
                                                                                                                                                                                                                                    (updated)
(first entry)
                                                                                                                                       ouery Match
Best Local Similarity 64.79
Matches 11, Conservative
                                                                                                                             116 AA;
                                                                                                                                                                                                                                                      puc-RVh-1220b.
                                                                                                                                                                                                                                    25-MAR-2003
30-MAR-1993
                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                             Sequence
                                                                                                                                                                                                                        AAR29016;
                                                                                                                                                                                                                                                                                                        Key
Peptide
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The sequences given in AAR29016-17 are portions of monoclonal antibodies which were encoded by plasmids contained within the mouse hybridoma, AUK12-20. The DNA encoding the complementarity determining regions (CDR s) was isolated by polymerase chain reaction. These antibodies recognise human interleukin-6 receptor (I.F.6R). The hybridoma cells were transformed with plasmids containing fragments of the antibody gene which caused the production of the antibody from the hybridoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, antibody, interleukin-6; receptor; IL-6R; light chain; L; H; heavy chain; variable region; mouse; monoclonal; hybridoma; AUK12-20; plasmid; p12-k2; p12-k2.
                                                                                                                                                                                                                                 Reconstituted human antibody to human interleukin.6 receptor - has low antigenicity and contains mouse V-region complementarity determining regions
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                                                                                                                                                      Tsuchiya M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.3%; Score 62; DB 13; 64.7%; Pred. No. 0.025;
                                                                                                                                                      Saldanha JW, Sato K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                Disclosure; Page 159-60; 207pp; Japanese.
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/note= "Signal peptide"
20..135
/note= "Mature peptide"
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92JP-0032084,
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                                            92WO-JP00544
                                                                          91JP-0095476.
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(first entry)
                                                                                                                      (CHUS ) CHUGAI SEIYAKU KK.
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Best Local Similarity 64.7
Matches 11, Conservative
                                                                                                                                                      Bendig MM, Jones ST,
                                                                                                                                                                                     WPI; 1992-398882/48.
N-PSDB; AAQ31391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 135 AA;
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19-FEB-1992;
                                                                          25-APR-1991;
19-FEB-1992;
                                            24-APR-1992;
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30-MAR-1993
             12-NOV-1992.
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                                                                                                                                                                                                                                                The sequences given in AAR29016-17 are portions of monoclonal antibodies which were encoded by plasmids contained within the mouse hybridoma, AUK12-20. The DNA encoding the complementarity determining regions (CDR'S) was isolated by polymerase chain reaction. These antibodies recognise human interleukin-6 receptor (IL-6R). The hybridoma cells were transformed with plasmids containing fragments of the antibody gene which caused the production of the antibody from the hybridoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse; complementarity determining region; monoclonal; hybridoma; PCR; plasmid; polymerase chain reaction; amplify.
                                                                                                                                                      Reconstituted human antibody to human interleukin-6 receptor - has low antigenicity and contains mouse V-region complementarity determining regions
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 64.7%; Pred. No. 0.025;
Matches 11; Conservative 2; Mismatches 4; Indels
                                                                            Tsuchiya M;
                                                                            Saldanha JW, Sato K,
                                                                                                                                                                                                                                                                                                                                                                                 (Updated on 25-MAR-2003 to correct PN field.
                                                                                                                                                                                                                       Disclosure; Page 157-8; 207pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..19
note= "Leader peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 YIDPFNGGTSYNQKFKG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YIDPYNGITIYDQNLKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69..85
/label= CDR2
86..117
/label= FR3
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/label= FR1
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/label= CDR1
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/label= CDR3
91JP-0095476.
92JP-0032084.
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/label= FR2
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/label= FR4
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(first entry)
                                             (CHUS ) CHUGAI SEIYAKU KK.
                                                                            Bendig MM, Jones ST,
                                                                                                          WPI; 1992-398882/48.
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 135 AA;
                                                                                                                          N-PSDB; AAQ31391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    puc-RVh-1220d
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25-APR-1991;
19-FEB-1992;
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30-MAR-1993
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Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
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RESULT 10 AAR2901

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Gaps

Tsuchiya M;

Sato K,

Saldanha JW,

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New polypeptide sequence having part or all of the primary structural conformation of one or more TSH receptor epitopes, useful for treating an autoimmune disease associated with an immune reaction to a TSH receptor, e.g. thyroid cancer -
                                                                                                                                                                                                 The sequences given in AAR28668-69 were encoded by plasmid sequences which were used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (IL-6R). The antibody comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma AUK12-20 which contained the plasmids pl2-k2 and pl2-h2.
                                                                                                              Reconstituted human antibody to human interleukin-6 receptor has low antigenicity and contains mouse V-region complementarity determining regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thyrotropin receptor; TSH receptor, epitope region; antibody; autoantibody; autoimmune disease; thyroid tissue; cytostatic; gene therapy; immune reaction; thyroid cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSH receptor antibody 17D2 heavy chain amino acid sequence.
                                                                                                                                                                                                                                                                                                      (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                          Disclosure; Page 119-20; 207pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP96759 standard; Protein; 214 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                         1 YIDPYNGITIYDQNLKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-AUG-2001; 2001GB-0020649.
01-JUL-2002; 2002GB-0015212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-AUG-2002; 2002WO-GB03831
                                                                                                                                                                                                                                                                                                                                                                                                                                          69 YIDPFNGGTSYNQKFKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
             CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 64.7
Matches 11; Conservative
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                                         Jones ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-290051/28.
N-PSDB; ACC44914.
                                                                     WPI; 1992-398882/48.
N-PSDB; AAQ30754.
                                                                                                                                                                                                                                                                                                                                     135 AA;
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                                           Bendig MM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                     Sequence
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The present invention describes a polypeptide sequence comprising part or all of the primary structural conformation of one or more thyrotropin (TSH) receptor repitopes with which autoantibodies and/or lymphocytes produced in response to a TSH receptor interact. Also described: (1) one or more receptor TSH epitopes with which the autoantibodies and/or! or more receptor TSH epitopes with which the autoantibodies and/or! or materact. Also described above; (2) a method of screening for autoantibodies or lymphocytes produced in response to a TSH receptor in a sample of body fluid obtained from a subject suspected of suffering from, susceptible to, having or recovering from autoimmune disease associated with an immune reaction to a TSH receptor; (3) a binding partner for a TSH receptor, which is capable of binding partner does not comprise TSH or naturally produced antibodies to binding partner does not comprise TSH or naturally produced antibodies to the TSH receptor; and (4) a combination comprising the binding partner does not comprise TSH or naturally produced antibodies to the TSH receptor; and/or tissue containing a TSH receptor, for simulating thyroid tissue, and/or tissue containing a TSH receptor, for simulating thyroid tissue the manufacture of a medicament for simulating thyroid can be used for treating an autoimmune disease associated with an immune reaction to a TSH receptor. The specific binding partner is useful for the manufacture of a medicament for stamilating thyroid cancer. Act or the manufacture of a medicament for stamilating thyroid cancer. Act of a medicament for stamilating thyroid cancer. Act of the manufacture of a medicament for stamilating thyroid cancer. Act of the medicament for stamilating thyroid cancer. Act of the medicament in ABP95719 to ABP95710 represent TSH receptor antibody when the present interest in the present interest in the present interest in the present interest in the present interest in the present interimple the present interest in the present interest in the presen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.3%; Score 62; DB 24; Length 214; 64.7%; Pred. No. 0.044; ive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISH receptor antibody 17D2 heavy chain amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP96760 standard; Protein; 214 AA.
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01-JUL-2002; 2002GB-0015212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-AUG-2002; 2002WO-GB03831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 64.73
Matches 11, Conservative
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Gaps

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4; Indels

2; Mismatches

65.3%; Score 62; DB 13; Length 135; 64.7%; Pred. No. 0.025;

New polypeptide sequence having part or all of the primary structural conformation of one or more TSH receptor epitopes, useful for treating

Sanders JF;

Smith BR, Furmaniak J, WPI; 2003-290051/28. N-PSDB; ACC44915

Sanders JF;

Claim 71; Fig 17; 196pp; English

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AAR38586
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The present invention describes a polypeptide sequence comprising part or all of the primary structural conformation of one or more thyrotropin (TSH) receptor epitopes with which autoantibodies and/or lymphocytes produced in response to a TSH receptor interact. Also described: (1) one or more receptor TSH epitopes with which the autoantibodies and/or lymphocytes interact. As with the polypeptide sequence described above; (2) a method of screening for autoantibodies or lymphocytes produced in response to a TSH receptor in a sample of body fluid obtained from a subject suspected of suffering from, susceptible to, having or recovering from autoimmune disease associated with an immune reaction to a TSH receptor to stimulate the TSH receptor, where the binding partner does not comprise TSH nor maturally produced antibodies to the TSH receptor; and (4) a combination comprising the binding partner and one or more further agents capable of stimulating thyroid tissue, and/or tissue containing a TSH receptor, for simultaneous, separate or sequential use in stimulating thyroid tissue, and/or tissue containing a TSH receptor. The specific binding partner in very more further agents capable of stimulating thyroid can be used for treating an autoimmune disease associated with an immune reaction to a PSH receptor. The specific binding partner is useful for the manufacture of a medicament for stimulating thyroid cancer. ACC4491 to ACC44905 and ABP96719 to ABP6750 represent TSH receptor antibody WH companies given in ABP96719 to ABP967710 represent TSH receptor antibody which exemplification of the present invention can in ABP96719 to ABP96770 represent TSH receptor antibody when the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heavy; light; variable; VH; VL; region; antidigitoxin; monoclonal; antibody; MAb; 26-10; Fv; fragment; antigen; binding site; linker; expression-secretion system; T7 promoter; signal peptide; molecule; polymerase chain reaction; PCR; single chain.
autoimmune disease associated with an immune reaction to a TSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.3%; Score 62; DB 24; Length 214; 64.7%; Pred. No. 0.044; ive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VH Fv fragment of antidigitoxin monoclonal antibody 26-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                         exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR34670 standard; Protein; 119 AA
                                        Claim 67; Fig 18; 196pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 YIDPYSGATSYHQKFKG 66
             receptor, e.g. thyroid cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YIDPYNGITIYDQNLKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ng SC, Wong S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92WO-US08881
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 11; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-1992;
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25-AUG-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR34670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
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The sequences given in AAR34670-71 represent the heavy and light variable portions (VH and VL) of antidigitoxin monoclonal antibody (MAb) contributed by the sequence of the smallest complete ante-examples of FV fragments. For its presently known. The DNA fragments encoding these FV fragments were used in the construction of an expression-secretion system for the production of biologically active FV fragments. The system also contains a DNA sequence encoding the TY promoter and one or DNA sequences encoding to or more signal peptides (see also AAR38527-28). The secretion-expression vector was produced by polymerase chain reaction. FV fragments may also be produced by polymerase chain reaction. FV fragments may also be produced as single chain FV molecules (see also AAR34672) which contain the VH and VL regions, a signal sequence and a linker between the two variable regions. Fy fragments and single chain molecules may be used to specifically bind one or more of the same antigens as the full length antibody from which it is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antidigoxin monoclonal antibody 26-10 heavy chain variable region.
                                                                             Expression-secretion vectors - for prodn. of biologically active antibody Fv fragments or single chain Fv molecules
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 60; DB 14; Length 119;
Pred. No. 0.046;
3; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR38586 standard; Protein; 119 AA.
                                                                                                                                                                Disclosure, Fig 1A, 51pp, English.
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58.8%;
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91EP-0923150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (updated)
(first entry)
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Best Local Similarity 58.8
Matches 10; Conservative
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UNIV CALGARY
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WPI; 1993-152491/18.
N-PSDB; AAQ41065.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 AA;
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18-DEC-1991;
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28-JUL-1995
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Expression-secretion vectors for prodn. of Fv fragments - used for similar applications as whole antibodies and specifically bind digoxin

Claim 13; Fig 1A; 55pp; English.

Antidigoxin monoclonal antibody 26-10 is a high affinity antibody produced against digoxin conjugated to BSA. cDNA clones of the genes encoding the VH and VL portions of the 26-10 antibody were made by PCR amplification of cDNA generated by reverse transcription of mRNA isolated from 2610 hybridoma. The VH and VL clones (encoding ARISBSB6 and ARISBSP7, respectively) were used in the construction of plasmids (Updated on 25-MAR-2003 to correct PN field.) 

119 AA; Sequence

Gaps . Query Match 63.2%; Score 60; DB 14; Length 119; Best Local Similarity 58.8%; Pred. No. 0.046; Matches 10; Conservative 3; Mismatches 4; Indels

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1 YIDPYNGITIYDQNLKG 17

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50 YISPYSGVTGYNQKFKG 66

Search completed: January 13, 2004, 12:38:29 Job time : 3.96419 Becs

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Length 17;
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100.0%; Score 95; DB 11;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 17; Conservative 0; Mismatches 0;
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US-10-223-880-5
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US-09-782-672-2
US-09-782-672-2
US-09-726-258-48
US-09-726-258-44
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US-09-940-7278-65
US-10-032-482-23
US-10-032-482-23
US-10-232-482-3
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US-10-207-655-348
US-10-389-155-23
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Publication No. US20030176664A1
GENERAL INPORMATION:
APPLICANT: JIAO, JIN-AN
APPLICANT: WONG, HING C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YIDPYNGITIYDONLKG 17
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       TYPE: PRT
ORGANISM: Homo sapiens
US-09-990-586-101
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            9, Appli
9, Appli
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                                                                                                                                                                   January 13, 2004, 12:43:20; Search time 2,71703 Seconds (without alignments) 1260.812 Million cell updates/sec
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14: /cgm2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
                                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-310-113-164
US-10-230-880-101
US-09-290-586-9
US-09-990-586-9
US-10-310-113-161
US-10-230-880-9
US-10-230-880-9
US-10-230-880-9
US-09-299-586-4
US-09-990-586-4
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                                                                                                                                                                                                                                                                                                                                                                                                                         747907 seqs, 201509753 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                            - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 YIDPYNGITIYDQNLKG 17
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Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                   Sequence:
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                                                                                                                                                                             Run on:
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No.
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Sequence 33, Appli Sequence 30, Appli Sequence 30, Appli Sequence 32, Appli Sequence 32, Appli Sequence 33, Appli Sequence 34, Appli Sequence 23, Appli

Sequence 90 Appl Sequence 7, Appli Sequence 7, Appli Sequence 65, Appl Sequence 12, Appl Sequence 12, Appl

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

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Gaps

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US-00-990-586-9
US-00-990-586-9
US-00-990-586-9
Sequence 9, Application US/0990586
Publication No. US20030109680A1
GENERAL INFORMATION:
APPLICANT: DIAO, JIN-AN
APPLICANT: WONG, HING C.
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION METHODS
TITLE OF INVENTION: OF USE THEREOF
FILE REFERENCE: 71758/46943-CIP2.
CURRENT APPLICATION NUMBER: US/09/990,586
CURRENT FILING DATE: 2001-11-21
PRIOR PELICATION NUMBER: 09/293,854
PRIOR FILING DATE: 1999-04-16
                                                                                                            Esperanza, Nieves
Lawrence, Luepeschen
TITLE OF INVENTION: ANTHEODIES FOR INHIBITING BLOOD
COAGULATION AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                               ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP STREET: 130 Water Street CITY: Boston STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM COMPACTURE
COMPUTER: IBM COMPACTURE
COMPAGE: FastSEQ Version 1.5
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/293,854
FILING DATE: 16-Apr-1999
CLASSIFICATION: CURNOWN>
PRIOR APPLICATION NUMBER: 08/814,806
FILING DATE: AURNOWN>
ATTORNY/AGENT INFORMATION:
NAME: COTIESS, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 46943
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 17 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 617-523-6440
TELEX: «Unknown»
INFORMATION FOR SEQ ID 00: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YIDPYNGITIYDQNLKG 17
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                                                         APPLICANT: Wong, Hing C.
                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
Patent No. US20020168357A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-
                                 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-293-854-9
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               APPLICANT: MOSQUERA, LUIS A.

TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
TITLE OF INVENTION: THROMBOSES
FILE REFERENCE: 58122 (1758)
CURRENT APPLICATION NUMBER: US/10/310,113
CURRENT APPLICATION NUMBER: 05/290,586
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-11-22
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 08/293,854
PRIOR FILING DATE: 1997-03-10
PRIOR APPLICATION NUMBER: 08/293,864
PRIOR FILING DATE: 1997-03-10
NUMBER OF SEQ ID NOS: 169
SOFTWARE: PALENTIN VEY: 2.1
SEQ ID NO 164
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Publication No. US2030190705A1

GENERAL INFORMATION:

APPLICANT: WONG, HING C.

APPLICANT: STINSON, JEFFREY L.

APPLICANT: STINSON, JEFFREY L.

APPLICANT: STINSON, JEFFREY L.

TILE OF INVENTION: WETHOO OF HUMANIZING INMUNE SYSTEM MOLECULES

FILE REFERENCE: 71758/58066

CURRENT APPLICATION NUMBER: 09/990, 880

CURRENT FILING DATE: 2001-12-23

PRIOR APPLICATION NUMBER: 09/990, 866

PRIOR PLILNG DATE: 2001-11-21

PRIOR APPLICATION NUMBER: 09/930, 854

PRIOR PLING DATE: 2001-10-29

PRIOR PLING DATE: 2001-10-29

PRIOR PLING DATE: 2001-10-29

PRIOR PLING DATE: 2001-10-29

PRIOR PLING DATE: 2001-10-29

PRIOR PLING DATE: 2001-10-29

PRIOR PLING DATE: 2001-10-29

PRIOR PLING DATE: 2001-10-29

PRIOR PLING DATE: 2001-10-29

PRIOR PLING DATE: 2001-10-29

PRIOR PLING DATE: 1099-04-16
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
STHER INFORMATION: humanized HC-08 CDR2 amino acid sequence
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100.0%; Score 95; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 17; Conservative 0; Mismatches 0; Indels
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100.0%; Score 95; DB 12;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 17; Conservative 0; Mismatches 0;
   NIEVES, ESPERANZA LILIANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 9, Application US/09293854
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ORGANISM: Artificial Sequence
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CORGANISM: Homo sapiens
US-10-230-880-101
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US-09-293-854-9
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Gaps
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APPLICANT: WONG, HING C.
APPLICANT: STINSON, JEFFREY L.
APPLICANT: STINSON, JEFFREY L.
APPLICANT: MOSQUEAR, LUIS A.
TILLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
FILE REFERENCE: 71758/58066
CURRENT APPLICATION NUMBER: US/10/230,880
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: 09/990,586
PRIOR PELING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 09/993,854
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PATCHTIN Ver. 2.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/10293417

Publication No. US20030082636A1

GENERAL INFORMATION:

APPLICANT: Wong, Hing C.
Jiao, Jin-an

Esperanza, Nieves

Lawrence, Luepechen

TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD

COAGULATION AND METHODS OF USE THEREOF
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CORRESPONDENCE ADDRESS:
ADDRESSE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                 Score 91, DB 12; Length 17; Pred. No. 2.5e-08; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 95.8%; Score 91; DB 12; Length 17; Best Local Similarity 94.1%; Pred. No. 2.5e-08; Matches 16; Conservative 0; Mismatches 1; Indels
PRIOR FILING DATE: 2001-10-29
PRIOR PILING DATE: 109/293,854
PRIOR PILING DATE: 1099-04-16
PRIOR APPLICATION NUMBER: 08/814,806
PRIOR PILING DATE: 1997-03-10
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 2.1
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/10230880 Publication No. US20030190705A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YIDPYNGITIYDQNLKG 17
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                                                                                                                                                                                                                                                                                                                                         95.8%;
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Best Local Similarity 94.1
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Murine sp
US-10-310-113-161
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; Sequence 161, Application US/10310113
; Publication No. US20030176664A1
; GENERAL INFORMATION:
APPLICANT: WONG, JIN-AN
; APPLICANT: WONG, HING C.
; APPLICANT: WONG, ESPERANZA LILIANA
APPLICANT: WOSQUERA, LUIS A.
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; CURRENT APPLICATION WUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR FILING DATE: 2001-11-71
                                                                                                                                                                                                                                                                      Gaps
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Sequence 9. Application US/10310113
Publication No. US20030176664A1
GENERAL INFORMATION:
APPLICANT: JIAO, JIN.AN
APPLICANT: WONG, HING C.
APPLICANT: WONG, HING C.
APPLICANT: MOSQUEA, LUIS A.
TITLE OF INVENTION: USE OF ANTI-TISSUE PACTOR ANTIBODIES FOR TREATING
TITLE OF INVENTION: THROMBOSES
FILE REPRESENCE: $812.7(1758)
CURRENT APPLICATION NUMBER: US/10/310,113
CURRENT FILING DATE: 2002-12-04
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95.8%; Score 91, DB 12, Length 17;
Best Local Similarity 94.1%; Pred. No. 2.5e-08;
Matches 16; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                              Score 91; DB 11; Length 17;
Pred. No. 2.5e-08;
                                                                                                                                                                                                                                                                   0; Mismatches
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PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/343,306
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 1999-04-16
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 08/814,806
PRIOR FILING DATE: 1997-03-10
NUMBER OF SEQ ID NOS: 169
SOFTWARE: PARCHIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/343,306
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                                                                                                                                                                                                                                                                                                                     1 YIDPYNGITIYDQNLKG 17
                                                                                                                                                                                                                 Query Match
Best Local Similarity 94.1%;
Matches 16; Conservative
        NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 17
                                                                                                            TYPE: PRT
, ORGANISM: Homo sapiens
US-09-990-586-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Murine sp
US-10-310-113-9
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Sequence 4, Application US/09990586

Sequence 4. Application US/0990586

Publication No. US20030109680A1

GENERAL INFORMATION:
APPLICANT: UNO, JIN-AN
APPLICANT: WONG, HING C.

TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
FILE REPERENCE: 71758/46943-CIPE
CURRENT APPLICATION NUMBER: US/09/990,586

CURRENT FILING DATE: 2001-11-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 94.1%; Pred. No. 2.2e-07;
Matches: 16; Conservative 0; Mismatches 1
                                                                                            APPLICATION NUMBER: 08/814,806
FILING DATE: «Unknown-
ATTORNEY/AGRNT INPORMATION:
NAME: Corless, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 46943
TELECOMMUNICATION INFORMATION:
TELEFAX: 617-523-3400
TELEFX: 617-523-3400
TELEFX: 617-523-3400
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TELEFX: 617-523-5410
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PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 117
FILING DATE: 16-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10310113
Publication No. US20030176664A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YIDPYNGITIYDQNLKG 17
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CRGANISM: Homo sapiens
US-09-990-586-4
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Sequence 4, Application US/09293854
Patent No. US20020168357A1
GENERAL INPORMATION:
APPLICANT WORN, Hing C.
Jiao, Jin-an
Beperanza, Nieves
Lawrence, Luepschen
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
COAGULATION AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
CITES SOSCHON
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

95.8%; Score 91, DB 15; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.5e-08;
Matches 16; Conservative 0; Mismatches 1; Indels
                                                                 COMPUTER REALACLE.

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OCMPUTER: IBM Compatible
OCMPUTER: IBM Compatible
OFERATING SYSTEM: DOS
SOFTWARE: FastEEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/293,417
FILING DATE: 12-No. US20030082636A1-2002
CLASSIPICATION NUMBER: US/09/293,854
FILING DATE: LO-ADP-1999
APPLICATION NUMBER: 08/814,806
FILING DATE: CUDKNOWN:
ATTORNEY/AGUT INFORMATION:
NAME: COrless, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 46943
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-5440
TELEPHONE: 617-523-5440
TELEPHONE: 617-523-5440
TELEPHONE: GIP-523-5440
TELERY: CUDKNOWN:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFFWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                      ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YIDPYNGITIYDQNLKG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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US-09-293-854-4
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GENERAL INFORMATION:
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                                                                  APPLICANT: NIEVEN, ENTERANGE, CHIS A.
TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
TITLE OF INVENTION: THROMEDES
TITLE OF INVENTION: THROMEDES
TITLE REFERENCE: $8122(1758)
CURRENT PILING DATE: 2002-12-04
CURRENT FILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 2001-10-29
PRIOR PLING DATE: 2001-10-29
PRIOR PLING DATE: 2001-10-29
PRIOR PLING DATE: 1999-04-16
PRIOR PLING DATE: 1999-04-16
PRIOR FILING DATE: 1999-04-16
PRIOR FILING DATE: 1999-04-16
PRIOR FILING DATE: 1997-03-10
NUMBER OF SEQ ID NOS: 169
SOUTHARE: ALCHING DATE: 201-10-29
SOUTHARE: ALCHING DATE: 1997-03-10
SOUTHARE: ALCHING DATE: 1997-03-10
SOUTHARE: ALCHING DATE: 1997-03-10
SOUTHARE: ALCHING DATE: 1997-03-10
SOUTHARE: ALCHING DATE: 1997-03-10
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| Bublication No. US20030190705A1
| GENERAL INFORMATION:
| APPLICANT: STINSON, USFREY L.
| APPLICANT: STINSON, USFREY L.
| APPLICANT: MOSQUERA, LUIS A.
| TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
| FILE REPERENCE: 71758/50066
| CURRENT FILING DATE: 2002-12-23
| PRIOR APPLICATION NUMBER: 05/990,586
| PRIOR APPLICATION NUMBER: 60/943,306
| PRIOR APPLICATION NUMBER: 60/143,306
| PRIOR PILING DATE: 2001-11-21
| PRIOR PILING DATE: 2001-10-29
| PRIOR PILING DATE: 1999-04-16
| NUMBER OF SEQ ID NOS: 174
| SEQ ID NOS: 174
| SEQ ID NOS: 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 91, DB 12; Length 117;
Pred. No. 2.2e-07;
0; Mismatches 1; Indels
   IAO, JIN-AN
WONG, HING C.
NIEVES, ESPERANZA LILIANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 4, Application US/10293417; Publication No. US20030082636A1
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Best Local Similarity 94.1%;
Matches 16; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Murine sp.
US-10-310-113-4
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US-10-293-417-4
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APPLICANT Won's High C.

Experience Lagraches

Lawrence Lagraches

Lawrence Largesches

TITLE OF INVENTION AND WITHOUS BLOOD

NUMBER OF EXUNDING COADMILITON AND WITHOUS OF USE THEREOF

COMPRESENT STATEMENTS AND ANTHOUSES OF USE THEREOF

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Search completed: January 13, 2004, 13:13:47 Job time : 2.71703 secs

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LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                RESULT 1
US-08-814-806-9
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Sequence 102, App
Sequence 27, App
Sequence 100, App
Sequence 100, App
Sequence 112, App
Sequence 7, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
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Sequence 11, App
Sequence 41, Appl
Sequence 41, Appl
Sequence 27, Appl
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Sequence 9, Appli
Sequence 4, Appli
                                                                                      January 13, 2004, 12:33:50; Search time 1.46987 Seconds (without alignments) 489.353 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-293-854-9
US-09-293-854-9
US-08-281-44
US-08-436-717-144
US-08-436-717-144
US-08-137-117D-102
US-08-137-117D-102
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US-08-137-117D-102
US-08-137-117D-102
US-08-137-117D-102
US-08-136-717-102
US-08-136-717-112
US-08-136-717-112
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US-08-136-717-112
US-08-136-717-112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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95
1 YIDPYNGITIYDQNLKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                               Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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                                                                                                                                                                                     Sequence:
                                                                                            Run on:
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Appl	Appl	Appl	Appl	App1	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	
48,	49,	48,	49,	48,	49,	50,	, 20,	50,	, 0 0 0	37,	37,	37,	37,	37,	58,	58,	28,	
Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Seguence	Sequence	Sequence	
985-4	US-09-026-985-49	US-09-121-952A-48	US-09-121-952A-49	US-09-234-340A-48	. US-09-234-340A-49		US-08-398-612A-50	-08-398-611A-	US-08-491-334A-50	US-09-027-449-37	US-08-804-444A-37	US-09-026-985-37	US-09-121-952A-37	US-09-234-340A-37	-398-613A-5	US-08-398-612A-58	US-08-398-611A-58	
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62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	62.1	
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## ALIGNMENTS

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Sequence 4, Application US/08814806
Patent No. 598665
GENERAL INFORMATION:
APPLICANT: Wong, Hing C.
APPLICANT: Jiao, Jin-an
APPLICANT: Esperanza, Nieves
APPLICANT: Lawrence, Luepschen
TITLE OF INVENTION: COAGULATION AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                       ADDRESSE: Dike, Bronstein, Roberts & Cushman, LLP STREET: 130 Water Street
CITY: Boston STATE: WA ZIATE: WA ZIP: USA ZIP: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 91; DB 2; 1
Pred. No. 8.9e-08;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09293854 Patent No. 655319 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COLLESS, Peter F
REGISTRATION NUMBER: 33,860
REFRENCE/DOCKET NUMBER: 4694
TELECHONE: 617-523-3400
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YIDPYNGITIYDQNLKG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wong, Hing C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: N-terminal ORIGINAL SOURCE: US-08-814-806-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
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                                                                                                                                                                                                                                                                                                                           APPLICANT: Wong, Hing C.
Jino, Jin-an
Esperanza, Nieves
Lawrence, Luupschen
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
COAGULATION AND METHODS OF USE THEREOF
                                                                                 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.8%; Score 91; DB 4; Length 17; 94.1%; Pred. No. 8.5e-09; tive 0; Mismatches 1; Indels
                                 Query Match 95.8%; Score 91; DB 2; Length 17; Best Local Similarity 94.1%; Pred. No. 8.5e-09; Matches 16; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02109

COMPUTER: ERADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: SASTEM: DOS
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION NUMBER: US/09/293,854
FILING DATE: 16-Apr-1999
CLASSIPICATION: cUnknown>
PRIOR APPLICATION NUMBER: 09/814,806
FILING DATE: cUnknown>
APPLICATION NUMBER: 09/814,806
FILING DATE: cUnknown>
ATTORNEY/AGBNT TRORMATION:
NAME: COTIESS, PETER F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 46943
TELEPRONE: 617-523-6440
TELEPRAN: 617-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
PRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-09-293-854-9
                                                                                                                                                                                                                                                                Sequence 9, Application US/09293854 Patent No. 6555319 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YIDPYNGITIYDQNLKG 17
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                                                                                                                       1 YIDPYNGITIYDQNLKG 17
                                                                                                                                                             1 YIDPYNGITIYDQNFKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 94.1;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston STATE: MA
                                                                                                                                                                                                                                              US-09-293-854-9
US-08-814-806-9
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Jiao, Jin-an
Esperanza, Nieves
Lawrence, Luepschen
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
COAGULATION AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 26
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Length 117;

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AFFLICATION NOMBER: US/08/12/11/10

FILING DATE: 20-DEC 1993
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HATCH C.
REFERENCE/DOCKET NUMBER: 53,258
REFERENCE/DOCKET NUMBER: 53,258
REFERENCE/DOCKET NUMBER: 53,258
TELLECOMMUNICATION INFORMATION:
TELLECOMMUNICATION INFORMATION:
TELLEPHONE: (202)672-5390
TELLEPHONE: 0203/672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNMER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
        CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/137,117D
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5-08-436-717-144
Sequence 144, Application US/08436717
Patent No. 5817790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YIDPFNGGTSYNOKFKG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 64.7%;
Matches 11; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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US-08-137-117D-144
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              COMMERCED DIRECTOR ADDRESS:
CONTRET: 130 Water Street
CITY: Boston
STREET: 130 Water Street
CITY: Boston
STRYE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FREESEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/293,854
FILING DATE: L-Apr-1999
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/814,806
FILING DATE: cUnknown>
ATTORNEY/AGENT INFORMATION:
NAME: COTIESS, PECET
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 33,860
TELEPROMICATION INFORMATION:
TELEPROMICATION INFORMATION:
TELEPROMICATION INFORMATION:
TELEPROMICATION INFORMATION:
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TELEPROMICATION INFORMATION:
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Patent No. 5795965

GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6.RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.8%; Score 91; DB 4; 3 94.1%; Pred. No. 8.9e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 117 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YIDPYNGITIYDQNLKG 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 94.1<sup>1</sup>
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: D.C.
COUNTRY: USA
ZIF: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d.
COMPUTER: IBM PC comp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-137-117D-144
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: STOCHIVA, MASSAYUKİ
APPLICANT: STOCHIVA, MASSAYUKİ
APPLICANT: STOCHIVA, MASSAYUKİ
APPLICANT: BENDIĞ, MAIY
APPLICANT: JONES, SLEVEN
APPLICANT: JONES, SLEVEN
APPLICANT: STORMATION: RESHAPED HUMAN ANTIBODY TO HUMAN
ITILE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Larcher
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRAT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
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Gaps

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APPLICANT: Bendig, Mary M. APPLICANT: Bendig, Mary M. APPLICANT: Leger, Olivier J. APPLICANT: Leger, Olivier J. APPLICANT: Saldanha, Jose APPLICANT: Saldanha, Jose APPLICANT: Saldanha, Jose APPLICANT: WORSE OF INVENTION: Humanized Antibodies Against Leukocyte TITLE OF INVENTION: Adhesion Molecule VLA-4 NUMBER OF ENCHORES: ASSESSED TOWNSENG AND SESS: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: COMPARED TOWNSENG AND STRATE: California CONTRY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.3%; Score 62; DB 5; Length 116; 64.7%; Pred. No. 0.0056;
                                                                                                                                                                                    Query Match
Best Local Similarity 64.7%; Pred. No. 0.0056;
Matches 11; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER TEADABLE FORM:

ZIP: 94105

COMFUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMFUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC-JUS95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 15-270-14
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: ATTORNEY/ENERGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US95-01219-41; Sequence 41, Application PC/TUS9501219; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-08-137-117D-27
; Sequence 27, Application US/08137117D
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                                                                                                                                                                                                                                                                                                                                 1 YIDPYNGITIYDQNLKG 17
                                                                                                                                                                                                                                                                                                                                                                                50 YIDPFNGGISYNQKFKG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 64.7<sup>3</sup>
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-41
                                    single
TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
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Fatent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Bendig, Mary M.
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Gones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 17;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 65.3%; Score 62; DB 2; I Best Local Similarity 64.7%; Pred. No. 0.00053; Matches 11; Conservative 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                               53466/126/AAOK
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                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION NUMBER: UP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 55,258
REFERENCE/DOCKET NUMBER: 53466/12
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
TELEPRAS.
                                                                                                                                                                                                                                                                                                                                                                                                            1 YIDPYNGITIYDQNLKG 17
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              24-APR-1992
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TOPOLOGY: linear
US-08-436-717-144
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              FILING DATE:
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US-08-561-521-41
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65.3%; Score 62; DB 1; Length 135;
Best Local Similarity 64.7%; Pred. No. 0.0067;
Matches 11; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 102, Application US/08137117D
; Sequence 102, Application US/08137117D
; Patent No. 5795956
; GENERAL INFORMATION:
APPLICANT: TSUGHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: SATO, Seven
APPLICANT: JONES, Steven
APPLICANT: JONES, Steven
APPLICANT: NUMBEN OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 3000 K Steven
CTTW.
                      ADDRESSENT ALLIAS ALLIAS ALLIAS ALLIAS SOUR STREET: 3000 K Street, N.W., Suite 500 CITY: Weahington STATE: D.C.
COUNTRY: USA
ZIP: D.C.
COMPUTER: D.C.
COMPUTER: FALDABLE FORM: WEBDIUM TYPE: FALDABLE FORM: MEBLIUM TYPE: FLORY MS-DOS SOUTHARR: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOUTHARR: BATCHING RAPELICATION DATA: APPLICATION NUMBER: US/08/137,117D FILING DATE: 20-DEC-1993
FILING DATE: 20-DEC-1993
FILING DATE: 20-DEC-1993
FILING DATE: 20-DEC-1993
FILING DATE: 20-DEC-1993
FILING DATE: 1992
FILING DATE: 19-FER-1992
FILING DATE: 19-FER-1992
FILING DATE: 19-FER-1992
FILING DATE: 19-FER-1992
FILING DATE: 21-FER-1992
ATPONEY/AGENT INFORMATION:
WANNEY MANDER: 19-19-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53466/126/AAOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFRENCE/DOCKET NUMBER: 5346(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 YIDPFNGGTSYNQKFKG 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d:
COMPUTER: IBM PC comp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-137-117D-100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 100. Application US/08137117D

Patent No. 5795965

GENERAL INFORMATION:

APPLICANT: SATO, Koh

APPLICANT: SATO, Koh

APPLICANT: SALO, Roh

APPLICANT: SALOANA, Mary

APPLICANT: SALOANA, Mary

APPLICANT: SALOANA, OSC

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR

NUMBER OF SEQUENCES: 158
Patent No. 5795965

GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: BENDIG, Mary
APPLICANT: JONEG, Steven
APPLICANT: JONEG, Steven
APPLICANT: JONEG, Steven
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
ITLE OF SEQUENCES: 158
CORRESPONDENCES: 158
CORRESPONDENCES: Lardner
ADDRESSEE: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                 CITY: N.C...
STATE: D.C.
COUNTRY: UGA
COUNTRY: UGA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPACEDS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: UG/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING APPLICATION DATA:
APPLICATION NUMBER: WP 4-32084
FILING DATE: 19-PEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HARCID C.
RETERRANCEDOCKET NUMBER: 53466/126/AAOK
TELEPHONE: (202)672-5390
TELEPHONE: C.202)672-5390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                    SEE: Foley & Lardner: 3000 K Street, N.W. Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YIDPYNGITIYDQNLKG 17
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 135 amino acids
amino acid
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Best Local Similarity 64.74
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-08-137-117D-100
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APPLICANT: SATO, Koh
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESEARED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
CORRESPONDENCE: 158
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: WEAL LOOP STATE: WEAL LOOP STATE: WEAL LOOP STATE: WEAL LOOP STATE: WEAL LOOP STATE: WEAL LOOP WEAL LOOP STATE: WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LOOP WEAL LO
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Pred. No. 0.0067;
                                                                   FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 39-95476
APPLICATION NUMBER: 39-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 33466/126/AAOK
TELEPHONE: (202)672-5300
TELEPHONE: (202)672-5300
TELEPACH: 135 anino acide
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 anino acide
TYPE: anino acide
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 27, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /AGENT INFOLL C. WEGNER, Harold C. Transfer: 25,258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 64.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-137-117D-112
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Patent No. 579565

GENERAL INFORMATION:

APPLICANT: SUCHIYA, Masayuki
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
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STATE: D.C.
COUNTRY: USA
COUNTRY: USA
ZIP: 20007-510
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRICK APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-AFR-1992
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 4-32084
FILING DATE: 19-FEB-1992
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 3-95476
FILING DATE: 25-AFR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNEY HORDER: 53,258
REFERENCE/DOCKET NUMBER: 53,466/126/AAOK
TELEPAX: (202)672-5399
TELEPAX: (202)672-5399
TELEFAX: (202)672-5399
TELEFAX: (302)672-5399
TELEFAX: (302)672-5399
TELEFAX: (302)672-5399
TELEFAX: 135 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: ATTORN: TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUNKESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 YIDPFNGGTSYNOKFKG 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 64.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-137-117D-102
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                                                                                                                                                                                                   Query Match
65.3%; Score 62; DB 2; Length 135;
Best Local Similarity 64.7%; Pred. No. 0.0067;
Matches 11; Conservative 2; Mismatches 4; Indels
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ZUNDYTRY: USA

ZUDY: 20007-5109

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: TSUCHIYA, Masayuki
APPLICANT: ARAO, Koh
APPLICANT: BRNDIG, Mary
APPLICANT: BONES, Steven
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, JOSE
TITLE OF INVENTION: INTELLEUKIN-6 RI
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: POLEY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 102, Application US/08436717
Patent No. 5817790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 YIDPFNGGTSYNOKFKG 85
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                     , MOLECULE TYPE: protein US-08-436-717-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
    amino acid
                                         TOPOLOGY: linear
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Pred. No. 0.0067;
2; Mismatches 4; Indels
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Patent No. 5817790

GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: BENDIG, Mary
APPLICANT: BENDIG, Mary
APPLICANT: SEALDANTA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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ZIP: 2000-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/436,717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:

RIGHS APPLICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WP PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
RACHISTRANICN NUMBER: 25-258
RACHISTRANICN NUMBER: 25-258
RACHISTRANICN NUMBER: 25-258
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REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: 90.17
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELEDECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
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: 3000 K Street, N.W., Suite 500
Washington
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INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
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INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 64.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                   135 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-436-717-27
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US-08-436-717-100
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Search completed: January 13, 2004, 12:46:36 Job time: 1.46987 secs